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OM protein - protein search, using sw model
Run on: October 9, 2002, 19:12:30 ; Search time 12.1071 Seconds
(without alignments)
1036.689 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 113
Sequence: 1 EIVLTOSPLSLPVTGEPAS.....MQLQSFRTGPGTKVDIKR 113

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : A_Geneseq_032802.*
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3: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
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20: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					Description	
Result No.	Score	Query Match	Length	ID		
1	113	100.0	113	22	AAE12705	Human PH1 Fab anti
2	113	100.0	220	22	AAE12714	Human recombinant
3	113	100.0	381	22	AAE12707	Human b1vPH1-IL-2
4	32	28.3	222	22	AAU04972	Synthetic antibody
5	32	28.3	222	22	AAU04976	Synthetic antibody
6	31	27.4	100	16	AAU04976	VK005 VK region
7	31	27.4	100	22	AAE12711	Antibody variable
8	31	27.4	111	21	AAV95225	Anti-platelet glyco
9	31	27.4	112	17	AAV95218	Human IgM GM607 va
10	31	27.4	113	21	AAV95220	Anti-platelet glyco
11	31	27.4	113	21	AAV95221	Anti-platelet glyco

12	31	27.4	114	18	AAW27544	Human Ab light cha
13	31	27.4	114	21	AAV95186	Anti-platelet glyco
14	31	27.4	131	21	AAV95226	Anti-platelet glyco
15	31	27.4	139	22	AAV99117	Human protein seq
16	31	27.4	157	22	AAW77307	Human bone marrow
17	31	27.4	248	22	AAV65590	Anti-hEDRF antibod
18	31	27.4	281	18	AAW27560	Consensus single c
19	30	26.5	239	21	AAV82613	Human PTHrp monocl
20	30	26.5	239	21	AAV82615	Human PTHrp monocl
21	29	25.7	112	22	AAV93587	Human anti-Rh(D) c
22	28	24.8	239	21	AAV82616	Human PTHrp monocl
23	27	23.9	109	20	AAV39809	TRI 6 antibody lig
24	27	23.9	112	19	AAV53586	Light chain of a h
25	27	23.9	148	20	AAV34309	IgM antibody CEM 1
26	27	23.9	239	21	AAV82612	Human PTHrp monocl
27	27	23.9	239	21	AAV82614	Human PTHrp monocl
28	27	23.9	239	21	AAV82617	Human PTHrp monocl
29	26	23.0	100	16	AAV72067	OF7K.7 VK-2 L cha
30	26	23.0	100	22	AAE06968	Mouse germline kap
31	26	23.0	108	14	AAV85894	Human lambda light
32	26	23.0	108	19	AAV58494	Human kappa light
33	25	22.1	112	19	AAV54015	Human Anti-CD4 ant
34	25	22.1	116	19	AAV76126	Human ICR-8.1 V-K
35	25	22.1	116	19	AAV71256	Humanised murine a
36	25	22.1	116	20	AAW81450	Humanised antibody
37	25	22.1	116	21	AAV13046	Protein sequence o
38	25	22.1	116	21	AAV82445	Humanised ICR-8.1
39	25	22.1	116	21	AAV50753	Humanised murine a
40	25	22.1	138	19	AAV53812	Light chain of a h
41	25	22.1	222	22	AAU04974	Synthetic antibody
42	24	21.2	112	14	AAV32239	Humanised MAB high
43	24	21.2	112	18	AAV27145	Mature light chain
44	24	21.2	112	21	AAV87571	Humanised ABL 364
45	24	21.2	143	20	AAV34313	IgM antibody CEM 1

ALIGNMENTS

RESULT 1
AAE12705
ID AAE12705 standard; Protein; 113 AA.
XX AC AAE12705;
XX AC AAE12705;
XX 04-JAN-2002 (first entry)
XX Human PH1 Fab antibody variable light chain region (VL).
XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VL;
XX variable light chain region; cancer; breast; ovary; lung; bladder;
XX Cytostatic; therapy; PH1 antibody.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Key 24..39
FT Region /label= CDR1
FT /note= "Complementarity determining region 1"
FT Region 55..61
FT /label= CDR2
FT /note= "Complementarity determining region 2"
FT Region 94..102
FT /label= CDR3
FT /note= "Complementarity determining region 3"
XX WO200175110-A2.
XX 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US10589.
XX 30-MAR-2000; 2000US-0538913.
PR

XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 PI WPI: 2001-626437/72.
 DR N-PSDB; AAD20730.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1
 XX Claim 3; Page 93; 126pp; English.
 PS The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is anti-MUC1 human PH1 Fab
 CC antibody VL region.
 XX SQ Sequence 113 AA;
 Query Match 100.0%; Score 113; DB 22; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.8e-102;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIVLTQSPVLPVTGEPASISCRSSQSLHNSGYTLQWYLDYKQPGQSPQLLIYSGSHRA 60
 DB 1 EIVLTQSPVLPVTGEPASISCRSSQSLHNSGYTLQWYLDYKQPGQSPQLLIYSGSHRA 60
 QY 61 SGVPRFSGSVSGTDFTLIRSRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKR 113
 DB 61 SGVPRFSGSVSGTDFTLIRSRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKR 113
 RESULT 2
 AAE12714
 ID AAE12714 standard; Protein: 220 AA.
 AC AAE12714;
 XX 04-JAN-2002 (first entry)
 DT Human recombinant immunoglobulin (Ig) light chain region.
 XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
 KW light chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy; immunoglobulin; Ig.
 XX Homo sapiens.
 OS WO200175110-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US10589.
 PF 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 PI WPI: 2001-626437/72.
 DR N-PSDB; AAD20732.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1
 XX Claim 3; Page 93; 126pp; English.
 PS The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is anti-MUC1 human PH1 Fab
 CC antibody VL region.
 XX SQ Sequence 113 AA;
 Query Match 100.0%; Score 113; DB 22; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.8e-102;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIVLTQSPVLPVTGEPASISCRSSQSLHNSGYTLQWYLDYKQPGQSPQLLIYSGSHRA 60
 DB 1 EIVLTQSPVLPVTGEPASISCRSSQSLHNSGYTLQWYLDYKQPGQSPQLLIYSGSHRA 60
 QY 61 SGVPRFSGSVSGTDFTLIRSRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKR 113
 DB 61 SGVPRFSGSVSGTDFTLIRSRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKR 113

PI Hoogenboom HRJM, Henderikx MPG;
 XX WPI: 2001-626437/72.
 DR N-PSDB; AAD20744.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1
 XX Claim 12; Page 103; 126pp; English.
 PS The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is human recombinant immunoglobulin
 CC (Ig) light chain region (variable VL and CL constant kappa light chain).
 XX SQ Sequence 220 AA;
 Query Match 100.0%; Score 113; DB 22; Length 220;
 Best Local Similarity 100.0%; Pred. No. 3.2e-102;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIVLTQSPVLPVTGEPASISCRSSQSLHNSGYTLQWYLDYKQPGQSPQLLIYSGSHRA 60
 DB 1 EIVLTQSPVLPVTGEPASISCRSSQSLHNSGYTLQWYLDYKQPGQSPQLLIYSGSHRA 60
 QY 61 SGVPRFSGSVSGTDFTLIRSRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKR 113
 DB 61 SGVPRFSGSVSGTDFTLIRSRVEAEADVGYVYCMQGLQSPFTFGPGTKVDIKR 113
 RESULT 3
 AAE12707
 ID AAE12707 standard; Protein: 381 AA.
 AC AAE12707;
 XX 04-JAN-2002 (first entry)
 DT Human b1vPH1-IL-2 immunocytokine protein.
 XX Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
 KW breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
 XX Homo sapiens.
 OS WO200175110-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-US10589.
 PF 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 PI WPI: 2001-626437/72.
 DR N-PSDB; AAD20732.

DT 24-OCT-2001 (first entry)
 XX Synthetic antibody scFv UBS-54, mutant B43.
 DE Human; Antibody; scFv UBS-54; VH1; VK2; phage display; B43;
 KW tumour; tissue penetration; complement activation; mutant; mutein.
 XX Homo sapiens.
 OS Synthetic.
 XX Key
 FH Region
 FT 1..25
 FT /label= FR1
 FT 26..32
 FT /label= CDR1
 FT /note= "Complementarity determining region"
 FT 33..51
 FT /label= FR2
 FT 52..57
 FT /label= CDR2
 FT /note= "Complementarity determining region"
 FT 58..98
 FT /label= FR3
 FT 99..104
 FT /label= CDR3
 FT /note= "Complementarity determining region"
 FT 105..112
 FT /label= FR4
 FT 113..135
 FT /label= FR1
 FT 136..151
 FT /label= CDR1
 FT /note= "Complementarity determining region"
 FT 152..166
 FT /label= FR1
 FT 167..173
 FT /label= CDR1
 FT /note= "Complementarity determining region"
 FT 174..205
 FT /label= FR4
 FT 206..214
 FT /label= CDR1
 FT /note= "Complementarity determining region"
 FT 215..222
 FT /label= FR1
 XX WO200148485-A2.
 XX
 XX 05-JUL-2001.
 XX
 XX 21-DEC-2000; 2000WO-NL00941.
 XX
 XX 27-DEC-1999; 99EP-0204561.
 XX
 XX (CRUC-) CRUCELL HOLLAND BV.
 XX Logtenberg T;
 XX WPI; 2001-441741/47.
 XX
 XX Use of a native group for selecting evolved binding members with
 FT enhanced group binding, complement activation and tissue penetration
 FT property from library of mutants of a protein capable of binding to the
 FT group -
 XX
 XX Example; Page - ; 42pp; English.
 XX
 CC The sequence represents the synthetic antibody scFv UBS-54, mutant B43,
 CC where VK2 forms the light chain (VH1 forming the heavy chain). The
 CC antibody molecule is used to demonstrate the method of the invention
 CC which involves using a cell displaying a group (e.g. a phage displayed
 CC antibody) to isolate an evolved (or mutated) molecule which has a
 CC higher affinity/enhanced property for the group. The method is useful for

CC obtaining an evolved group binding molecule with enhanced group binding,
 CC tissue penetration or complement activation property. The selection
 CC procedure is useful for selecting high affinity mutant antibody fragments
 CC which are useful for targeted tumour cell lysis. Mutants of proteinaceous
 CC molecule are physically linked to a vehicle comprising nucleic acid
 CC encoding the mutant molecule and this has the advantage that when the
 CC member is recovered from the cells and/or its functional equivalent, the
 CC nucleic acid encoding the proteinaceous molecule can also be
 CC simultaneously recovered.
 CC Note: The present sequence is not displayed in the specification
 CC but is derived from the scFv UBS-54 sequence given in figure 2.
 XX
 SQ Sequence 222 AA;
 Query Match 28.3%; Score 32; DB 22; Length 222;
 Best Local Similarity 100.0%; Pred. No. 3.3e-23;
 Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 LTQSPFLSLPVTGPSPASISCRSSQSLLHSNGY 35
 DB 116 LTQSPFLSLPVTGPSPASISCRSSQSLLHSNGY 147
 RESULT 6
 AAR72066
 ID AAR72066 standard; Protein; 100 AA.
 XX
 AC AAR72066;
 DT 26-SEP-1995 (first entry)
 XX
 DE VK005 VK region.
 XX
 KW Graves ophthalmopathy associated immunoglobulin protein;
 KW orbital antigen; monoclonal antibody; light chain; L chain;
 KW variable region; autoimmunity.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Region
 FT 23..38
 FT /label= CDR1
 FT 54..60
 FT /label= CDR2
 FT 93..100
 FT /label= CDR3
 XX
 XX WO9508336-A.
 XX
 XX 30-MAR-1995.
 XX
 XX 22-SEP-1994; 94WO-US10756.
 XX
 XX 22-SEP-1993; 93US-0124469.
 XX
 XX (NICH-) NICHOLS INST DIAGNOSTICS.
 XX
 XX McLaughlan SM, Rapoport B;
 XX
 XX WPI; 1995-139383/18.
 XX
 XX N-PSDB; AAQ89325.
 XX
 XX Graves' ophthalmopathy-associated monoclonal antibody - produced
 FT by molecular cloning of immunoglobulin genes by PCR
 XX
 XX Disclosure; Page 67; 94pp; English.
 XX
 CC L- and H-chain DNA was amplified by PCR from Graves' orbital
 CC tissue and clones encoding autoimmune-associated immunoglobulin
 CC fragments were obtained. 14/15 clones of L chain (kappa) regions
 CC showed homology to the putative VK germline gene KL012 (given in
 CC AAQ89317) and the remaining clone, OF7K.7 (AAQ89326), to the VK005
 CC gene.

XX SQ Sequence 100 AA; Query Match 27.4%; Score 31; DB 16; Length 100; Best Local Similarity 100.0%; Pred. No. 1.6e-22; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPSPASISCRSSQSLHNSGY 35
 DB 5 TQSPSLPVTGPSPASISCRSSQSLHNSGY 35

RESULT 7
 AAEL1711
 ID AAEL1711 standard; peptide; 100 AA.
 AC AAEL1711;
 XX 04-JAN-2002 (first entry)
 XX Antibody variable light chain region (VL) from DP47 germ line.
 XX Tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VL;
 KW variable light chain region; cancer; breast; ovary; lung; bladder;
 KW cytostatic; therapy.
 XX Unidentified.
 OS WO200175110-A2.
 XX 11-OCT-2001.
 XX 30-MAR-2001; 2001WO-US10589.
 XX 30-MAR-2000; 2000US-0538913.
 XX (DYAX-) DYAX CORP.
 XX Hoogenboom HRJM, Henderikx MPG;
 PI WPI; 2001-626437/72.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Example 1; Page 35; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1
 CC (MUC-1)-specific binding member comprising an antigen binding domain
 CC region having an antibody variable light (VL) or heavy (VH) region,
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 CC The binding of MUC1-specific binding member to MUC1 is detected by a
 CC detection method selected from enzyme-linked immunosorbent assay,
 CC magnetic resonance imaging, scintillation counting, and X-ray film.
 CC MUC1-specific binding member is useful for treating cancer, preferably
 CC adenocarcinoma, in an individual, where the cancer is present in tissue
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 CC binding member is useful for diagnosing and imaging MUC1-expressing
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 CC containing molecules, and for therapeutically or prophylactically
 CC treating cancer. The present sequence is antibody variable light chain
 CC region (VL) from DP47 germ line.

XX SQ Sequence 100 AA; Query Match 27.4%; Score 31; DB 22; Length 100; Best Local Similarity 100.0%; Pred. No. 1.6e-22; Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPSPASISCRSSQSLHNSGY 35

Db 5 TQSPSLPVTGPSPASISCRSSQSLHNSGY 35

RESULT 8
 AAY95225
 ID AAY95225 standard; Protein; 111 AA.
 XX AAY95225;
 AC AAY95225;
 XX 29-AUG-2000 (first entry)
 XX Anti-platelet glycoprotein Ib human HIB-5 VL.
 XX Variable light chain; single chain antibody; scFv; human; HIB-5;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 XX 1..23 /note= "framework region 1"
 FT Region
 XX 24..39 /note= "complementarity determining region 1"
 FT Region
 XX 40..54 /note= "framework region 2"
 FT Region
 XX 55..61 /note= "complementarity determining region 2"
 FT Region
 XX 62..93 /note= "framework region 3"
 FT Region
 XX 94..99 /note= "complementarity determining region 3"
 FT Region
 XX 100..111 /note= "framework region 4"
 FT Region
 XX WO200026667-A1.
 XX 11-MAY-2000.
 XX 29-OCT-1999; 99WO-US25495.
 XX 30-OCT-1998; 98US-0106275.
 XX (MILL) MILLER J L.
 XX Miller JL;
 XX WPI; 2000-365744/31.
 XX Isolated nucleic acid molecule encoding anti-human platelet
 PT glycoprotein Ib alpha molecule useful for producing antibodies which
 PT inhibit platelet aggregation -
 XX Claim 21; Fig 8; 89pp; English.

XX The present sequence is that of the light chain variable region
 CC (VL) of human single chain antibody (scFv) HIB-5, which is directed
 CC against platelet glycoprotein Ib (GPiB). The HIB series of scFv
 CC was isolated from a human synthetic VH and VL scFv library by 3
 CC rounds of phagemid selection against transfected CHO cells
 CC expressing the GPiB alpha component of the GPiB/IX/V complex
 CC on their surface, followed by a 4th round of selection against
 CC washed human platelets, and 2 final rounds in which attempts were
 CC made to displace scFv from washed platelets by flooding with
 CC murine monoclonal antibody or mimotope peptide (see AAY95229).
 CC Whether displayed as surface proteins on a phagemid or secreted
 CC as free scFv by Escherichia coli, the HIB scFv clones are capable
 CC of inhibiting von Willebrand factor-dependent aggregation of
 CC platelets. The scFv are composed of native human protein sequences
 CC and are therefore attractive potential reagents for therapeutic
 CC purposes. They provide a new class of antithrombotic agents,
 CC useful for the prevention of platelet-dependent thrombi in

CC diseased arteries, bypass grafts, dialysis etc., and can also be
 CC used as diagnostic reagents. Methods of inhibiting aggregation
 CC of platelets, of binding human platelet GPIb alpha and of selecting
 CC a VH or VL region of an antibody that inhibits platelet aggregation
 CC are claimed.
 CC Note: The present sequence is not shown in the specification but is
 CC derived from the H1B-5 VH sequence given in Fig 8 (see AAY95220).
 XX
 SQ Sequence 111 AA;

Query Match 27.4%; Score 31; DB 21; Length 111;
 Best Local Similarity 100.0%; Pred. No. 1.7e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TQSPSLPVTGPGEPAISCRSSQSLHSHNGY 35
 |||||
 Db 5 TQSPSLPVTGPGEPAISCRSSQSLHSHNGY 35

RESULT 9
 AAR95218
 ID AAR95218 standard; protein; 112 AA.
 XX
 AC AAR95218;

DT 16-DEC-1996 (first entry)
 XX
 DE Human IgM GM607 variable light chain.

XX Antibody: fusion protein; single chain; inhibition; tumour;
 KW diagnosis; detection; imaging; immunotoxin; targeting; assay;
 KW immunoassay; Lewis(Y) carbohydrate antigen.
 XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 24..39
 FT /label= CDR 1.
 FT Domain 55..61
 FT /label= CDR 2.
 FT Domain 89..97
 FT /label= CDR 3.

XX W09613594-AL.
 XX
 XX 09-MAY-1996.
 XX
 XX 26-OCT-1995; 95WO-US13811.
 XX
 XX 28-OCT-1994; 94US-0331398.
 XX
 XX 28-OCT-1994; 94US-0331396.
 XX
 XX 28-OCT-1994; 94US-0331397.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Benhar I, Brinkmann U, Fitzgerald D, Jung S, Lee B;
 PI Padlan EA, Pai L, Pastan I, Willingham M;

XX WPI: 1996-251462/25.

XX Single chain fusion proteins and antibodies - useful to diagnose and
 PT treat cancer, specifically bind Lewis(Y) related carbohydrate
 PT antigen

XX Example 13; Figure 11B; 116pp; English.

XX A novel recombinant DNA molecule which encodes a single chain fusion
 CC protein or antibody comprising the Fv region of both the light and
 CC heavy chains of an antibody (Ab) fused together, and an effector
 CC molecule, where the fusion protein or Ab has the binding specificity
 CC of monoclonal Ab (MAb) B1, B3 or B5, can be used for the production
 CC -of such fusion proteins or antibodies. The fusion proteins can be
 CC used in compositions as an immunotoxin to inhibit tumour cell growth.

CC The single chain antibody can be used to detect the presence or
 CC absence of cells bearing a Lewis(Y) carbohydrate antigen in a
 CC patient. The antibodies are also useful as multiple targeting
 CC moieties, providing at least 2 kinds of biological activity. They
 CC can also be used in diagnostic assays and for the imaging of tumours
 CC when attached to a radiolabel and for the pathological diagnosis of
 CC tumours. Humanised antibodies are less immunogenic than the mouse
 CC MAb B1, B3 and B5, making them more suitable for long term
 CC treatment.

XX
 SQ Sequence 112 AA;

Query Match 27.4%; Score 31; DB 17; Length 112;
 Best Local Similarity 100.0%; Pred. No. 1.7e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TQSPSLPVTGPGEPAISCRSSQSLHSHNGY 35
 |||||
 Db 5 TQSPSLPVTGPGEPAISCRSSQSLHSHNGY 35

RESULT 10
 AAY95220
 ID AAY95220 standard; protein; 113 AA.
 XX
 AC AAY95220;

XX 29-AUG-2000 (first entry)

DE Anti-platelet glycoprotein Ib human H1B-5 VL.

XX Variable light chain; single chain antibody; scFv; human; H1B-5;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic.

XX Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Region 1..23
 FT /note= "framework region 1"
 FT Region 24..39
 FT /note= "complementarity determining region 1"
 FT Region 40..54
 FT /note= "framework region 2"
 FT Region 55..61
 FT /note= "complementarity determining region 2"
 FT Region 62..93
 FT /note= "framework region 3"
 FT Region 94..101
 FT /note= "complementarity determining region 3"
 FT Region 102..113
 FT /note= "framework region 4"

XX W0200026667-AL.

XX 11-MAY-2000.

XX 29-OCT-1999; 99WO-US25495.

XX 30-OCT-1998; 98US-0106275.

XX (MILL) MILLER J L.

XX Miller JL;

XX WPI: 2000-365744/31.

XX Isolated nucleic acid molecule encoding anti-human platelet
 PT glycoprotein Ib alpha molecule useful for producing antibodies which
 PT inhibit platelet aggregation -
 XX Claim 18; Fig 8; 89pp; English.

CC The present sequence is that of the light chain variable region
 CC (VL) of human single chain antibody (scFv) H1b-5, which is directed
 CC against platelet glycoprotein Ib (GPIb). The H1b series of scFv
 CC was isolated from a human synthetic VH and VL scFv library by 3
 CC rounds of phagemid selection against transfected CHO cells
 CC expressing the GPIb alpha component of the GPIb/IX/V complex
 CC on their surface, followed by a 4th round of selection against
 CC washed human platelets, and 2 final rounds in which attempts were
 CC made to displace scFv from washed platelets by flooding with
 CC murine monoclonal antibody or mimotope peptide (see AA95229).
 CC Whether displayed as surface proteins on a phagemid or secreted
 CC as free scFv by *Escherichia coli*, the H1b scFv clones are capable
 CC of inhibiting von Willebrand factor-dependent aggregation of
 CC platelets. The scFv are composed of native human protein sequences
 CC and are therefore attractive potential reagents for therapeutic
 CC purposes. They provide a new class of antithrombotic agents,
 CC useful for the prevention of platelet-dependent thrombi in
 CC diseased arteries, bypass grafts, dialysis etc., and can also be
 CC used as diagnostic reagents. Methods of inhibiting aggregation
 CC of platelets, of binding human platelet GPIb alpha and of selecting
 CC a VH or VL region of an antibody that inhibits platelet aggregation
 CC are claimed.

XX
 SQ Sequence 113 AA;

Query Match 27.4%; Score 31; DB 21; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.7e-22; Mismatches 0; Indels 0; Gaps 0;
 Matches 31; Conservative 0;

QY 5 TQSPILSLPVTGPGEASISCRSSQSLHSHNGY 35
 DB 5 TQSPILSLPVTGPGEASISCRSSQSLHSHNGY 35
 |||||

RESULT 11
 AA95221
 ID AA95221 standard; Protein; 113 AA.
 XX
 AC AA95221;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Anti-platelet glycoprotein Ib human H1b-5 VL.
 XX
 KW Variable light chain; single chain antibody; scFv; human; H1b-5;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 1..23 /note= "framework region 1"
 FT Region 24..39 /note= "framework region 1"
 FT Region 40..54 /note= "framework region 2"
 FT Region 55..61 /note= "framework region 2"
 FT Region 62..93 /note= "framework region 3"
 FT Region 94..101 /note= "framework region 3"
 FT Region 102..113 /note= "framework region 3"
 FT Region /note= "framework region 4"
 XX
 PN WO200026667-A1.
 XX
 XX 11-MAY-2000.
 XX
 XX 29-OCT-1999; 99WO-US25495.
 XX
 XX 30-OCT-1998; 98US-0106275.
 PR

XX (MILLER) MILLER J L.
 XX
 XX Miller JL;
 XX
 XX WPI; 2000-365744/31.
 XX
 XX Isolated nucleic acid molecule encoding anti-human platelet
 XX glycoprotein Ib alpha molecule useful for producing antibodies which
 XX inhibit platelet aggregation -
 XX
 XX Claim 18; Fig 8; 89pp; English.
 XX
 XX The present sequence is that of the light chain variable region
 XX (VL) of human single chain antibody (scFv) H1b-5, which is directed
 XX against platelet glycoprotein Ib (GPIb). The H1b series of scFv
 XX was isolated from a human synthetic VH and VL scFv library by 3
 XX rounds of phagemid selection against transfected CHO cells
 XX expressing the GPIb alpha component of the GPIb/IX/V complex
 XX on their surface, followed by a 4th round of selection against
 XX washed human platelets, and 2 final rounds in which attempts were
 XX made to displace scFv from washed platelets by flooding with
 XX murine monoclonal antibody or mimotope peptide (see AA95229).
 XX Whether displayed as surface proteins on a phagemid or secreted
 XX as free scFv by *Escherichia coli*, the H1b scFv clones are capable
 XX of inhibiting von Willebrand factor-dependent aggregation of
 XX platelets. The scFv are composed of native human protein sequences
 XX and are therefore attractive potential reagents for therapeutic
 XX purposes. They provide a new class of antithrombotic agents,
 XX useful for the prevention of platelet-dependent thrombi in
 XX diseased arteries, bypass grafts, dialysis etc., and can also be
 XX used as diagnostic reagents. Methods of inhibiting aggregation
 XX of platelets, of binding human platelet GPIb alpha and of selecting
 XX a VH or VL region of an antibody that inhibits platelet aggregation
 XX are claimed.
 XX Note: The present sequence is not shown in the specification but is
 XX derived from the H1b-5 VH sequence given in Fig 8 (see AA95220).
 XX
 XX Sequence 113 AA;

Query Match 27.4%; Score 31; DB 21; Length 113;
 Best Local Similarity 100.0%; Pred. No. 1.7e-22; Mismatches 0; Indels 0; Gaps 0;
 Matches 31; Conservative 0;

QY 5 TQSPILSLPVTGPGEASISCRSSQSLHSHNGY 35
 DB 5 TQSPILSLPVTGPGEASISCRSSQSLHSHNGY 35
 |||||

RESULT 12
 AA27544
 ID AA27544 standard; Protein; 114 AA.
 XX
 AC AA27544;
 XX
 DT 22-JAN-1998 (first entry)
 XX
 DE Human Ab light chain variable region V-kappa-2 consensus.
 XX
 KW Human; antibody; preparation; library; V-kappa-2; variable region;
 KW light chain; consensus.
 XX
 OS Homo sapiens.
 XX
 PN WO9708320-A1.
 XX
 XX 06-MAR-1997.
 XX
 XX 19-AUG-1996; 96WO-EP03647.
 XX
 XX 18-AUG-1995; 95EP-0113021.
 XX
 XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
 PA

```

XX  Ge L, Ilag V, Knappik A, Moroney S, Pack P, Plueckthun A;
XX  WPI; 1997-179277/16.
XX  N-PSDB; AAT87942.
XX  Preparation of human derived antibody gene library - using synthetic
XX  consensus sequences, and signal consensus antibody gene as universal
XX  framework for highly diverse antibody libraries
XX  Example 1; Fig 3B; 436pp; English.
XX  The present sequence is the human antibody light chain
XX  variable region synthetic kappa sequence V-kappa-2, used in the
XX  preparation of a human derived antibody gene library.
XX  Sequence 114 AA;
SQ  Query Match 27.4%; Score 31; DB 18; Length 114;
    Best Local Similarity 100.0%; Pred. No. 1.8e-22;
    Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy  5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35
    |||||
Db  5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35
    |||||
RESULT 13
AAAY95186
ID  AAY95186 standard; Protein; 114 AA.
XX  AAY95186;
XX  29-AUG-2000 (first entry)
XX  Anti-platelet glycoprotein Ib human Hib-5 VL.
XX  Variable light chain; single chain antibody; scFv; human; Hib-5;
XX  glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
XX  antithrombotic; thrombus; therapy; diagnostic.
XX  Homo sapiens.
XX  Key Location/Qualifiers
XX  Region 1..23 /note= "framework region 1"
XX  Region 24..39 /note= "complementarity determining region 1"
XX  Region 40..54 /note= "framework region 2"
XX  Region 55..61 /note= "complementarity determining region 2"
XX  Region 62..93 /note= "framework region 3"
XX  Region 94..101 /note= "complementarity determining region 3"
XX  Region 102..114 /note= "framework region 4"
XX  WO200026667-A1.
XX  11-MAY-2000.
XX  29-OCT-1999; 99WO-US25495.
XX  30-OCT-1998; 98US-0106275.
XX  (MILLER) MILLER J L.
XX  Miller JL;
XX  WPI; 2000-365744/31.
XX  N-PSDB; AAA27664.

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XX  Isolated nucleic acid molecule encoding anti-human platelet
XX  glycoprotein Ib alpha molecule useful for producing antibodies which
XX  inhibit platelet aggregation -
XX  Claim 11; Page 77; 89pp; English.
XX  The present sequence is that of the light chain variable region
XX  (VL) of human single chain antibody (scFv) Hib-5, which is directed
XX  against platelet glycoprotein Ib (GP1b). The Hib series of scFv
XX  was isolated from a human synthetic VH and VL scFv library by 3
XX  rounds of phagemid selection against transfected CHO cells
XX  expressing the GP1b alpha component of the GP1b/IX/V complex
XX  on their surface, followed by a 4th round of selection against
XX  washed human platelets, and 2 final rounds in which attempts were
XX  made to displace scFv from washed platelets by flooding with
XX  murine monoclonal antibody or mimotope peptide (see AAY95229).
XX  Whether displayed as surface proteins on a phagemid or secreted
XX  as free scFv by Escherichia coli, the Hib scFv clones are capable
XX  of inhibiting von Willebrand factor-dependent aggregation of
XX  platelets. The scFv are composed of native human protein sequences
XX  and are therefore attractive potential reagents for therapeutic
XX  purposes. They provide a new class of antithrombotic agents,
XX  useful for the prevention of platelet-dependent thrombi in
XX  diseased arteries, bypass grafts, dialysis etc., and can also be
XX  used as diagnostic reagents. Methods of inhibiting aggregation
XX  of platelets, of binding human platelet GP1b alpha and of selecting
XX  a VH or VL region of an antibody that inhibits platelet aggregation
XX  are claimed.
XX  Sequence 114 AA;
SQ  Query Match 27.4%; Score 31; DB 21; Length 114;
    Best Local Similarity 100.0%; Pred. No. 1.8e-22;
    Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy  5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35
    |||||
Db  5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35
    |||||
RESULT 14
AAAY95226
ID  AAY95226 standard; Protein; 131 AA.
XX  AAY95226;
XX  29-AUG-2000 (first entry)
XX  Anti-platelet glycoprotein Ib human Hib-5 VL region and linker.
XX  Variable light chain; single chain antibody; scFv; human; Hib-5;
XX  glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
XX  antithrombotic; thrombus; therapy; diagnostic.
XX  Chimeric - Synthetic.
XX  Chimeric - Homo sapiens.
XX  Key Location/Qualifiers
XX  Peptide 1..17 /note= "vector-derived linker"
XX  Region 18..131 /note= "light chain variable region"
XX  Region 18..40 /note= "framework region 1"
XX  Region 41..56 /note= "complementarity determining region 1"
XX  Region 57..71 /note= "framework region 2"
XX  Region 72..78 /note= "complementarity determining region 2"
XX  Region 79..110 /note= "framework region 3"

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FT Region 111..119
FT /note="complementarity determining region 3"
FT Region 120..131
FT /note="framework region 4"
XX WO200026667-A1.
XX 11-MAY-2000.
XX 29-OCT-1999; 99WO-US25495.
XX 30-OCT-1998; 98US-0106275.
XX (MILLER) MILLER J L.
XX Miller JI;
XX WPI; 2000-365744/31.
XX Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which
PT inhibit platelet aggregation -
XX Disclosure; Fig 8; 89pp; English.
XX The present sequence is that of the light chain variable region
CC (VL) plus linker peptide of human single chain antibody (scFv)
CC HIB-5, which is directed against platelet glycoprotein Ib (GPIb).
CC HIB-5 is composed of a heavy chain variable region and light chain
CC variable region joined via a vector-derived peptide linker. The
CC HIB series of scFv was isolated from a human synthetic VH and VL
CC scFv library by 3 rounds of phagemid selection against transfected
CC CHO cells expressing the GPIb alpha component of the GPIb/IX/V
CC complex on their surface, followed by a 4th round of selection
CC against washed human platelets, and 2 final rounds in which
CC attempts were made to displace scFv from washed platelets by
CC flooding with murine monoclonal antibody or minotope peptide (see
CC AY95229). Whether displayed as surface proteins on a phagemid or
CC secreted as free scFv by Escherichia coli, the HIB scFv clones are
CC capable of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences
CC and are therefore attractive potential reagents for therapeutic
CC purposes. They provide a new class of antithrombotic agents,
CC useful for the prevention of platelet-dependent thrombi in
CC diseased arteries, bypass grafts, dialysis etc., and can also be
CC used as diagnostic reagents. Methods of inhibiting aggregation
CC of platelets, of binding human platelet GPIb alpha and of selecting
CC a VH or VL region of an antibody that inhibits platelet aggregation
CC are claimed.
XX
XX Sequence 131 AA;
Query Match 27.4%; Score 31; DB 21; Length 131;
Best Local Similarity 100.0%; Pred. No. 2e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TQSPSLPVTGPGEPASTICRSQSLLHNGY 35
Db 22 TQSPSLPVTGPGEPASTICRSQSLLHNGY 52
RESULT 15
AAB99117
ID AAB99117 standard; Protein; 139 AA.
XX
AC AAB99117;
XX
DT 22-AUG-2001 (first entry)
XX
DE Human protein SEQ ID 16.
XX
KW Human; antiarthritic; cardiatic; monoclonal antibody; keloid; arthritis;
Tumour Growth Factor-beta II receptor; TGF-beta II receptor; atopy;

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KW signal transduction inhibition; tissue fibrosis; atherosclerosis.
XX Homo sapiens.
OS WO200136642-A1.
PN 25-MAY-2001.
XX 17-NOV-2000; 2000WO-JP08129.
XX 18-NOV-1999; 99JP-0328681.
PR 08-NOV-2000; 2000JP-0340216.
XX (NISE) JAPAN TOBACCO INC.
XX Sakamoto S, Kamada M;
XX WPI; 2001-343825/36.
DR N-PSDB; AAH41159.
XX Human monoclonal antibodies recognizing human TGF-beta II receptor,
PT useful for treating TGF-beta associated diseases such as tissue
PT fibrosis -
XX Claim 11; Page 109-110; 118pp; Japanese.
XX The present invention relates to novel human monoclonal antibodies. The
CC antibodies can bind to human Tumour Growth Factor-beta (TGF-beta) II
CC receptor, resulting in the inhibition of the signal transduction of human
CC TGF-beta into cells. The antibodies can be used for the prevention and
CC treatment of diseases associated with the production of TGF-beta, such as
CC tissue fibrosis in the lung, liver, skin, kidney or other tissues,
CC atherosclerosis, atopy, keloid and arthritis. The present sequence was
CC used in the present invention.
XX
XX Sequence 139 AA;
Query Match 27.4%; Score 31; DB 22; Length 139;
Best Local Similarity 100.0%; Pred. No. 2.1e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TQSPSLPVTGPGEPASTICRSQSLLHNGY 35
Db 25 TQSPSLPVTGPGEPASTICRSQSLLHNGY 55
Search completed: October 9, 2002, 19:22:59
Job time : 12.1071 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:21:30 ; Search time 4.61224 Seconds
(without alignments)
598.427 Million cell updates/sec

Title: US-09-822-698A-1
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	27.4	112	1	US-08-331-398A-49
2	31	27.4	112	2	US-08-331-397B-49
3	31	27.4	112	2	US-08-759-804A-49
4	31	27.4	112	4	US-09-227-693-49
5	31	27.4	113	4	US-09-025-769B-15
6	31	27.4	114	4	US-09-025-769B-29
7	31	27.4	114	4	US-09-025-769B-45
8	31	27.4	281	4	US-09-025-769B-178
9	29	25.7	112	4	US-09-240-374-30
10	28	24.8	112	1	US-08-053-171-16
11	26	23.0	108	1	US-08-488-113B-151
12	26	23.0	108	1	US-08-477-484B-151
13	26	23.0	108	1	US-08-107-669D-15
14	26	23.0	108	1	US-08-472-788A-15
15	26	23.0	108	2	US-08-477-531B-15
16	26	23.0	108	2	US-08-646-360-151
17	26	23.0	108	2	US-08-082-842A-15
18	26	23.0	108	4	US-08-839-765-151
19	26	23.0	112	4	US-09-136-389-151
20	25	22.1	112	1	US-08-478-039-88
21	25	22.1	112	1	US-08-476-349A-88
22	25	22.1	116	1	US-08-482-882-66
23	25	22.1	116	2	US-08-483-389-66
24	25	22.1	116	2	US-08-487-113D-66
25	25	22.1	116	2	US-08-473-503-66
26	25	22.1	116	2	US-08-483-932-66
27	25	22.1	116	2	US-08-720-420A-66

28	25	22.1	116	3	US-08-714-017-66	Sequence 66, Appl
29	25	22.1	116	3	US-08-475-680-66	Sequence 66, Appl
30	24	21.2	112	1	US-08-053-171-15	Sequence 15, Appl
31	24	21.2	112	3	US-08-815-190A-14	Sequence 14, Appl
32	23	20.4	112	1	US-08-331-398A-50	Sequence 50, Appl
33	23	20.4	112	2	US-08-331-397B-50	Sequence 50, Appl
34	23	20.4	112	2	US-08-759-804A-50	Sequence 50, Appl
35	23	20.4	112	4	US-09-227-693-50	Sequence 50, Appl
36	23	20.4	113	1	US-08-264-093-10	Sequence 10, Appl
37	22	19.5	132	1	US-08-392-419-4	Sequence 4, Appl
38	22	19.5	365	3	US-08-875-811-53	Sequence 53, Appl
39	22	19.5	366	3	US-08-875-811-55	Sequence 55, Appl
40	21	18.6	131	1	US-08-129-930B-95	Sequence 95, Appl
41	21	18.6	131	4	US-08-134-346A-50	Sequence 50, Appl
42	21	18.6	131	4	US-08-976-288A-95	Sequence 95, Appl
43	20	17.7	108	1	US-08-468-661-3	Sequence 3, Appl
44	20	17.7	108	1	US-08-466-272A-3	Sequence 3, Appl
45	20	17.7	108	1	US-08-478-857-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-331-398A-49
; Sequence 49, Application US/08331398A
; Patent No. 5608039
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pai, Lee
; TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
; TITLE OF INVENTION: and Their Uses (as amended)
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,398A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126110US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:

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; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-331-398A-49

Query Match 27.4%; Score 31; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TOSPLSLPVTGPEPASISCRSSQSLHNSGY 35
DB 5 TOSPLSLPVTGPEPASISCRSSQSLHNSGY 35

RESULT 2
US-08-331-397B-49
; Sequence 49, Application US/08331397B
; Patent No. 5981726
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
; TITLE OF INVENTION: Specific Antibody Fragments, Fusion Proteins, and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Street Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,397B
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA: US 07/596,289
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126120US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-331-397B-49

Query Match 27.4%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5 TOSPLSLPVTGPEPASISCRSSQSLHNSGY 35
DB 5 TOSPLSLPVTGPEPASISCRSSQSLHNSGY 35

RESULT 3
US-08-759-804A-49
; Sequence 49, Application US/08759804A
; Patent No. 5990296
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Willingham, Mark
; APPLICANT: Fitzgerald, David J.
; APPLICANT: Brinkmann, Ulrich
; APPLICANT: Pal, Lee
; TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,804A
; FILING DATE: 03-DEC-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/331,398
; FILING DATE: 28-OCT-1994
; PRIOR APPLICATION DATA: US 07/767,331
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-126140US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-759-804A-49

Query Match 27.4%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 5 TOSPLSLPVTGPEPASISCRSSQSLHNSGY 35
DB 5 TOSPLSLPVTGPEPASISCRSSQSLHNSGY 35
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RESULT 4
US-09-227-693-49
; Sequence 49, Application US/09227693
; Patent No. 6287562
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, ByungKook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourlie and Crew
; STREET: Steuart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/227,693
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/331,396
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM GM607 VL region"
US-09-227-693-49

Query Match 27.4%; Score 31; DB 4; Length 112;
Best Local Similarity 100.0%; Pred.No.1.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEPAISICRSSQSLLHSNGY 35
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Db 5 TQSPSLPVTGPGEPAISICRSSQSLLHSNGY 35

RESULT 5
US-09-025-769B-15
; Sequence 15, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter

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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-29

Query Match 27.4%; Score 31; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35
|||||
DB 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35

RESULT 7

US-09-025-769B-45
Sequence 45, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-45

Query Match 27.4%; Score 31; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35
|||||
DB 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35

RESULT 8

US-09-025-769B-178
Sequence 178, Application US/09025769B
Patent No. 6300064
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Liming
APPLICANT: Moroney, Simon
APPLICANT: Plueckthun, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-025-769B-178

Query Match 27.4%; Score 31; DB 4; Length 281;
Best Local Similarity 100.0%; Pred. No. 3.3e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35
|||||
DB 170 TQSPSLPVTGEPASISCRSSQSLHNSGY 200

RESULT 9

US-09-240-274-30
Sequence 30, Application US/09240274
Patent No. 6255455

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; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 30
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-30

Query Match      25.7%   Score 29; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTQSPSLPVTGPGPASPISCRSSQSLHLS 32
Db 3 LTQSPSLPVTGPGPASPISCRSSQSLHLS 31

RESULT 10
US-08-053-171-16
; Sequence 16; Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co, Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/053,171
; FILING DATE: 22-APR-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-54-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Sequence of Tew antibody
; Patent No. 5562903

; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 30
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-30

Query Match      25.7%   Score 29; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.2e-20;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LTQSPSLPVTGPGPASPISCRSSQSLHLS 32
Db 3 LTQSPSLPVTGPGPASPISCRSSQSLHLS 31

RESULT 11
US-08-488-113B-151
; Sequence 151; Application US/08488113B
; Patent No. 5744580
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Carroll, Stephen F.
; APPLICANT: Studnika, Gary M.
; TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
; TITLE OF INVENTION: Proteins
; NUMBER OF SEQUENCES: 169
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McAndrews, Held & Malloy, Ltd.
; STREET: 500 West Madison Street, 34th floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60661
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,113B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/425,336
; FILING DATE: 18-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/064,691
; FILING DATE: 12-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/988,430
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/901,707
; FILING DATE: 19-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/787,567
; FILING DATE: 04-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McNicholas, Janet M.
; REGISTRATION NUMBER: 32,918
; REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.CZA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/707-8889
; TELEFAX: 312/707-9155
; TELEX: 650 388-1248
; INFORMATION FOR SEQ ID NO: 151:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 108 amino acids
; TYPE: amino acid
; STRANDEDNESS: double
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COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/472,788A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/082,842

FILING DATE: 23-JUN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10906

FILING DATE: 14-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/808,464

FILING DATE: 13-DEC-1991

ATTORNEY/AGENT INFORMATION:

NAME: Cimbala, Michele A.

REGISTRATION NUMBER: 33,851

REFERENCE/DOCKET NUMBER: 0610.1000003

TELEPHONE: 202/371-2600

TELEFAX: 202/371-2540

TELEX:

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-472-788A-15

Query Match 23.0%; Score 26; DB 1; Length 108;

Best Local Similarity 100.0%; Pred. No. 8.7e-18;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TQSPSLPVTGPGEPASISCRSSQSL 30

Db 5 TQSPSLPVTGPGEPASISCRSSQSL 30

RESULT 15

US-08-477-531B-15

Sequence 15, Application US/08477531B

Patent No. 5821123

GENERAL INFORMATION:

APPLICANT: Studnicka, Gary M.

TITLE OF INVENTION: Modified Antibody Variable Domains (as amended)

NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein and Fox P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,531B

FILING DATE: 07-JUN-1995

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/107,669

FILING DATE: 13-AUG-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/10906
FILING DATE: 14-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/808,464
FILING DATE: 13-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Michele A. Cimbala
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 0610.1000004/MAC
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 108 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-477-531B-15

Query Match 23.0%; Score 26; DB 2; Length 108;

Best Local Similarity 100.0%; Pred. No. 8.7e-18;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TQSPSLPVTGPGEPASISCRSSQSL 30

Db 5 TQSPSLPVTGPGEPASISCRSSQSL 30

Search completed: October 9, 2002, 19:26:36

Job time : 4.61224 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:23:10 ; Search time 44.3929 Seconds
(without alignments)
895.951 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 113
Sequence: 1 EIVLTQSPSLPVTGPGEAS.....MOGLQSPFTFGPTKVDIKR 113

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 3502263 seqs, 351980561 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	113	100.0	113	22	US-09-822-698A-1
3	113	100.0	220	22	US-09-822-698A-24
4	113	100.0	381	19	US-09-538-913-5
5	113	100.0	381	22	US-09-822-698A-5
6	31	27.4	64	26	US-60-173-469-1652
7	31	27.4	80	26	US-60-160-203-4277

8	31	27.4	98	26	US-60-169-840-6274
9	31	27.4	100	5	US-08-124-469-19
10	31	27.4	100	8	US-08-472-771-19
11	31	27.4	100	8	US-08-486-202-19
12	31	27.4	100	18	US-09-430-048-60
13	31	27.4	100	18	US-09-472-087-115
14	31	27.4	100	19	US-09-538-913-19
15	31	27.4	100	22	US-09-822-698A-19
16	31	27.4	102	18	US-09-430-048-59
17	31	27.4	104	26	US-60-160-203-3582
18	31	27.4	112	7	US-08-331-396-49
19	31	27.4	112	7	US-08-331-396A-49
20	31	27.4	112	7	US-08-331-396C-49
21	31	27.4	112	7	US-08-331-396D-49
22	31	27.4	112	7	US-08-331-397-49
23	31	27.4	112	7	US-08-331-398-49
24	31	27.4	112	11	US-08-700-737-8
25	31	27.4	112	11	US-08-759-804-49
26	31	27.4	112	18	US-09-430-048-20
27	31	27.4	113	18	US-09-490-070-15
28	31	27.4	114	18	US-09-430-048-19
29	31	27.4	114	18	US-09-490-070-29
30	31	27.4	114	18	US-09-490-070-45
31	31	27.4	121	26	US-60-160-203-4767
32	31	27.4	131	18	US-09-430-048-25
33	31	27.4	157	22	US-09-864-761-48255
34	31	27.4	174	26	US-60-189-458-192
35	31	27.4	219	23	US-09-972-656-104
36	31	27.4	248	19	US-09-517-225E-6
37	31	27.4	262	1	PCT-US01-19110-2081
38	31	27.4	262	22	US-09-880-748-2081
39	31	27.4	281	18	US-09-490-070-178
40	30	26.5	260	1	PCT-US01-19110-1039
41	30	26.5	260	22	US-09-880-748-1039
42	29	25.7	112	22	US-09-848-798-30
43	29	25.7	112	22	US-09-848-798A-30
44	28	24.8	101	23	US-09-972-656-132
45	28	24.8	114	11	US-08-700-737-51

ALIGNMENTS

RESULT 1
US-09-538-913-1
; Sequence 1, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE REFERENCE: seglist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 113
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-1

Query Match	100.0%	Score 113;	DB 19;	Length 113;
Best Local Similarity	100.0%	Pred. No. 3e-102;		
Matches 113;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	EIVLTQSPSLPVTGPGEASISCRSSQSLLSHNGYTYLDWYLNKPGQSPQLIYSGSHRA	60	
Db	1	EIVLTQSPSLPVTGPGEASISCRSSQSLLSHNGYTYLDWYLNKPGQSPQLIYSGSHRA	60	
QY	61	SGVPDRFSSVSGTDFTLRISRVAEADVGVYCYMGLQSPFTFGPTKVDIKR	113	
Db	61	SGVPDRFSSVSGTDFTLRISRVAEADVGVYCYMGLQSPFTFGPTKVDIKR	113	

```
RESULT 2
US-09-822-698A-1
; Sequence 1, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 113
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of PH1 Fab antibody
US-09-822-698A-1
Query Match 100.0%; Score 113; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 3e-102;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Db 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113

RESULT 3
US-09-822-698A-24
; Sequence 24, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-IgG1
US-09-822-698A-24
Query Match 100.0%; Score 113; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 5.3e-102;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Db 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
```

```
RESULT 4
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for bivPHI-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
US-09-538-913-5
Query Match 100.0%; Score 113; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.4e-102;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Db 127 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 186
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 187 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 239

RESULT 5
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine bivPHI-IL-2
US-09-822-698A-5
Query Match 100.0%; Score 113; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 8.4e-102;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Db 127 EIVLTQSPVLSPLPTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSPQLLIYSGSHRA 186
Qy 61 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 187 SGVPDRFSGSVSGTDTFLRISRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 239

RESULT 6
US-60-173-469-1652
```

```
; Sequence 1652, Application US/60173469
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000185
; CURRENT APPLICATION NUMBER: US/60/173,469
; CURRENT FILING DATE: 1999-12-29
; NUMBER OF SEQ ID NOS: 2120
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1652
; LENGTH: 64
; TYPE: PRT
; ORGANISM: HUMAN
US-60-173-469-1652

Query Match      27.4%; Score 31; DB 26; Length 64;
Best Local Similarity 100.0%; Pred. No. 4.4e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEPAISCRSSQSLHNSGY 35
   |||||
DB 25 TQSPSLPVTGPGEPAISCRSSQSLHNSGY 55
   |||||

RESULT 7
US-60-160-203-4277
; Sequence 4277, Application US/60160203
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CLG00116
; CURRENT APPLICATION NUMBER: US/60/160,203
; CURRENT FILING DATE: 1999-10-19
; NUMBER OF SEQ ID NOS: 6374
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4277
; LENGTH: 80
; TYPE: PRT
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(80)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-160-203-4277

Query Match      27.4%; Score 31; DB 26; Length 80;
Best Local Similarity 100.0%; Pred. No. 5.3e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEPAISCRSSQSLHNSGY 35
   |||||
DB 7 TQSPSLPVTGPGEPAISCRSSQSLHNSGY 37
   |||||

RESULT 8
US-60-169-840-6274
; Sequence 6274, Application US/60169840
; GENERAL INFORMATION:
; APPLICANT: BONAZZI, VIVIEN
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: CL000164
; CURRENT APPLICATION NUMBER: US/60/169,840
; CURRENT FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 9628
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6274
; LENGTH: 98
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; TYPE: PRT
; ORGANISM: Human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(98)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-60-169-840-6274

Query Match      27.4%; Score 31; DB 26; Length 98;
Best Local Similarity 100.0%; Pred. No. 6.2e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEPAISCRSSQSLHNSGY 35
   |||||
DB 24 TQSPSLPVTGPGEPAISCRSSQSLHNSGY 54
   |||||

RESULT 9
US-08-124-469-19
; Sequence 19, Application US/08124469
; GENERAL INFORMATION:
; APPLICANT: RAPOPORT, Basil
; APPLICANT: MCLACHLAN, Sandra M.
; TITLE OF INVENTION: GRAVES' OPTHALMOPATHY ASSOCIATED
; TITLE OF INVENTION: ANTIBODIES, GRAVES' OPTHALMOPATHY ORBITAL ANTIGEN,
; TITLE OF INVENTION: AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DORR
; STREET: 1455 PENNSYLVANIA AVE., N.W.
; CITY: WASHINGTON,
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/124,469
; FILING DATE: 22-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: WIXON, HENRY N.
; REGISTRATION NUMBER: 32,073
; REFERENCE/DOCKET NUMBER: 102.105.301
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)942-8400
; TELEFAX: (202)942-8484
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 100 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-124-469-19

Query Match      27.4%; Score 31; DB 5; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.3e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEPAISCRSSQSLHNSGY 35
   |||||
DB 5 TQSPSLPVTGPGEPAISCRSSQSLHNSGY 35
   |||||

RESULT 10
US-08-472-771-19
; Sequence 19, Application US/08472771
; GENERAL INFORMATION:
; APPLICANT: RAPOPORT, Basil
; APPLICANT: MCLACHLAN, Sandra M.
```


; SEQ ID NO 115
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-115

Query Match 27.4%; Score 31; DB 18; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.3e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35
|||||
Db 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35

RESULT 14

US-09-538-913-19
; Sequence 19, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE REFERENCE: seqlist.DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-538-913-19

Query Match 27.4%; Score 31; DB 19; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.3e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35
|||||
Db 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35

RESULT 15

US-09-822-698A-19
; Sequence 19, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 19
; LENGTH: 100
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region from a DPK 15 germ line
US-09-822-698A-19

Query Match 27.4%; Score 31; DB 22; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.3e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35
|||||
Db 5 TQSPSLPVTGEPASISCRSSQSLHNSGY 35

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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:23:45 ; Search time 14.9898 Seconds
(without alignments)
2085.589 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 113
Sequence: 1 EIVLTQSPVLPVTPGEPAS.....MQGLQSPFTFGTKVDIKR 113

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Gapop 60.0 , Gapext 60.0

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3: /cgcn2_6/ptodata/1/paa/US07_NEW_COMB.pep.*
4: /cgcn2_6/ptodata/1/paa/US08_NEW_COMB.pep.*
5: /cgcn2_6/ptodata/1/paa/US09_NEW_COMB.pep.*
6: /cgcn2_6/ptodata/1/paa/US10_NEW_COMB.pep.*
7: /cgcn2_6/ptodata/1/paa/US60_NEW_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB	ID	Description
1	54	47.8	112	5	US-09-791-537-110202		Sequence 110202,
2	37	32.7	138	1	PCT-US02-09694-52		Sequence 52, Appl
3	32	28.3	118	5	US-09-791-537-54839		Sequence 54839, A
4	31	27.4	99	6	US-10-041-860-323		Sequence 323, App
5	31	27.4	99	6	US-10-041-860-365		Sequence 365, App
6	31	27.4	100	1	PCT-US02-12202-24		Sequence 24, Appl
7	31	27.4	100	5	US-09-791-537-24898		Sequence 24898, A
8	31	27.4	100	6	US-10-025-687-24		Sequence 24, Appl
9	31	27.4	100	6	US-10-153-382-38		Sequence 38, Appl
10	31	27.4	100	6	US-10-125-687-24		Sequence 24, Appl
11	31	27.4	100	6	US-10-041-860-8		Sequence 8, Appl
12	31	27.4	100	6	US-10-041-860-280		Sequence 280, App
13	31	27.4	100	6	US-10-041-860-321		Sequence 321, App
14	31	27.4	100	6	US-10-041-860-364		Sequence 364, App
15	31	27.4	100	6	US-10-010-942B-7		Sequence 7, Appl
16	31	27.4	109	5	US-09-791-537-88611		Sequence 88611, A
17	31	27.4	110	5	US-09-791-537-109684		Sequence 109684,
18	31	27.4	111	6	US-10-041-860-45		Sequence 45, Appl
19	31	27.4	111	6	US-10-041-860-219		Sequence 219, App
20	31	27.4	111	6	US-10-041-860-253		Sequence 253, App
21	31	27.4	111	6	US-10-041-860-363		Sequence 363, App
22	31	27.4	112	5	US-09-791-537-21281		Sequence 21281, A
23	31	27.4	112	5	US-09-791-537-21285		Sequence 21285, A
24	31	27.4	112	5	US-09-791-537-85986		Sequence 85986, A
25	31	27.4	113	1	PCT-US02-12202-9		Sequence 9, Appl
26	31	27.4	113	5	US-09-791-537-59499		Sequence 59499, A

27	31	27.4	113	6	US-10-025-687-9	Sequence 9, Appl
28	31	27.4	113	6	US-10-125-687-9	Sequence 9, Appl
29	31	27.4	113	6	US-10-041-860-30	Sequence 30, Appl
30	31	27.4	113	6	US-10-041-860-221	Sequence 221, App
31	31	27.4	113	6	US-10-041-860-255	Sequence 255, App
32	31	27.4	114	5	US-09-791-537-64706	Sequence 64706, A
33	31	27.4	114	5	US-09-791-537-86001	Sequence 86001, A
34	31	27.4	114	5	US-09-791-537-86326	Sequence 86326, A
35	31	27.4	114	5	US-09-791-537-122965	Sequence 122965,
36	31	27.4	114	5	US-09-791-537-137519	Sequence 137519,
37	31	27.4	114	6	US-10-041-860-322	Sequence 322, App
38	31	27.4	115	5	US-09-791-537-137518	Sequence 137518,
39	31	27.4	116	5	US-09-791-537-43479	Sequence 43479, A
40	31	27.4	116	5	US-09-791-537-104602	Sequence 104602,
41	31	27.4	117	5	US-09-791-537-48291	Sequence 48291, A
42	31	27.4	117	5	US-09-791-537-107503	Sequence 107503,
43	31	27.4	118	5	US-09-791-537-129360	Sequence 129360,
44	31	27.4	123	5	US-09-791-537-71832	Sequence 71832, A
45	31	27.4	125	6	US-10-010-942B-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-09-791-537-110202
; Sequence 110202, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO. 110202
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-110202

Query Match 47.8%; Score 54; DB 5; Length 112;
Best Local Similarity 100.0%; Pred. No. 4.2e-42;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDMYLQKPGQSPOLLIIY 54
Db 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDMYLQKPGQSPOLLIIY 54

RESULT 2
PCT-US02-09694-52

; Sequence 52, Application PC/TUS0209694
; GENERAL INFORMATION:
; APPLICANT: GERSHWIN, M. ERIC
; TITLE OF INVENTION: ANTIBODIES AGAINST AUTOANTIGENS OF PRIMARY BILIARY
; FILE REFERENCE: ABX-UCD PCT
; CURRENT APPLICATION NUMBER: PCT/US02/09694
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Human mAb
; NAME/KEY: MOD_RES

; LOCATION: (10)
; OTHER INFORMATION: Any amino acid
; NAME/KEY: MOD_RES
; LOCATION: (130)
; OTHER INFORMATION: Any amino acid
PCT-US02-09694-52

Query Match 32.7%; Score 37; DB 1; Length 138;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 PASISCRSSQSLHNSGYLDWYLRKPGSQPOLLIY 54
|||||
Db 11 PASISCRSSQSLHNSGYLDWYLRKPGSQPOLLIY 47

RESULT 3

US-09-791-537-54839
; Sequence 54839, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 54839
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-54839

Query Match 28.3%; Score 32; DB 5; Length 118;
Best Local Similarity 100.0%; Pred. No. 9e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VLTQSPSLPVTGPEPASISCRSSQSLHNSG 34
|||||
Db 5 VLTQSPSLPVTGPEPASISCRSSQSLHNSG 36

RESULT 4

US-10-041-860-323
; Sequence 323, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX 051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 323
; LENGTH: 99
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-323

Query Match 27.4%; Score 31; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.5e-21;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TQSPSLPVTGPEPASISCRSSQSLHNSGY 35
|||||
Db 5 TQSPSLPVTGPEPASISCRSSQSLHNSGY 35

RESULT 5

US-10-041-860-365
; Sequence 365, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadl
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX 051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 365
; LENGTH: 99
; TYPE: PRT
; ORGANISM: homo sapiens
; NAME/KEY: VARIANT
; LOCATION: 43, 58, 96
; OTHER INFORMATION: Xaa = Any Amino Acid
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 43, 58, 96
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-041-860-365

Query Match 27.4%; Score 31; DB 6; Length 99;
Best Local Similarity 100.0%; Pred. No. 6.5e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHNSGY 35
|||||
Db 5 TQSPSLPVTGPEPASISCRSSQSLHNSGY 35

RESULT 6

PCT-US02-12202-24
; Sequence 24, Application PC/TUS0212202
; GENERAL INFORMATION:
; APPLICANT: abmaxis, Inc.
; APPLICANT: Luo, Peizhi
; TITLE OF INVENTION: STRUCTURE-BASED CONSTRUCTION OF HUMAN ANTIBODY LIBRARY
; FILE REFERENCE: 26050-706
; CURRENT APPLICATION NUMBER: PCT/US02/12202
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/284,407
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-12202-24

Query Match 27.4%; Score 31; DB 1; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 100
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-280

Query Match      27.4%; Score 31; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35
Db 5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35

RESULT 13
US-10-041-860-321
; Sequence 321, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 321
; LENGTH: 100
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-321

Query Match      27.4%; Score 31; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35
Db 5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35

RESULT 14
US-10-041-860-364
; Sequence 364, Application US/10041860
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: AGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 364
; LENGTH: 100
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-364

Query Match      27.4%; Score 31; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35
Db 5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35

RESULT 15
US-10-010-942B-7
; Sequence 7, Application US/10010942B
; GENERAL INFORMATION:
; APPLICANT: Basl, Gurid
; APPLICANT: Saidanah, Jose
; APPLICANT: Yednock, Ted
; TITLE OF INVENTION: HUMANIZED ANTIBODIES THAT RECOGNIZE
; FILE REFERENCE: ELN-002
; CURRENT APPLICATION NUMBER: US/10/010,942B
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 60/251,892
; PRIOR FILING DATE: 2000-12-06
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-010-942B-7

Query Match      27.4%; Score 31; DB 6; Length 100;
Best Local Similarity 100.0%; Pred. No. 6.6e-21;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35
Db 5 TQSPSLPVTGPEPASISCRSSQSLHSHNGY 35

Search completed: October 9, 2002, 19:33:55
Job time : 15.9898 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model
Run on: October 9, 2002, 19:19:35 : Search time 6.05357 Seconds
(without alignments)
1793.668 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 113
Sequence: 1 EIVLTQSLPLVTPGEPAS.....MQGLQSFPTGPGTKVDIKR 113
Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues
Word size : 0
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_71.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	27.4	112	2 S58207	Ig light chain V r
2	31	27.4	112	2 S58206	Ig light chain V r
3	31	27.4	117	1 K2HUGM	Ig kappa chain pre
4	31	27.4	123	2 S40319	Ig kappa chain V r
5	31	27.4	132	2 S26882	Ig kappa chain V r
6	31	27.4	135	2 S40342	Ig kappa chain - h
7	31	27.4	136	2 S40357	Ig kappa chain V-J
8	30	26.5	114	2 S40375	Ig kappa chain - h
9	28	24.8	113	1 K2HUTW	Ig kappa chain V-I
10	27	23.9	100	2 S24681	Ig kappa chain - h
11	27	23.9	125	2 S40356	Ig kappa chain - h
12	27	23.9	126	2 S40339	Ig kappa chain - h
13	26	23.0	112	1 K2HUGL	Ig kappa chain V-I
14	26	23.0	121	2 S40371	Ig kappa chain - h
15	24	21.2	120	2 A49043	Ig kappa chain V r
16	23	20.4	115	1 K2HUCM	Ig kappa chain V-I
17	23	20.4	121	2 S24205	Ig kappa chain V r
18	23	20.4	127	2 S40323	Ig kappa chain - h
19	23	20.4	130	2 S40321	Ig kappa chain - h
20	22	19.5	87	2 S34091	Ig kappa chain V r
21	22	19.5	100	2 H33730	Ig kappa chain V r
22	22	19.5	112	1 KVMSS1	Ig kappa chain V r
23	22	19.5	113	2 S38716	Ig light chain V r
24	22	19.5	113	1 KVMSS17	Ig kappa chain V r
25	22	19.5	116	2 S20708	Ig kappa chain V r
26	22	19.5	119	2 B27588	Ig kappa chain pre
27	22	19.5	119	2 A27588	Ig kappa chain pre
28	22	19.5	124	2 S03876	Ig kappa chain V-I
29	20	17.7	112	2 126317	Ig kappa chain V r

30 20 17.7 112 2 E26317 Ig kappa chain V r
31 20 17.7 112 2 G26317 Ig kappa chain V r
32 20 17.7 112 2 A26317 Ig kappa chain V r
33 20 17.7 112 2 B26317 Ig kappa chain V r
34 20 17.7 112 2 D26317 Ig kappa chain V r
35 20 17.7 112 2 F26317 Ig kappa chain V r
36 20 17.7 112 2 PL0275 Ig kappa chain V r
37 20 17.7 112 2 PL0274 Ig kappa chain V r
38 20 17.7 113 1 KVMSS7S Ig kappa chain V r
39 20 17.7 249 2 S41374 single chain Fv an
40 19 16.8 114 2 S40340 Ig kappa chain V-J
41 19 16.8 120 2 S41815 Ig kappa chain V r
42 18 15.9 54 2 S34093 Ig kappa chain V r
43 18 15.9 96 2 S40320 Ig kappa chain - h
44 18 15.9 131 2 S40372 Ig kappa chain V-J
45 17 15.0 83 2 S34095 Ig kappa chain V r

ALIGNMENTS

RESULT 1
S58207
Ig light chain V region anti-F(ab')2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C:Accession: S58207
R:Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebe, S.; Breitlin
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable regi
A:Reference number: S58206
A:Accession: S58207
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEL>
A:Cross-references: EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PID:g929643
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 27.4%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPLSLPVTPGEPASISCRSSQSLHNSGY 35
|||||
DB 5 TQSPLSLPVTPGEPASISCRSSQSLHNSGY 35

RESULT 2
S58206
Ig light chain V region anti-F(ab')2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 21-Jan-2000
C:Accession: S58206
R:Welschhof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebe, S.; Breitlin
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable regi
A:Reference number: S58206
A:Accession: S58206
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-112 <WEL>
A:Cross-references: EMBL:X89054; NID:g929640; PIDN:CAA61441.1; PID:g929641
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 27.4%; Score 31; DB 2; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.6e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPLSLPVTPGEPASISCRSSQSLHNSGY 35

```
Db 5 TQSPSLPVTGEPASISCRSSQSLHSNGY 35
|||||
RESULT 3
K2HUCM
Ig kappa chain precursor V-II region (GM607) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C:Accession: A01889; B24452
R:Klobeck, H.G.; Solomon, A.; Zachau, H.G.
Nature 309, 73-76, 1984
A:Title: Contribution of human V-kappaII germ-line genes to light-chain diversity.
A:Reference number: A01889; MUID:84191506
A:Accession: A01889
A:Molecule type: mRNA
A:Residues: 1-117 <KLO>
A:Note: the sequence was determined from the differentiated gene
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>
F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAP>
F:20-99/Domain: immunoglobulin homology <IMM>
F:27-97/Disulfide bonds: #status predicted

Query Match 27.4%; Score 31; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHSNGY 35
|||||
Db 9 TQSPSLPVTGEPASISCRSSQSLHSNGY 39
|||||

RESULT 4
S40319
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40319
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40319; MUID:94080891
A:Accession: S40319
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72429; NID:9441326; PIDN:CAA51097.1; PID:9441327
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:26-105/Domain: immunoglobulin homology <IMM>

Query Match 27.4%; Score 31; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 1.8e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHSNGY 35
|||||
Db 15 TQSPSLPVTGEPASISCRSSQSLHSNGY 45
|||||

RESULT 5
S26882
Ig kappa chain V region (V607) - human
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
```

```
C:Accession: S26882
R:Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combriato, G.; Zachau, H.G.
Nature 347, 90-92, 1990
A:Title: Megabase inversions in the human genome as physiological events.
A:Reference number: S26882; MUID:90370099
A:Accession: S26882
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-132 <WEI>
A:Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 27.4%; Score 31; DB 2; Length 132;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHSNGY 35
|||||
Db 25 TQSPSLPVTGEPASISCRSSQSLHSNGY 55
|||||

RESULT 6
S40342
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40342
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40342; MUID:94080891
A:Accession: S40342
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-135 <KLE>
A:Cross-references: EMBL:X72452; NID:9441372; PID:9441373
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 27.4%; Score 31; DB 2; Length 135;
Best Local Similarity 100.0%; Pred. No. 1.9e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGEPASISCRSSQSLHSNGY 35
|||||
Db 18 TQSPSLPVTGEPASISCRSSQSLHSNGY 48
|||||

RESULT 7
S40357
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40357
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40357; MUID:94080891
A:Accession: S40357
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-136 <KLE>
A:Cross-references: EMBL:X72467
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 27.4%; Score 31; DB 2; Length 136;
```

```

Best Local Similarity 100.0%; Pred. NO. 1.9e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHSGY 35
|||||
Db 25 TQSPSLPVTGPEPASISCRSSQSLHSGY 55

RESULT 8
S40375
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40375
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-114 <KLE>
A:Cross-references: EMBL:X72485; NID:g441438; PIDN:CAA51153.1; PID:g441439
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-92/Domain: immunoglobulin homology <IMM>

Query Match 26.5%; Score 30; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. NO. 1.8e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHSG 34
|||||
Db 2 TQSPSLPVTGPEPASISCRSSQSLHSG 31

RESULT 9
K2HUTW
Ig kappa chain V-II region (Tew) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A90370; A92764; A01888
R:Putnam, F.W.; Whitley, Jr., E.J.; Paul, C.; Davidson, J.N.
Biochemistry 12, 3763-3780, 1973
A:Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary amyloid
A:Reference number: A90370; MUID:74148480
A:Contents: Bence Jones protein Tew
A:Accession: A90370
A:Molecule type: protein
A:Residues: 1-113 <PPT>
A:Note: this protein was isolated from the urine of a patient with plasma cell dyscrasia
A:Note: the C region of this chain has the Inv (1,2) marker
R:Terry, W.D.; Page, D.L.; Kimura, S.; Isobe, T.; Osserman, E.F.; Glennner, G.G.
J. Clin. Invest. 52, 1276-1281, 1973
A:Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient with
A:Reference number: A92764; MUID:73166638
A:Contents: amyloid protein Tew
A:Accession: A92764
A:Molecule type: protein
A:Residues: 1-27 <TER>
A:Note: the major amyloid protein appears to be identical with the Bence Jones protein in
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:136265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: amyloid; heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>
F:23-93/Disulfide bonds: #status predicted

Query Match 24.8%; Score 28; DB 1; Length 113;

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Best Local Similarity 100.0%; Pred. NO. 2.1e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHLS 32
|||||
Db 5 TQSPSLPVTGPEPASISCRSSQSLHLS 32

RESULT 10
S24681
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
C:Accession: S24681
R:van Es, J.H.
Submitted to the EMBL Data Library, July 1992
A:Reference number: S24679
A:Accession: S24681
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-100 <VAN>
A:Cross-references: EMBL:X67904; NID:g33435; PIDN:CAA48102.1; PID:g33436
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 23.9%; Score 27; DB 2; Length 100;
Best Local Similarity 100.0%; Pred. NO. 2e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLH 31
|||||
Db 5 TQSPSLPVTGPEPASISCRSSQSLH 31

RESULT 11
S40356
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40356
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40356
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72466; NID:g441400; PIDN:CAA51134.1; PID:g441401
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-104/Domain: immunoglobulin homology <IMM>

Query Match 23.9%; Score 27; DB 2; Length 125;
Best Local Similarity 100.0%; Pred. NO. 2.5e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLH 31
|||||
Db 14 TQSPSLPVTGPEPASISCRSSQSLH 40

RESULT 12
S40339
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40339
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891

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A:Accession: S40339
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-126 <KLE>
A:Cross-references: EMBL:X72449; NID:g441366; PIDN:CAA51117.1; PID:g441367
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:31-110/Domain: immunoglobulin homology <IMM>

Query Match      23.9%; Score 27; DB 2; Length 126;
Best Local Similarity 100.0%; Pred. No. 2.5e-20;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEPASISCRSSQSLH 31
   |||||
Db 20 TQSPSLPVTGPGEPASISCRSSQSLH 46
   |||||

RESULT 13
K2HUML
Ig kappa chain V-II region (Mil) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A01887
R:Dreyer, W.J.; Gray, W.R.; Hood, L.
Cold Spring Harb. Symp. Quant. Biol. 32, 353-367, 1967
A:Title: The genetic, molecular, and cellular basis of antibody formation: some facts and
A:Reference number: A01887
A:Accession: A01887
A:Molecule type: protein
A:Residues: 1-112 <DRE>
A:Note: the C region of this chain has the Inv (3) marker
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB: IGV2
A:Cross-references: GDB: I36265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 12
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer
F:16-94/Domain: immunoglobulin homology <IMM>
F:23-92/Disulfide bonds: #status predicted

Query Match      23.0%; Score 26; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVLTQSPSLPVTGPGEPASISCRSSQ 27
   |||||
Db 2 IVLTQSPSLPVTGPGEPASISCRSSQ 27
   |||||

RESULT 14
S40371
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40371
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40371
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <KLE>
A:Cross-references: EMBL:X72481; NID:g441430; PIDN:CAA51149.1; PID:g441431
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:31-92/Domain: immunoglobulin homology <IMM>

Query Match      23.0%; Score 26; DB 2; Length 121;
Best Local Similarity 100.0%; Pred. No. 2.4e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVLTQSPSLPVTGPGEPASISCRSSQ 27
   |||||
Db 2 IVLTQSPSLPVTGPGEPASISCRSSQ 27
   |||||
```

```
Best Local Similarity 100.0%; Pred. No. 2.6e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPGEPASISCRSSQSL 30
   |||||
Db 2 TQSPSLPVTGPGEPASISCRSSQSL 27
   |||||

RESULT 15
A49043
Ig kappa chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49043
R:Lautner-Rieske, A.; Huber, C.; Meindl, A.; Pargent, W.; Schaeble, K.F.; Thiebe, R.;
Eur. J. Immunol. 22, 1023-1029, 1992
A:Title: The human immunoglobulin kappa locus. Characterization of the duplicated A r
A:Reference number: A49043; MUID:92201291
A:Accession: A49043
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-120 <LAU>
A:Note: sequence extracted from NCBI backbone (NCBIN:92557, NCBI:92566)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match      21.2%; Score 24; DB 2; Length 120;
Best Local Similarity 100.0%; Pred. No. 3e-17;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGEPAISCRSSQSLHNGYTYL 38
   |||||
Db 35 PGEPAISCRSSQSLHNGYTYL 58
   |||||

Search completed: October 9, 2002, 19:25:51
Job time : 6.05357 secs
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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:13:25 ; Search time 3 45918 Seconds
(without alignments)
1264.839 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 113
Sequence: 1 EIVLTQSLPLVTPGEPAS.....MQGLQSPFTFGTKVDIKR 113

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Swissprot_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	31	27.4	117	1 KV2E_HUMAN	P06309 homo sapien
2	28	24.8	113	1 KV2D_HUMAN	P01617 homo sapien
3	26	23.0	112	1 KV2C_HUMAN	P01616 homo sapien
4	23	20.4	115	1 KV2A_HUMAN	P01614 homo sapien
5	22	19.5	112	1 KV2D_MOUSE	P01629 mus musculu
6	22	19.5	113	1 KV2E_MOUSE	P03976 mus musculu
7	20	17.7	113	1 KV2F_MOUSE	P01630 mus musculu
8	17	15.0	133	1 KV2F_HUMAN	P06310 homo sapien
9	14	12.4	108	1 KV1CANFA	P01618 canis famil
10	13	11.5	107	1 KV1D_HUMAN	P01596 homo sapien
11	11	9.7	113	1 KV2B_HUMAN	P01615 homo sapien
12	11	9.7	113	1 KV2G_MOUSE	P01631 mus musculu
13	10	8.8	109	1 LV1F_HUMAN	P04208 homo sapien
14	10	8.8	109	1 LV2E_HUMAN	P01708 homo sapien
15	10	8.8	111	1 LV1A_HUMAN	P01699 homo sapien
16	10	8.8	111	1 LV2F_HUMAN	P01709 homo sapien
17	10	8.8	111	1 LV2G_HUMAN	P01710 homo sapien
18	10	8.8	111	1 LV2I_HUMAN	P01712 homo sapien
19	10	8.8	111	1 LV6C_HUMAN	P06317 homo sapien
20	10	8.8	112	1 LV1B_HUMAN	P01700 homo sapien
21	10	8.8	112	1 LV6A_HUMAN	P01721 homo sapien
22	10	8.8	114	1 KV4A_HUMAN	P01625 homo sapien
23	10	8.8	120	1 KV2B_MOUSE	P01627 mus musculu
24	10	8.8	121	1 KV40_HUMAN	P06312 homo sapien
25	10	8.8	133	1 KV4B_HUMAN	P06313 homo sapien
26	10	8.8	134	1 KV4C_HUMAN	P06314 homo sapien
27	9	8.0	108	1 KV5P_MOUSE	P01649 mus musculu
28	9	8.0	112	1 KV2A_MOUSE	P01626 mus musculu
29	9	8.0	113	1 KV2C_MOUSE	P01628 mus musculu
30	9	8.0	131	1 LV6E_HUMAN	P06319 homo sapien
31	8	7.1	100	1 KV3C_HUMAN	P01621 homo sapien
32	8	7.1	107	1 KV6A_MOUSE	P01675 mus musculu
33	8	7.1	107	1 KV6B_MOUSE	P01676 mus musculu

34	8	7.1	107	1 KV6C_MOUSE	P01677 mus musculu
35	8	7.1	107	1 KV6D_MOUSE	P01678 mus musculu
36	8	7.1	107	1 KV6E_MOUSE	P01679 mus musculu
37	8	7.1	108	1 KV1E_HUMAN	P01597 homo sapien
38	8	7.1	108	1 KV1Y_HUMAN	P03622 homo sapien
39	8	7.1	109	1 KV3B_HUMAN	P01620 homo sapien
40	8	7.1	109	1 KV3D_HUMAN	P01622 homo sapien
41	8	7.1	109	1 KV3E_HUMAN	P01623 homo sapien
42	8	7.1	109	1 KV3G_HUMAN	P04206 homo sapien
43	8	7.1	111	1 LV6D_HUMAN	P06318 homo sapien
44	8	7.1	112	1 LV1H_HUMAN	P06887 homo sapien
45	8	7.1	115	1 KV31_HUMAN	P04433 homo sapien

ALIGNMENTS

RESULT 1
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobeck H.G.; Solomon A.; Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain diversity";
RL Nature 309:73-76(1984).
CC -----
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CC -----
CC EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117
FT DOMAIN 5 27
FT DOMAIN 28 43
FT DOMAIN 44 58
FT DOMAIN 59 65
FT DOMAIN 66 97
FT DOMAIN 98 106
FT DOMAIN 107 116
FT DISULFID 27 97
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

IG KAPPA CHAIN V-II REGION GM607.
FRAMEWORK-1.
COMPLEMENTARITY-DETERMINING-1.
FRAMEWORK-2.
COMPLEMENTARITY-DETERMINING-2.
FRAMEWORK-3.
COMPLEMENTARITY-DETERMINING-3.
FRAMEWORK-4.
BY SIMILARITY.

Query Match 27.4%; Score 31; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.8e-25;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHNSGY 35

|||||
9 TQSPSLPVTGPEPASISCRSSQSLHNSGY 39

Db

```

RESULT 2
KV2D_HUMAN          STANDARD;          PRT;    113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
(1)
RN PIR; A01888; K2HUTW.
RP InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 23.0%; Score 26; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVLTQSPSLPVTGPEPASISCRSSQ 27
DB 2 IVLTQSPSLPVTGPEPASISCRSSQ 27

RESULT 4
KV2A_HUMAN          STANDARD;          PRT;    115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
(1)
RN PIR; A01885; K2HUCM.
RP InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 20.4%; Score 23; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 4.9e-17;

KV2C_HUMAN          STANDARD;          PRT;    112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

Query Match 24.8%; Score 28; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 2.6e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQLLHS 32
DB 5 TQSPSLPVTGPEPASISCRSSQLLHS 32

RESULT 3
KV2C_HUMAN          STANDARD;          PRT;    112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region MIL.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

```



```
OY 76 FTLRISRVEADVGVYCMQ 95
      |||||||
Db 76 FTLRISRVEADVGVYCMQ 95

RESULT 8
KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combrato G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids res. 13:6499-6513(1985).
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CC -----
DR EMBL: Z00020; CAA77315.1; -
DR PIR: A01890; K2HURP.
DR InterPro: IPR003506; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 60 74 FRAMEWORK-2.
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 82 113 FRAMEWORK-3.
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 123 132 FRAMEWORK-4.
FT DISULFID 43 113 BY SIMILARITY.
FT NON_TER 133 133
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 15.0%; Score 17; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 1.2e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 80 ISRVEADVGVYCMQ 96
      |||||||
Db 100 ISRVEADVGVYCMQ 116

RESULT 9
KVL_CANFA STANDARD; PRT; 108 AA.
AC P01618;
DT 21-JUL-1986 (Rel. 01, Created)
DE 15-JUL-1999 (Rel. 38, Last sequence update)
DE Ig kappa chain V region GOM.
OS * Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RX MEDLINE=79026193; PubMed=100411;
RA Wasserman R.L., Capra J.D.;
RT "The amino acid sequence of the light chain variable region of a
RT canine myeloma immunoglobulin: evidence that the VK subgroups
RT predated mammalian speciation.";
RL Immunohemistry 15:303-305(1978).
CC -!- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLOGY WITH HUMAN KAPPA
CC CHAINS.
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF
CC THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.
DR PIR: A01907; K2DGM.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
DR Immunoglobulin V region.
KW DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 107 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;

Query Match 12.4%; Score 14; DB 1; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 PGPASISCRSSOS 28
      |||||||
Db 15 PGPASISCRSSOS 28

RESULT 10
KVLD_HUMAN STANDARD; PRT; 107 AA.
AC P01596;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region CAR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=75075135; PubMed=4216454;
RA Milstein C.P., Deverson E.V.;
RT "Primary structure of kappa light chain from a human myeloma
RT protein.";
RL Eur. J. Biochem. 49:377-391(1974).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR HSSP; P80362; IWTLL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Glycoprotein.
FT CARBOHYD 28 N-LINKED (GLCNAC. . .).
FT NON_TER 107 107
SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;
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Query Match          11.5%; Score 13; DB 1; Length 107;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 FTFGPGTKVDIKR 113
DB 95 FTFGPGTKVDIKR 107
|||||

RESULT 11
KV2B_HUMAN          STANDARD;          PRT;          113 AA.
AC P01615;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=76253627; PubMed=821524;
RX Riesen W.F., Jaton J.-C.;
RT "Variable region sequence of the light chain from a Waldenstroms IgM
with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
DR PIR; A01886; K2HUFF.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match          9.7%; Score 11; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AEDVGYYCMQ 95
DB 85 AEDVGYYCMQ 95
|||||

RESULT 12
KV2G_MOUSE          STANDARD;          PRT;          113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
```

```
*Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KVNS26.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match          9.7%; Score 11; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00021;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ASISCRSSQSL 29
DB 19 ASISCRSSQSL 29
|||||

RESULT 13
LV1F_HUMAN          STANDARD;          PRT;          109 AA.
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
the lambda light chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR PIR; A01967; L1HUWA.
DR HSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97
FT DOMAIN 98 109
FT DISULFID 22 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match          8.8%; Score 10; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0023;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVPPDRFSGS 70
DB 57 SGVPPDRFSGS 66
|||||

RESULT 14
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FT  MOD_RES      1  PYRROLIDONE CARBOXYLIC ACID.
FT  DISULFID     22  BY SIMILARITY.
FT  NON_TER      111
FT  SEQUENCE     111 AA: 11514 MW: 21D9F64250DFC8E0 CRC64:
SQ
Query Match      8.0%; Score 10; DB 1; Length 111;
Best Local Similarity 100.0%; Pred. NO. 0.0024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      61 SGVPDRFSGS 70
Db      57 SGVPDRFSGS 66
Search completed: October 9, 2002, 19:23:36
Job time : 3.45918 secs

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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:14:10 ; Search time 9.65689 seconds
(without alignments)
2024.299 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 113
Sequence: 1 EIVLTQSPLSLPTVPGEPAS.....MGLQSPFTFGTKVDIKR 113

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SPTREMBL19.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mbc.*
- 8: sp_organelle.*
- 9: sp_plant.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	15.0	114	4 Q9UL80	Q9ul80 homo sapien
2	14	12.4	108	4 Q9UL83	Q9ul83 homo sapien
3	13	11.5	109	4 Q9UL86	Q9ul86 homo sapien
4	11	9.7	104	11 Q9UL82	Q9i182 mus musculus
5	11	9.7	116	4 Q96PF6	Q96pf6 homo sapien
6	10	8.8	107	4 Q9UL81	Q9ul81 homo sapien
7	10	8.8	108	4 Q96SB0	Q96sb0 homo sapien
8	10	8.8	112	4 Q96JD2	Q96jd2 homo sapien
9	10	8.8	112	4 Q96JD1	Q96jd1 homo sapien
10	10	8.8	116	4 Q96JD0	Q96jd0 homo sapien
11	10	8.8	235	11 Q91W12	Q91w12 mus musculus
12	10	8.8	236	4 Q96E61	Q96e61 homo sapien
13	10	8.8	238	11 Q9NM37	Q9nm37 mus musculus
14	8	7.1	97	11 Q9JL76	Q9j176 mus musculus
15	8	7.1	109	4 Q9UL78	Q9ul78 homo sapien
16	8	7.1	480	4 Q96JV4	Q96jv4 homo sapien

17	7	6.2	99	11	Q9JL74	Q9j174 mus musculus
18	7	6.2	106	5	Q9U410	Q9u410 schistosoma
19	7	6.2	107	4	Q9NSD6	Q9nsd6 homo sapien
20	7	6.2	107	4	Q96SA9	Q96sa9 homo sapien
21	7	6.2	107	11	Q9ERZ9	Q9erz9 mus musculus
22	7	6.2	108	4	Q9UL79	Q9ul79 homo sapien
23	7	6.2	108	4	Q9UL77	Q9ul77 homo sapien
24	7	6.2	108	4	Q9UL70	Q9ul70 homo sapien
25	7	6.2	111	11	Q920E9	Q920e9 mus musculus
26	7	6.2	116	16	Q92CR3	Q92cr3 listeria in
27	7	6.2	130	4	Q9NP29	Q9np29 homo sapien
28	7	6.2	159	16	Q9RXE4	Q9rx4 deinococcus
29	7	6.2	164	5	Q9GN43	Q9gn43 schistosoma
30	7	6.2	186	17	Q9HJE4	Q9hj4 thermoplasma
31	7	6.2	214	11	Q9CRX7	Q9cr7 mus musculus
32	7	6.2	218	11	Q925S1	Q925s1 mus musculus
33	7	6.2	258	2	Q933Q6	Q933q6 shigella fl
34	7	6.2	265	2	Q9WX68	Q9wx68 acetobacter
35	7	6.2	330	10	Q9FM86	Q9fm86 arabidopsis
36	7	6.2	337	2	Q9RJB9	Q9rjb9 streptomyce
37	7	6.2	343	16	Q92VC2	Q92yc2 rhizobium m
38	7	6.2	408	16	Q34765	Q34765 bacillus su
39	7	6.2	443	5	Q9GR71	Q9gr71 leishmania
40	7	6.2	516	3	Q9P340	Q9p340 penicillium
41	7	6.2	581	10	Q9XEK4	Q9xek4 brassica na
42	7	6.2	600	10	Q9SZ13	Q9sz13 arabidopsis
43	7	6.2	763	4	Q9UPX0	Q9upx0 homo sapien
44	7	6.2	801	2	Q9EUH6	Q9euh6 salmonella
45	7	6.2	802	2	Q9EUK1	Q9euk1 salmonella

ALIGNMENTS

RESULT 1

Q9UL80	PRELIMINARY;	PRT;	114 AA.
ID	Q9UL80		
AC	Q9UL80;		
DT	01-MAY-2000 (Tremblrel. 13, Created)		
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)		
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)		
DE	MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=98277139; PubMed=9614934;		
RA	Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,		
RA	Young D.C.;		
RT	"Myosin-reactive autoantibodies in rheumatic carditis and normal fetus".		
RL	Clin. Immunol. Immunopathol. 87:184-192(1998).		
DR	EMBL; AF035034; AAD56270.1; -.		
DR	RSSP; P80362; IWL.		
DR	InterPro; IPR003006; Ig_MHC.		
DR	InterPro; IPR003596; Ig_V.		
DR	Pfam; PF00047; Ig; 1.		
DR	SMART; SM00406; IGV; 1.		
FT	NON_TER 1		
FT	NON_TER 114 114		
SQ	SEQUENCE 114 AA; 12775 MW; 070E31E210D1CB01 CRC64;		

Query Match 15.0%; Score 17; DB 4; Length 114;
Best Local Similarity 100.0%; Pred. No. 1.1e-10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ISRVEADGVVYCMQG 96
IIIIIIIIIIIIIIIIIIII
DB 80 ISRVEADGVVYCMQG 96

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RESULT 2
Q9UL83
ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSP; P80362; IWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 12.4%; Score 14; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.1e-07;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 PFTGPGTKVDIKR 113
Db 95 PFTGPGTKVDIKR 108

RESULT 3
Q9UL86
ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Werwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR HSP; P80362; IWTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DACC83 CRC64;

Query Match 11.5%; Score 13; DB 4; Length 109;

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Best Local Similarity 100.0%; Pred. No. 2.7e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 FTFGPGTKVDIKR 113
Db 97 FTFGPGTKVDIKR 109

RESULT 4
Q9JL82
ID Q9JL82 PRELIMINARY; PRT; 104 AA.
AC Q9JL82;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BA1B/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.";
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206024; AAF69322.1; -.
DR HSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 104 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFDF5F0AALAE CRC64;

Query Match 9.7%; Score 11; DB 11; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ASISCRSSQSL 29
Db 11 ASISCRSSQSL 21

RESULT 5
Q96PF6
ID Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN SDNK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden.";
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
FT NON_TER 1
FT NON_TER 116 116

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```
SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;
Query Match 9.7%; Score 11; DB 4; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.00045;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 PFTGPGTKVD 110
      |||||
Db 95 PFTGPGTKVD 105

RESULT 6
Q9UL81 ID Q9UL81 PRELIMINARY; PRT; 107 AA.
AC Q9UL81;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.D., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035033; AAD56269.1; -
DR HSP: P01607; IREI.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IgV; 1.
FT NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 8.8%; Score 10; DB 4; Length 107;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 TFGPGTKVDI 111
      |||||
Db 96 TFGPGTKVDI 105

RESULT 7
Q96SH0 ID Q96SH0 PRELIMINARY; PRT; 108 AA.
AC Q96SH0;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Addison E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes."
RL J. Immunol. 161:2020-2031(1998).
DR EMBL: U96394; AAB68783.1; -
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FT NON_TER 1
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;
Query Match 8.8%; Score 10; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 0.0054;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVDPDRFSGS 70
      |||||
Db 57 SGVDPDRFSGS 66

RESULT 8
Q96JD2 ID Q96JD2 PRELIMINARY; PRT; 112 AA.
AC Q96JD2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION NEG (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BONE MARROW;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT "Amyloid lambda 6 light chain variable region NEG."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF267873; AAK58585.1; -
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 11908 MW; 080B4B37E2360B06 CRC64;

Query Match 8.8%; Score 10; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVDPDRFSGS 70
      |||||
Db 57 SGVDPDRFSGS 66

RESULT 9
Q96JDI ID Q96JDI PRELIMINARY; PRT; 112 AA.
AC Q96JDI;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION PIP (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BONE MARROW;
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;
RT "Amyloid lambda 6 light chain variable region PIP."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF267874; AAK58586.1; -
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;

Query Match 8.8%; Score 10; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.0056;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVDPDRFSGS 70
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DBA/2;
 RA MEDLINE=20448942; PubMed=1092488;
 RX Malkiel S., Liao L., Cunningham M.W., Diamond B.;
 RT "T-Cell-dependent antibody response to the dominant epitope of
 streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
 with cardiac myosin";
 RL Infect. Immun. 68:5803-5808(2000).
 DR EMBL; AF206030; AAF69328.1; -;
 DR HSSP; P01679; 2FBJ.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 97
 SQ SEQUENCE 97 AA; 10542 MW; C9EE1FFE1F49DA1C CRC64;

Query Match 7.1%; Score 8; DB 11; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.78; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 80 ISRVEAED 87
 Db 64 ISRVEAED 71
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RESULT 15
 Q9UL78 PRELIMINARY; PRT; 109 AA.
 AC Q9UL78;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
 DE (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98277139; PubMed=9614934;
 RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
 RA Young D.C.;
 RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus";
 RL Clin. Immunol. Immunopathol. 87:184-192(1998).
 DR EMBL; AF035036; AAD56272.1; -;
 DR HSSP; P80362; 1WTL.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 FT NON_TER 1
 FT NON_TER 109
 SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EB197 CRC64;

Query Match 7.1%; Score 8; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.86; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 EIVLTQSP 8
 Db 1 EIVLTQSP 8
 |||||

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:04:24 ; Search time 12.1071 Seconds
(Without alignments)
1036.689 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 592
Sequence: 1 EIVLTQSLPLPTGEPAS.....MQGLQSPFTRGPGTKVDIKR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*		
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22:	/SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB ID	Description
1	592	100.0	113 22 AAEL12705	Human PH1 Fab anti
2	592	100.0	220 22 AAEL12714	Human recombinant
3	592	100.0	381 22 AAEL12707	Human b1vPH1-II-2
4	540	91.2	239 21 AAY82615	Human PTHR monocl
5	537	90.7	239 21 AAY82616	Human PTHR monocl
6	528	89.2	239 21 AAY82617	Human PTHR monocl
7	528	89.2	239 21 AAY82618	Human PTHR monocl
8	527	88.5	112 19 AAY82610	Light chain of a h
9	524	88.0	112 19 AAY82610	Anti-platelet glyc
10	523.5	88.4	114 21 AAY95186	Anti-platelet glyc
11	523.5	88.4	131 21 AAY95226	Anti-platelet glyc

12	522	88.2	112	17	AAR95218	Human IgM GM607 va
13	521	88.0	239	21	AA82611	Human PTHR monocl
14	520	87.8	239	21	AA82614	Human PTHR monocl
15	519.5	87.8	113	21	AA95221	Anti-platelet glyc
16	518.5	87.6	113	21	AA95220	Anti-platelet glyc
17	517.5	87.4	112	21	AA95187	Anti-platelet glyc
18	517.5	87.4	222	22	AA04972	Synthetic antibody
19	517.5	87.4	222	22	AA04976	Synthetic antibody
20	517.5	87.4	248	22	AA68590	Anti-platelet glyc
21	512.5	86.6	111	21	AA95225	Synthetic antibody
22	512.5	86.6	222	22	AA04974	Anti-platelet glyc
23	511	86.3	109	20	AA93909	Human Ab light cha
24	510	86.1	114	18	AAW27544	Consensus single c
25	510	86.1	281	18	AAW27560	Amino acid sequenc
26	507	85.6	112	21	AA818883	Human anti-Rh(D) c
27	505	85.3	112	22	AA93587	Human PTHR monocl
28	504	85.1	239	21	AA82619	Human PTHR monocl
29	502	84.8	113	15	AA85652	Anti-CMV monoclon
30	501	84.6	112	19	AAWS4015	Human Anti-CD4 ant
31	501	84.6	139	22	AA899117	Human protein SEQ
32	497	84.0	239	21	AA82612	Human PTHR monocl
33	497	84.0	239	21	AA82613	Human PTHR monocl
34	488	82.4	143	20	AA934313	IgM antibody CEM 1
35	487	82.3	148	20	AA934309	IgM antibody CEM 1
36	484.5	81.8	113	17	AA889508	Vikappa for antio
37	483	81.6	116	19	AAW76126	Human ICR-8.1 V-K
38	483	81.6	116	19	AAW71256	Humanised murine a
39	483	81.6	116	20	AAW81450	Humanised antibody
40	483	81.6	116	21	AA813046	Protein sequence o
41	483	81.6	116	21	AA82445	Humanised ICR-8.1
42	483	81.6	116	21	AA950753	Humanised murine a
43	482	81.4	112	14	AA932239	Humanised MAB ligh
44	482	81.4	112	18	AAW27145	Mature light chain
45	482	81.4	112	19	AAW40133	Human Mab AB17.1.4

ALIGNMENTS

RESULT 1			
AAEL12705			
ID	AAEL12705 standard; Protein; 113 AA.		
XX	AAEL12705;		
AC	AAEL12705;		
XX			
DT	04-JAN-2002 (first entry)		
XX	Human PH1 Fab antibody variable light chain region (VL).		
DE	Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VL;		
KW	variable light chain region; cancer; breast; ovary; lung; bladder;		
KW	cytostatic; therapy; PH1 antibody.		
XX			
OS	Homo sapiens.		
XX			
FT	Key	Location/Qualifiers	
FT	Region	24..39	
FT		/label= CDR1	
FT		/note= "Complementarity determining region 1"	
FT	Region	55..61	
FT		/label= CDR2	
FT		/note= "Complementarity determining region 2"	
FT	Region	94..102	
FT		/label= CDR3	
FT		/note= "Complementarity determining region 3"	

WO200175110-A2.

11-OCT-2001.

30-MAR-2001; 2001WO-US10589.

30-MAR-2000; 2000US-0538913.

XX PA (DYAX-) DYAX CORP.
 XX PI Hoogenboom HRJM, Henderikx MPG;
 XX DR WPI; 2001-626437/72.
 XX DR N-PSDB; AAD20730.
 XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member
 XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 XX PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX PS Claim 3; Page 93; 126pp; English.
 XX CC The invention relates to an isolated tumour-associated antigen mucin-1
 XX CC (MUC-1)-specific binding member comprising an antigen binding domain
 XX CC region having an antibody variable light (VL) or heavy (VH) region,
 XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
 XX CC detection method selected from enzyme-linked immunosorbent assay,
 XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
 XX CC MUC1-specific binding member is useful for treating cancer, preferably
 XX CC adenocarcinoma, in an individual, where the cancer is present in tissue
 XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 XX CC binding member is useful for diagnosing and imaging MUC1-expressing
 XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 XX CC containing molecules, and for therapeutically or prophylactically
 XX CC treating cancer. The present sequence is anti-MUC1 human PH1 Fab
 XX CC antibody VL region.
 XX SQ Sequence 113 AA;
 Query Match 100.0%; Score 592; DB 22; Length 113;
 Best Local Similarity 100.0%; Pred. No. 7.7e-42;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EIVLTQSPSLPTPGEPASISCRSSQSLHNSNGVTYLDWYIQKPGQSPQLLIYSGSHRA 60
 Db 1 EIVLTQSPSLPTPGEPASISCRSSQSLHNSNGVTYLDWYIQKPGQSPQLLIYSGSHRA 60
 Qy 61 SGVPDRFSGSVSGTDFTLRISRVEADVGYYCMQGLQSPFTFGPTGKVDIKR 113
 Db 61 SGVPDRFSGSVSGTDFTLRISRVEADVGYYCMQGLQSPFTFGPTGKVDIKR 113
 RESULT 2
 AAE12714
 ID AAE12714 standard; Protein; 220 AA.
 XX AC AAE12714;
 XX DT 04-JAN-2002 (first entry)
 XX DE Human recombinant immunoglobulin (Ig) light chain region.
 XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;
 XX KW light chain region; cancer; breast; ovary; lung; bladder;
 XX KW cytostatic; therapy; immunoglobulin; Ig.
 XX OS Homo sapiens.
 XX PN WO200175110-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US10589.
 XX PR 30-MAR-2000; 2000US-0538913.
 XX PA (DYAX-) DYAX CORP.
 XX PI Hoogenboom HRJM, Henderikx MPG;
 XX DR WPI; 2001-626437/72.
 XX DR N-PSDB; AAD20732.

PI Hoogenboom HRJM, Henderikx MPG;
 XX WPI; 2001-626437/72.
 DR N-PSDB; AAD20744.
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
 PT its portion for binding to an epitope of the protein core of mucin-1 -
 XX Claim 12; Page 103; 126pp; English.
 XX CC The invention relates to an isolated tumour-associated antigen mucin-1
 XX CC (MUC-1)-specific binding member comprising an antigen binding domain
 XX CC region having an antibody variable light (VL) or heavy (VH) region,
 XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
 XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
 XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
 XX CC detection method selected from enzyme-linked immunosorbent assay,
 XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
 XX CC MUC1-specific binding member is useful for treating cancer, preferably
 XX CC adenocarcinoma, in an individual, where the cancer is present in tissue
 XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
 XX CC binding member is useful for diagnosing and imaging MUC1-expressing
 XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,
 XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
 XX CC containing molecules, and for therapeutically or prophylactically
 XX CC treating cancer. The present sequence is human recombinant immunoglobulin
 XX CC (Ig) light chain region (variable VL and CL constant kappa light chain).
 XX SQ Sequence 220 AA;
 Query Match 100.0%; Score 592; DB 22; Length 220;
 Best Local Similarity 100.0%; Pred. No. 1.5e-41;
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 EIVLTQSPSLPTPGEPASISCRSSQSLHNSNGVTYLDWYIQKPGQSPQLLIYSGSHRA 60
 Db 1 EIVLTQSPSLPTPGEPASISCRSSQSLHNSNGVTYLDWYIQKPGQSPQLLIYSGSHRA 60
 Qy 61 SGVPDRFSGSVSGTDFTLRISRVEADVGYYCMQGLQSPFTFGPTGKVDIKR 113
 Db 61 SGVPDRFSGSVSGTDFTLRISRVEADVGYYCMQGLQSPFTFGPTGKVDIKR 113
 RESULT 3
 AAE12707
 ID AAE12707 standard; Protein; 381 AA.
 XX AC AAE12707;
 XX DT 04-JAN-2002 (first entry)
 XX DE Human blyPHI-IL-2 immunocytokine protein.
 XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
 XX KW breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
 XX OS Homo sapiens.
 XX PN WO200175110-A2.
 XX PD 11-OCT-2001.
 XX PF 30-MAR-2001; 2001WO-US10589.
 XX PR 30-MAR-2000; 2000US-0538913.
 XX PA (DYAX-) DYAX CORP.
 XX PI Hoogenboom HRJM, Henderikx MPG;
 XX DR WPI; 2001-626437/72.
 XX DR N-PSDB; AAD20732.

XX Novel isolated tumor-associated antigen mucin-1-specific binding member
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
PT its portion for binding to an epitope of the protein core of mucin-1
XX
PS Claim 9; Page 95-97; 126pp; English.
XX
CC The invention relates to an isolated tumour-associated antigen mucin-1
CC (MUC-1)-specific binding member comprising an antigen binding domain
CC region having an antibody variable light (VL) or heavy (VH) region,
CC or a complementarily determining region (CDR) of VL or VH. MUC1-specific
CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
CC The binding of MUC1-specific binding member to MUC1 is detected by a
CC detection method selected from enzyme-linked immunosorbent assay,
CC magnetic resonance imaging, scintillation counting, and X-ray film.
CC MUC1-specific binding member is useful for treating cancer, preferably
CC adenocarcinoma, in an individual, where the cancer is present in tissue
CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
CC binding member is useful for diagnosing and imaging MUC1-expressing
CC cancer cells and tissues, for purifying or isolating non-glycosylated,
CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
CC containing molecules, and for therapeutically or prophylactically
CC treating cancer. The present sequence is human bivPH1-IL-2
CC immunocytokine protein. bivPH1 is mucin specific binding portion.
XX
XX Sequence 381 AA;
SQ
Query Match 100.0%; Score 592; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 2.7e-41;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYKQKQSPQLLIYSGSHRA 60
DB 127 EIVLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYKQKQSPQLLIYSGSHRA 186
QY 61 SGVPRFSGSVSGTDFTLIRSRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
DB 187 SGVPRFSGSVSGTDFTLIRSRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 239
RESULT 4
ID AAY82615
XX AAY82615 standard; Protein; 239 AA.
XX
AC AAY82615;
XX
DT 02-AUG-2000 (first entry)
XX
DE Human PTHrP monoclonal antibody clone 1C1-3 protein SEQ ID NO:14.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 155
FT /note= "possible Ala"
XX
XX JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NISR) JAPAN TOBACCO INC.
XX

DR WPI: 2000-286723/25.
DR N-PSDB: AAA13925.
XX
PT A human monoclonal antibody to parathyroid hormone related protein.
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
XX Claim 31; Page 45-46; 88pp; Japanese.
XX
CC The present invention describes a human monoclonal antibody to
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
CC present invention.
XX
XX Sequence 239 AA;
SQ
Query Match 91.2%; Score 540; DB 21; Length 239;
Best Local Similarity 90.3%; Pred. No. 3.2e-37;
Matches 102; Conservative 6; Mismatches 5; Indels 0; Gaps 0;
QY 1 EIVLTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYKQKQSPQLLIYSGSHRA 60
DB 21 DIVMTQSPSLSPVTPGEPASISCRSSQSLHNSGYTYLDWYKQKQSPQLLIYSGSHRA 80
QY 61 SGVPRFSGSVSGTDFTLIRSRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
DB 81 SGVPRFSGSVSGTDFTLIRSRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 133
RESULT 5
ID AAY82616
XX AAY82616 standard; Protein; 239 AA.
XX
AC AAY82616;
XX
DT 02-AUG-2000 (first entry)
XX
DE Human PTHrP monoclonal antibody clone 2G4-12-20 protein SEQ ID NO:16.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 5
FT /label= Val, Ala, Asp, Gly
FT Misc-difference 13
FT /note= "possibly Leu"
FT Misc-difference 25
FT /label= Ile, Thr, Asn, Ser
FT Misc-difference 27
FT /label= Phe, Ser, Tyr, Cys
FT Misc-difference 216
FT /note= "possible Val"
XX
XX JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX

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XX 17-JUN-1998; 98JP-0188196.
PR 26-JUN-1998; 98JP-0196729.
XX
PA (NISB ) JAPAN TOBACCO INC.
XX
DR WPI: 2000-286723/25.
DR N-PSDB: AAA13926.
XX
PT A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
PS Claim 31; Page 48-49; 88pp; Japanese.
XX
CC The present invention describes a human monoclonal antibody to
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of teeth, periodontal
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
CC present invention.
XX
SQ Sequence 239 AA;
Query Match 90.7%; Score 537; DB 21; Length 239;
Best Local Similarity 89.4%; Pred. NO. 5.7e-37;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 1 EIVTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGSPQLLIYSGSHRA 60
DB 21 DIVMXQPLSLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGSPQLLIYSGSHRA 80
QY 61 SGVPDRFSGSGVTDFTLRIKSRVEADGVVYCMQGLASPTFTFGTKVDIKR 113
DB 81 SGVPDRFSGSGVTDFTLRIKSRVEADGVVYCMQALQTPFTFGTKVDIKR 133
RESULT 6
AAV82617
XX
XX AA82617 standard; Protein; 239 AA.
XX
XX AA82617;
XX
DT 02-AUG-2000 (first entry)
XX
XX Human PTHrP monoclonal antibody clone 3G4-3 protein SEQ ID NO:18.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH MISC-difference 3 /label= Phe, Leu, Ile, Val
FT MISC-difference 4 /label= Leu, Pro, His, Arg
FT MISC-difference 27 /label= Phe, Ser, Tyr, Cys
FT MISC-difference 117 /label= Leu, Ile, Val
XX
XX JP2000080100-A.

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XX 21-MAR-2000.
PD
XX 12-OCT-1998; 98JP-0304793.
PF
XX 17-JUN-1998; 98JP-0188196.
PR 26-JUN-1998; 98JP-0196729.
XX
PA (NISB ) JAPAN TOBACCO INC.
XX
XX WPI: 2000-286723/25.
DR N-PSDB: AAA13927.
XX
PT A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain
XX
PS Claim 31; Page 51-52; 88pp; Japanese.
XX
CC The present invention describes a human monoclonal antibody to
CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of teeth, periodontal
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHrP monoclonal antibody clone protein sequence from the
CC present invention.
XX
SQ Sequence 239 AA;
Query Match 89.2%; Score 528; DB 21; Length 239;
Best Local Similarity 88.5%; Pred. NO. 3.2e-36;
Matches 100; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 EIVTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGSPQLLIYSGSHRA 60
DB 21 DIVMTQPLSLVPTGEPASISCRSSQSLHNSGNLYLDWLQKPGSPQLLIYSGSHRA 80
QY 61 SGVPDRFSGSGVTDFTLRIKSRVEADGVVYCMQGLASPTFTFGTKVDIKR 113
DB 81 SGVPDRFSGSGVTDFTLRIKSRVEADGVVYCMQAXOTPTFTFGTKVDIKR 133
RESULT 7
AAV82618
XX
XX AA82618 standard; Protein; 239 AA.
XX
XX AA82618;
XX
DT 02-AUG-2000 (first entry)
XX
XX Human PTHrP monoclonal antibody clone 4B4-6-21 protein SEQ ID NO:20.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
KW sepsis; systemic inflammatory response syndrome; SIRS;
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FH MISC-difference 25 /label= Ile, Thr, Asn, Ser
FT MISC-difference 27 /label= Phe, Ser, Tyr, Cys
FT MISC-difference 213 /label= Gln, Lys, Glu
FT

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FT Misc-difference 215 /label= Gln, Lys, Glu
FT Misc-difference 219 /label= Cys, Trp
FT Misc-difference 220 /label= Val, Ala, Glu, Gly
FT Misc-difference 222 /label= Ile, Thr, Asn, Ser
XX JP2000080100-A.
XX
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NISB ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX N-PSDB; AAA13928.
XX
XX A human monoclonal antibody to parathyroid hormone related protein.
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain
XX
XX Claim 31; Page 55; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
XX
XX Sequence 239 AA;
XX
Query Match 89.2%; Score 528; DB 21; Length 239;
Best Local Similarity 88.5%; Pred. No. 3.2e-36;
Matches 100; Conservative 6; Mismatches 7; Indels 0; Gaps 0;
QY 1 EIVLTQSPFLSLPVTGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
DB 21 DIVMQXPLSLPVTGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYLSNRA 80
QY 61 SGVPDRFSGSVSGTDFTLRIKSRVEAEADVGVYICMQGLQSPFTFGPGTKVDIKR 113
DB 81 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYICMQTLQPTFTFGPGTKVDIKR 133
RESULT 8
AY82610
ID AAY82610 standard; Protein; 239 AA.
XX
XX AAY82610;
XX
XX 02-AUG-2000 (first entry)
XX
XX Human PTHrP monoclonal antibody clone 15H7-8-3 protein SEQ ID NO:4.
XX
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
XX hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
XX fracture; cachexia; tooth disease; periodontal disease; gingiva;
XX sepsis; systemic inflammatory response syndrome; SIRS;
XX hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

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XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 156 /label= Phe, Ser, Tyr, Cys
FT Misc-difference 164 /label= Phe, Ser, Tyr, Cys
FT
FT
XX JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-0304793.
XX
XX 17-JUN-1998; 98JP-0188196.
XX 26-JUN-1998; 98JP-0196729.
XX
XX (NISB ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
XX N-PSDB; AAA13920.
XX
XX A human monoclonal antibody to parathyroid hormone related protein.
XX useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX including metastasis, and pain
XX
XX Claim 31; Page 33; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment
XX of hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a
XX human PTHrP monoclonal antibody clone protein sequence from the
XX present invention.
XX
XX Sequence 239 AA;
XX
Query Match 89.0%; Score 527; DB 21; Length 239;
Best Local Similarity 88.5%; Pred. No. 3.8e-36;
Matches 100; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 EIVLTQSPFLSLPVTGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
DB 21 DIVMQXPLSLPVTGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYLSNRA 80
QY 61 SGVPDRFSGSVSGTDFTLRIKSRVEAEADVGVYICMQGLQSPFTFGPGTKVDIKR 113
DB 81 SGVPDRFSGSGGTDFTLKISRVEAEDVGVYICMQALQPTFTFGPGTKVDIKR 133
RESULT 9
AAW53586
ID AAW53586 standard; Protein; 112 AA.
XX
XX AAW53586;
XX
XX 23-JUL-1998 (first entry)
XX
XX Light chain of a human antibody.
XX
XX Light chain; human; humanised immunoglobulin; NOK2; Fas ligand;
XX inhibition; apoptosis; Fas expression; treatment; AIDS; rejection;
XX transplant surgery; autoimmune disease; SLE; RA; diabetes.

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XX OS Homo sapiens.
XX PN WO9810070-A1.
XX XX 12-MAR-1998.
XX PD 27-AUG-1997; 97WO-JP02983.
XX PF 20-SEP-1996; 96JP-0271546.
XX PR 02-SEP-1996; 96JP-0231742.
XX XX (SUME ) SUMITOMO ELECTRIC IND CO.
XX XX Eda Y, Higuchi H, Maeda H, Nakata M, Okumura K;
XX PI Ushio Y;
XX XX WPI; 1998-193620/17.
XX XX Human immunoglobulin or its active fragment specific for Fas ligand
XX PT - for treatment of AIDS, organ rejection, autoimmune diseases e.g.
XX PT systemic lupus erythematosus and diabetes
XX XX Disclosure; Page 261; 348pp; Japanese.
XX PS The present sequence represents the light chain of a human antibody, and
XX CC can be used in the humanised immunoglobulin of the invention. The
XX CC humanised immunoglobulin reacts specifically with a region of a Fas
XX CC ligand that is important in inhibiting apoptosis induced by cells with
XX CC Fas expression. The immunoglobulin of the invention can inhibit
XX CC physiological reactions between a Fas ligand and Fas, typified by
XX CC apoptosis. The humanised immunoglobulin is used for treatment of AIDS,
XX CC rejection following transplant surgery, autoimmune diseases such as
XX CC SLE or RA, and diabetes.
XX XX Sequence 112 AA;
XX SQ Query Match 88.5%; Score 524; DB 19; Length 112;
XX Best Local Similarity 87.5%; Pred. No. 3.le-36;
XX Matches 98; Conservative 9; Mismatches 5; Indels 0; Gaps 0;
QY 1 EIVLTQSLPLVTPPEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYSGSHRA 60
DB 1 DIVMTQSLPLVTPPEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYSGNRA 60
QY 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQGLQSPFTFGPTKVDIK 112
DB 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQALQTPYTFGGQTKLEIK 112
RESULT 10
XX AAY95186
XX ID AAY95186 standard; Protein; 114 AA.
XX AC AAY95186;
XX XX 29-AUG-2000 (first entry)
XX DE Anti-platelet glycoprotein Ib human Hib-5 VL.
XX XX Variable light chain; single chain antibody; scFv; human; Hib-5;
XX KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
XX KW antithrombotic; thrombus; therapy; diagnostic.
XX XX Homo sapiens.
XX XX Location/Qualifiers
XX FH Key 1..23
XX FT Region /note= "framework region 1"
XX FT Region 24..39
XX FT Region /note= "complementarity determining region 1"
XX FT Region 40..54
XX FT Region /note= "framework region 2"

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FT Region 55..61 /note= "complementarity determining region 2"
FT Region 62..93 /note= "framework region 3"
FT Region 94..101 /note= "complementarity determining region 3"
FT Region 102..114 /note= "framework region 4"
XX WO200026667-A1.
XX 11-MAY-2000.
XX 29-OCT-1999; 99WO-US25495.
XX 30-OCT-1998; 98US-0106275.
XX (MILL/) MILLER J L.
XX PI Miller JL;
XX WPI; 2000-365744/31.
XX N-PSDB; AAA27664.
XX Isolated nucleic acid molecule encoding anti-human platelet
XX glycoprotein Ib alpha molecule useful for producing antibodies which
XX inhibit platelet aggregation -
XX Claim 11; Page 77; 89pp; English.
XX The present sequence is that of the light chain variable region
XX (VL) of human single chain antibody (scFv) Hib-5, which is directed
XX against platelet glycoprotein Ib (GPiB). The Hib series of scFv
XX was isolated from a human synthetic VH and VL scFv library by 3
XX rounds of phagemid selection against transfected CHO cells
XX expressing the GPiB alpha component of the GPiB/IX/V complex
XX on their surface, followed by a 4th round of selection against
XX washed human platelets, and 2 final rounds in which attempts were
XX made to displace scFv from washed platelets by flooding with
XX murine monoclonal antibody or mimotope peptide (see AAY95229).
XX Whether displayed as surface proteins on a phagemid or secreted
XX as free scFv by Escherichia coli, the Hib scFv clones are capable
XX of inhibiting von Willebrand factor-dependent aggregation of
XX platelets. The scFv are composed of native human protein sequences
XX and are therefore attractive potential reagents for therapeutic
XX purposes. They provide a new class of antithrombotic agents,
XX useful for the prevention of platelet-dependent thrombi in
XX diseased arteries, bypass grafts, dialysis etc., and can also be
XX used as diagnostic reagents. Methods of inhibiting aggregation
XX of platelets, of binding human platelet GPiB alpha and of selecting
XX a VH or VL region of an antibody that inhibits platelet aggregation
XX are claimed.
XX SQ Sequence 114 AA;
XX Query Match 88.4%; Score 523.5; DB 21; Length 114;
XX Best Local Similarity 87.7%; Pred. No. 3.5e-36;
XX Matches 100; Conservative 8; Mismatches 5; Indels 1; Gaps 1;
QY 1 EIVLTQSLPLVTPPEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYSGSHRA 60
DB 1 DIVMTQSLPLVTPPEPASISCRSSQSLHNSGYTYLDWLQKPGSQPLLIIYSGNRA 60
QY 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQGLQSPFTFGPTKVDIKR 113
DB 61 SGVPDRFSGSVSGTDFTLKISRVEAEDVGYYCMQALQTPPFTFGQTKLEIKR 114
RESULT 11
XX AAY95226
XX ID AAY95226 standard; Protein; 131 AA.
XX XX AAY95226;

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XX 29-AUG-2000 (first entry)
 XX DE Anti-platelet glycoprotein Ib human H1b-5 VL region and linker.
 XX DE
 XX KW Variable light chain: single chain antibody; scfv; human; H1b-5;
 KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
 KW antithrombotic; thrombus; therapy; diagnostic.
 XX OS
 XX OS Chimeric - Synthetic.
 XX OS Chimeric - Homo sapiens.
 XX PH
 XX FT Key Location/Qualifiers
 FT Peptide 1..17 "vector-derived linker"
 FT Region 18..131
 FT Region /note= "light chain variable region"
 FT Region 18..40
 FT Region /note= "framework region 1"
 FT Region 41..56
 FT Region /note= "complementarity determining region 1"
 FT Region 57..71
 FT Region /note= "framework region 2"
 FT Region 72..78
 FT Region /note= "complementarity determining region 2"
 FT Region 79..110
 FT Region /note= "framework region 3"
 FT Region 111..119
 FT Region /note= "complementarity determining region 3"
 FT Region 120..131
 FT Region /note= "framework region 4"
 XX WO200026667-A1.
 XX 11-MAY-2000.
 XX 29-OCT-1999; 99WO-US25495.
 XX 30-OCT-1998; 98US-0106275.
 XX (MILLER) MILLER J L.
 XX PI Miller JL;
 XX WPI: 2000-365744/31.
 XX Isolated nucleic acid molecule encoding anti-human platelet
 XX glycoprotein Ib alpha molecule useful for producing antibodies which
 XX inhibit platelet aggregation -
 XX Disclosure; Fig 8; 89pp; English.
 XX The present sequence is that of the light chain variable region
 XX (VL) plus linker peptide of human single chain antibody (scfv)
 XX H1b-5, which is directed against platelet glycoprotein Ib (GP1b).
 XX H1b-5 is composed of a heavy chain variable region and light chain
 XX variable region joined by a vector-derived peptide linker. The
 XX H1b series of scfv was isolated from a human synthetic VH and VL
 XX scfv library by 3 rounds of phagemid selection against transfected
 XX CHO cells expressing the GP1b alpha component of the GP1b/IX/V
 XX complex on their surface, followed by a 4th round of selection
 XX against washed human platelets, and 2 final rounds in which
 XX attempts were made to displace scfv from washed platelets by
 XX flooding with murine monoclonal antibody or mimotope peptide (see
 XX AA95229). Whether displayed as surface proteins on a phagemid or
 XX secreted as free scfv by Escherichia coli, the H1b scfv clones are
 XX capable of inhibiting von Willebrand factor-dependent aggregation of
 XX platelets. The scfv are composed of native human protein sequences
 XX and are therefore attractive potential reagents for therapeutic
 XX purposes. They provide a new class of antithrombotic agents,
 XX useful for the prevention of platelet-dependent thrombi in
 XX diseased arteries, bypass grafts, dialysis etc., and can also be
 XX used as diagnostic reagents. Methods of inhibiting aggregation

CC of platelets, of binding human platelet GP1b alpha and of selecting
 CC a VH or VL region of an antibody that inhibits platelet aggregation
 CC are claimed.
 XX Sequence 131 AA;
 SQ
 Query Match 88.4%; Score 523.5; DB 21; Length 131;
 Best Local Similarity 87.7%; Pred. No. 4.1e-36;
 Matches 100; Conservative 8; Mismatches 5; Indels 1; Gaps 1;
 QY 1 EIVLTQSPPLSLPVTPGEPASISCRSSQSLHNSGYTVLDWYLOKPGQSPQLLIYGSNRA 60
 DB 18 DVMTQSPPLSLPVTPGEPASISCRSSQSLHNSGYNLDWYLOKPGQSPQLLIYGSNRA 77
 QY 61 SGVPRFSGSVSGTDTFLIRISRVEAEADVGVYCMQGLQS-PFTFGPGTKVDIKR 113
 DB 78 SGVPRFSGSVSGTDTFLIRISRVEAEADVGVYCMQALQTPPTFGGQTKLEIKR 131
 RESULT 12
 AAR95218
 ID AAR95218 standard; protein; 112 AA.
 XX AC AAR95218;
 XX DT 16-DEC-1996 (first entry)
 XX DE Human IgM GM607 variable light chain.
 XX KW Antibody; fusion protein; single chain; inhibition; tumour;
 KW diagnosis; detection; imaging; immunotoxin; targeting; assay;
 KW immunosay; Lewis(X) carbohydrate antigen.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FT Domain 24..39
 FT Domain /label= CDR 1.
 FT Domain 55..61
 FT Domain /label= CDR 2.
 FT Domain 89..97
 FT Domain /label= CDR 3.
 XX WO9613594-A1.
 XX 09-MAY-1996.
 XX 26-OCT-1995; 95WO-US13811.
 XX 28-OCT-1994; 94US-0331398.
 XX 28-OCT-1994; 94US-0331396.
 XX 28-OCT-1994; 94US-0331397.
 XX {USSH } US DEPT HEALTH & HUMAN SERVICES.
 XX Benhar I, Brinkmann U, Fitzgerald D, Jung S, Lee B;
 XX Padlan EA, Pai L, Pastan I, Willingham M;
 XX WPI: 1996-251462/25.
 XX Single chain fusion proteins and antibodies - useful to diagnose and
 XX treat cancer, specifically bind Lewis(X) related carbohydrate
 XX antigen
 XX Example 13; Figure 11B; 116pp; English.
 XX A novel recombinant DNA molecule which encodes a single chain fusion
 XX protein or antibody comprising the Fv region of both the light and
 XX heavy chains of an antibody (Ab) fused together, and an effector
 XX molecule, where the fusion protein or Ab has the binding specificity
 XX of monoclonal Ab (MAb) B1, B3 or B5, can be used for the production
 XX of such fusion proteins or antibodies. The fusion proteins can be
 XX used in compositions as an immunotoxin to inhibit tumour cell growth.

CC The single chain antibody can be used to detect the presence or
 CC absence of cells bearing a Lewis(X) carbohydrate antigen in a
 CC patient. The antibodies are also useful as multiple targeting
 CC moieties, providing at least 2 kinds of biological activity. They
 CC can also be used in diagnostic assays and for the imaging of tumours
 CC when attached to a radiolabel and for the pathological diagnosis of
 CC tumours. Humanised antibodies are less immunogenic than the mouse
 CC Mabs B1, B3 and B5, making them more suitable for long term
 CC treatment.

XX Sequence 112 AA;
 SQ Query Match 88.2%; Score 522; DB 17; Length 112;
 Best Local Similarity 89.3%; Pred. No. 4.6e-36;
 Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYSGSHRA 60
 Db 1 DIVMTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYLSNRA 60

Qy 61 SGVPDRFSGVSGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPTKVDIK 112
 Db 61 SGVPDRFSGVSGTDFTLRISRVEAEDGVYVCMQGLQTPQTGGTKVEIK 112

RESULT 13
 AAY82611
 ID AAY82611 standard; Protein; 239 AA.
 XX
 AC AAY82611;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 DE Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.
 XX
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 PN JP2000080100-A.
 XX
 PD 21-MAR-2000.
 XX
 PF 12-OCT-1998; 98JP-0304793.
 XX
 PR 17-JUN-1998; 98JP-0188196.
 XX
 PR 26-JUN-1998; 98JP-0196729.
 XX
 PA (NTSB) JAPAN TOBACCO INC.
 XX
 DR WPI; 2000-286723/25.
 DR N-PSDB; AAA13921.
 XX
 PT A human monoclonal antibody to parathyroid hormone related protein.
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 XX
 PS Claim 31; Page 34-35; 86pp; Japanese.
 XX

CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
 CC the release of calcium from bone; or (c) inhibits elevation of blood
 CC calcium content. The monoclonal antibody can be used in the treatment
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
 CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and

CC antiinflammatory activities. The present sequence represents a
 CC human PTHrP monoclonal antibody clone protein sequence from the
 CC present invention.

XX Sequence 239 AA;
 SQ Query Match 88.0%; Score 521; DB 21; Length 239;
 Best Local Similarity 86.7%; Pred. No. 1.2e-35;
 Matches 98; Conservative 8; Mismatches 7; Indels 0; Gaps 0;

Qy 1 EIVTQSLPLVPTGEPASISCRSSQSLHNSGYTYLDWLQKPGQSPQLLIYSGSHRA 60
 Db 21 DIVMTQSLPLVPTGEPATISCRSSQSLHNRNYYLDWFLQKPGQSPQLLIYLSNRA 80

Qy 61 SGVPDRFSGVSGTDFTLRISRVEAEDGVYVCMQGLQSPFTFGPTKVDIKR 113
 Db 81 SGVPDRFSGVSGTDFTLKLSRVEAEDGVLYYCMQALQIPFTFGPTKVDIKR 133

RESULT 14
 AAY82614
 ID AAY82614 standard; Protein; 239 AA.
 XX
 AC AAY82614;
 XX
 DT 02-AUG-2000 (first entry)
 XX
 DE Human PTHrP monoclonal antibody clone 2F8-10-3 protein SEQ ID NO:12.
 XX
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;
 KW sepsis; systemic inflammatory response syndrome; SIRS;
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 25 /label= Ile, Thr, Asn, Ser
 FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys
 FT Misc-difference 117 /label= Leu, Ile, Val
 FT Misc-difference 146 /label= Phe, Ser, Tyr, Cys
 FT Misc-difference 216 /note= "possible Val"
 XX
 PN JP2000080100-A.
 XX
 PD 21-MAR-2000.
 XX
 PF 12-OCT-1998; 98JP-0304793.
 XX
 PR 17-JUN-1998; 98JP-0188196.
 PR 26-JUN-1998; 98JP-0196729.
 XX
 PA (NTSB) JAPAN TOBACCO INC.
 XX
 DR WPI; 2000-286723/25.
 DR N-PSDB; AAA13924.
 XX
 PT A human monoclonal antibody to parathyroid hormone related protein.
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
 PT including metastasis, and pain
 XX
 PS Claim 31; Page 43; 88pp; Japanese.
 XX

CC The present invention describes a human monoclonal antibody to
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
 CC its fragments, following the stimulation of PTHrP has the following
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits

CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment
CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a
CC human PTHR monoclonal antibody clone protein sequence from the
CC present invention.

XX SQ Sequence 239 AA;

Query Match 87.8%; Score 520; DB 21; Length 239;
Best Local Similarity 87.6%; Pred. No. 1.5e-35;
Matches 99; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYSGSHRA 60
DB 21 DIVMXQXPLSLPVTPGEPASISCRSSQSLHNSGNNYLDWYLOKPGSQPLLIIYSGSNRA 80
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 81 SGVPDRFSGSVSGTDFTLKISRVEAEDGVVYCMQAXQIPFTFGPGTKVDIKR 133

RESULT 15

AAAY95221 standard; Protein; 113 AA.

XX AC AAAY95221;
XX DT 29-AUG-2000 (first entry)
XX DE Anti-platelet glycoprotein Ib human HIB-5 VL.
XX KW Variable light chain; single chain antibody; scFv; human; HIB-5;
KW glycoprotein Ib alpha; platelet; aggregation; antiaggregant;
XX antithrombotic; thrombus; therapy; diagnostic.

XX OS Homo sapiens.
FH Key Location/Qualifiers
FT 1..23 "framework region 1"
FT 24..39 "framework region 1"
FT 40..54 "complementarity determining region 1"
FT 55..61 "framework region 2"
FT 62..93 "complementarity determining region 2"
FT 94..101 "framework region 3"
FT 102..113 "complementarity determining region 3"
FT /note= "framework region 4"

WO2000026667-A1.
11-MAY-2000.
29-OCT-1999; 99WO-US25495.
30-OCT-1998; 98US-0106275.
(MILLER) MILLER J L.
Miller JL;
WPI: 2000-365744/31.

XX Isolated nucleic acid molecule encoding anti-human platelet
PT glycoprotein Ib alpha molecule useful for producing antibodies which

PT inhibit platelet aggregation -
XX Claim 18; Fig 8; 89pp; English.
XX The present sequence is that of the light chain variable region
CC (VL) of human single chain antibody (scFv) HIB-5, which is directed
CC against platelet glycoprotein Ib (GPiB). The HIB series of scFv
CC was isolated from a human synthetic VH and VL scFv library by 3
CC rounds of phagemid selection against transfected CHO cells
CC expressing the GPiB alpha component of the GPIb/IX/V complex
CC on their surface, followed by a 4th round of selection against
CC washed human platelets, and 2 final rounds in which attempts were
CC made to displace scFv from washed platelets by flooding with
CC murine monoclonal antibody or mimotope peptide (see AAY95229).
CC Whether displayed as surface proteins on a phagemid or secreted
CC as free scFv by Escherichia coli, the HIB scFv clones are capable
CC of inhibiting von Willebrand factor-dependent aggregation of
CC platelets. The scFv are composed of native human protein sequences
CC and are therefore attractive potential reagents for therapeutic
CC purposes. They provide a new class of antithrombotic agents,
CC useful for the prevention of platelet-dependent thrombi in
CC diseased arteries, bypass grafts, dialysis etc., and can also be
CC used as diagnostic reagents. Methods of inhibiting aggregation
CC of platelets, of binding human platelet GPiB alpha and of selecting
CC a VH or VL region of an antibody that inhibits platelet aggregation
CC are claimed.
CC Note: The present sequence is not shown in the specification but is
CC derived from the HIB-5 VH sequence given in Fig 8 (see AAY95220).

XX SQ Sequence 113 AA;

Query Match 87.8%; Score 519.5; DB 21; Length 113;
Best Local Similarity 88.5%; Pred. No. 7.5e-36;
Matches 100; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYSGSHRA 60
DB 1 DIVMTQSPLESLPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYSGSNRA 60
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 112
DB 61 SGVPDRFSGSVSGTDFTLKISRVEAEDGVVYCMQALQTPFTFGGQTKLEIK 113

Search completed: October 9, 2002, 19:10:27

Job time : 13.1071 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:09:15 ; Search time 4.61224 Seconds
(without alignments)
598.427 Million cell updates/sec

Title: US-09-822-698A-1
Perfect score: 592
Sequence: 1 EIVLTQSPLSLPVTCPGPAS.....MQGLQSPFTGPGKVKDIKR 113

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep: *
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep: *
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep: *
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep: *
5: /cgn2_6/ptodata/2/iaa/FCRUS_COMB.pep: *
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	532	89.9	113	4	US-09-025-769B-15	Sequence 15, Appl
2	522	88.2	112	1	US-08-331-398A-49	Sequence 49, Appl
3	522	88.2	112	2	US-08-331-397B-49	Sequence 49, Appl
4	522	88.2	112	2	US-08-759-804A-49	Sequence 49, Appl
5	522	88.2	112	4	US-09-227-693-49	Sequence 49, Appl
6	510	86.1	114	4	US-09-025-769B-29	Sequence 29, Appl
7	510	86.1	114	4	US-09-025-769B-45	Sequence 45, Appl
8	510	86.1	281	4	US-09-025-769B-178	Sequence 178, Appl
9	505	85.3	112	4	US-09-240-274-30	Sequence 30, Appl
10	502	84.8	113	1	US-08-082-623-4	Sequence 4, Appl
11	501	84.6	112	1	US-08-478-039-88	Sequence 88, Appl
12	501	84.6	112	1	US-08-476-319A-88	Sequence 88, Appl
13	499	84.3	112	1	US-08-053-171-16	Sequence 16, Appl
14	484.5	81.8	113	1	US-08-264-093-10	Sequence 10, Appl
15	484	81.8	112	1	US-08-331-398A-50	Sequence 50, Appl
16	484	81.8	112	2	US-08-331-397B-50	Sequence 50, Appl
17	484	81.8	112	2	US-08-759-804A-50	Sequence 50, Appl
18	484	81.8	112	4	US-09-227-693-50	Sequence 50, Appl
19	483	81.6	116	1	US-08-482-882-66	Sequence 66, Appl
20	483	81.6	116	2	US-08-483-389-66	Sequence 66, Appl
21	483	81.6	116	2	US-08-487-113D-66	Sequence 66, Appl
22	483	81.6	116	2	US-08-473-503-66	Sequence 66, Appl
23	483	81.6	116	2	US-08-483-932-66	Sequence 66, Appl
24	483	81.6	116	2	US-08-720-420A-66	Sequence 66, Appl
25	483	81.6	116	3	US-08-714-017-66	Sequence 66, Appl
26	483	81.6	116	3	US-08-475-680-66	Sequence 66, Appl
27	482	81.4	112	1	US-08-053-171-15	Sequence 15, Appl

28	482	81.4	112	3	US-08-815-190A-14	Sequence 14, Appl
29	482	81.4	112	4	US-09-000-088-2	Sequence 2, Appl
30	475	80.2	131	1	US-08-129-930B-95	Sequence 95, Appl
31	475	80.2	131	4	US-08-134-346A-50	Sequence 50, Appl
32	475	80.2	131	4	US-08-976-288A-95	Sequence 95, Appl
33	474	80.1	108	1	US-08-488-113B-151	Sequence 151, App
34	474	80.1	108	1	US-08-477-484B-151	Sequence 151, App
35	474	80.1	108	1	US-08-107-669D-15	Sequence 15, Appl
36	474	80.1	108	1	US-08-472-788A-15	Sequence 15, Appl
37	474	80.1	108	2	US-08-477-531B-15	Sequence 15, Appl
38	474	80.1	108	2	US-08-646-360-151	Sequence 151, App
39	474	80.1	108	2	US-08-082-842A-15	Sequence 15, App
40	474	80.1	108	4	US-08-839-765-151	Sequence 151, App
41	474	80.1	108	4	US-09-136-389-151	Sequence 151, App
42	473	79.9	112	1	US-08-478-039-89	Sequence 89, Appl
43	473	79.9	112	1	US-08-476-349A-89	Sequence 89, Appl
44	459	77.5	125	1	US-08-331-398A-67	Sequence 67, Appl
45	459	77.5	125	2	US-08-331-397B-67	Sequence 67, Appl

ALIGNMENTS

RESULT 1
US-09-025-769B-15
; Sequence 15, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-15

Query Match 89.9%; Score 532; DB 4; Length 113;
Best Local Similarity 88.5%; Pred. No. 4.2e-43;
Matches 100; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

US-09-025-769B-29
; Sequence 29, Application US/09025769B
; Patent No. 6300064

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RESOL 6
US-09-025-769B-178
; Sequence 178, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995

```



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; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 178:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 281 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769b-178
;

Query Match 86.1%; Score 510; DB 4; Length 281;
Best Local Similarity 86.7%; Pred. No. 1.3e-40;
Matches 98; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLRKPGSPOLLIIYSGSHRA 60
Db 166 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLRKPGSPOLLIIYSGNRA 225

Qy 61 SGVPDRFSGSVSGTDFTLIRSRVEADGVYVCMQGLQSPFTFGGTVKDIKR 113
Db 226 SGVPDRFSGSVSGTDFTLIRSRVEADGVYVCMQGLQSPFTFGGTVKDIKR 278

RESULT 9
US-09-240-274-30
; Sequence 30, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 112
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain G01
US-09-240-274-30

Query Match 85.3%; Score 505; DB 4; Length 112;
Best Local Similarity 87.3%; Pred. No. 1.4e-40;
Matches 96; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 4 LTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLRKPGSPOLLIIYSGSHRASGV 63
Db 3 LTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLRKPGSPOLLIIYSGSHRASGV 62

Qy 64 PDRFSGSVSGTDFTLIRSRVEADGVYVCMQGLQSPFTFGGTVKDIKR 113
Db 63 PDRFSGSVSGTDFTLIRSRVEADGVYVCMQGLQSPFTFGGTVKDIKR 112

RESULT 10
US-08-082-623-4
; Sequence 4, Application US/08082623
; Patent No. 5750106
; GENERAL INFORMATION:
; APPLICANT: Ostberg, Lars G.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO

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; TITLE OF INVENTION: CYTOMEGALOVIRUS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,623
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010,228
; FILING DATE: 28-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-055-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..113
; OTHER INFORMATION: /note= "The peptide sequence of the
; OTHER INFORMATION: V-1 region of SDZ MSL 109"
US-08-082-623-4

Query Match 84.8%; Score 502; DB 1; Length 113;
Best Local Similarity 85.0%; Pred. No. 2.7e-40;
Matches 96; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

Qy 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLRKPGSPOLLIIYSGSHRA 60
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLRKPGSPOLLIIYSGNRA 60

Qy 61 SGVPDRFSGSVSGTDFTLIRSRVEADGVYVCMQGLQSPFTFGGTVKDIKR 113
Db 61 SGVPDRFSGSVSGTDFTLIRSRVEADGVYVCMQGLQSPFTFGGTVKDIKR 113

RESULT 11
US-08-478-039-88
; Sequence 88, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VK2 consensus
;
; US-08-478-039-88
;
; Query Match 84.6%; Score 501; DB 1; Length 112;
; Best Local Similarity 85.7%; Pred. No. 3.4e-40;
; Matches 96; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
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; Qy 1 EIVLTQSLPLVPTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
; Db 1 DIVMTQSLPLVPTPGEPASISCRSSQSLVHNSGNTYLNWYLQKPGQSPQLLIYKVSNR 60
;
; Qy 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYVYCMQGLQSPFTFGPTKVDIK 112
; Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYVYCMQALQSPYTFGGQTKNEIK 112
;
; RESULT 12
; US-08-476-349A-88
; Sequence 88, Application US/08476349A
; Patent No. 5750105
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; APPLICATION NUMBER: US 07/735,064
; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 88:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: VK2 consensus
;
; US-08-476-349A-88
;
; Query Match 84.6%; Score 501; DB 1; Length 112;
; Best Local Similarity 85.7%; Pred. No. 3.4e-40;
; Matches 96; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
;
; Qy 1 EIVLTQSLPLVPTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
; Db 1 DIVMTQSLPLVPTPGEPASISCRSSQSLVHNSGNTYLNWYLQKPGQSPQLLIYKVSNR 60
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; Qy 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYVYCMQGLQSPFTFGPTKVDIK 112
; Db 61 SGVPDRFSGSGGTDFTLKISRVEAEDVGYVYCMQALQSPYTFGGQTKNEIK 112
;
; RESULT 13
; US-08-053-171-16
; Sequence 16, Application US/08053171
; Patent No. 5562903
; GENERAL INFORMATION:
; APPLICANT: Co. Loibner
; TITLE OF INVENTION: Antibody Derivatives
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-10

Query Match      81.8%; Score 484.5; DB 1; Length 113;
Best Local Similarity 84.1%; Pred. No. 1.2e-38;
Matches 95; Conservative 10; Mismatches 7; Indels 1; Gaps

QY   1 EVLVQTGSLPVTTPGEPAISCRSSSGLIHS -NGVYLDWYLQKPGQSPLLIIYSGR 59
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db    1 DVMVTQTPLSLPTTPEPASISCRSSLSLSDSGNTYLDWYLQKPGSQPLLIIYTL 60
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:

QY   60 ASGVPDFRFGSSGSGTFTLIIRSRVEADVGYYICMGLSPETTFGPKKYVDIK 112
      :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||:
Db    61 ASGVPDFRFGSSGSGTFTLIKISRVEADVGYYICMQRIEFPFFTGCKTKVEIK 113
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RESULT 15
US-08-331-398A-50
Sequence 50. Application US/08331398A
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; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Humanized B3 Variable Light
; OTHER INFORMATION: chain (V-L) (HumB3V-L)"
US-08-331-398A-50

Query Match      81.8%; Score 484; DB 1; Length 112;
Best Local Similarity 81.2%; Pred. No. 1.3e-38;
Matches 91; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

Qy 1 EIVLTQSPLSLPVTGPEPASISCRSSQSLHSHNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
   ::::|||||
Db 1 DVLMTQSPLSLPVTGPEPASISCRSSQIIIVHSHNGTYLEWYLQKPGQSPQLLIYKVSNR 60
   ::::|||||

Qy 61 SGVPDRFSGSVGTDFTLRISVEAEDVGVYCMGLOSPETFGPTKVDIK 112
   |||||
Db 61 SGVPDRFSGSGTDFTLRISVEAEDVGVYCFQGSHPVFTFGQGRKVEIK 112
   |||||

Search completed: October 9, 2002, 19:14:04
Job time : 5.61224 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

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Run on:      October 9, 2002, 19:10:35 ; Search time 44.537 Seconds
              (without alignments)
              893.051 Million cell updates/sec
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Title: US-09-822-698A-1

perfect score:

Sequence: 1 EIVLTQSPLSLPVTGPAS.....MQGLQSPFTFGPGTKVDIKR 113

Scoring table: BLOSUM62

Scoring code: BLOSOM2
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seas, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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post-processing: Minimum Match 0%

Post-processing: Minimum Match 0%
Maximum Match 100%

Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents AA Main:*

- ```

database :
pending_patients_AA_Main1 :
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2: /cgn2_6/pdata/2/paa/US06_COMB.pcp.*
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25: /cgn2_6/pdata/2/paa/US101_COMB.pcp.*
26: /cgn2_6/pdata/2/paa/US106_COMB.pcp.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query |        | DB | ID                  | Description        |
|------------|-------|-------|--------|----|---------------------|--------------------|
|            |       | Match | Length |    |                     |                    |
| 1          | 592   | 100.0 | 113    | 19 | US-09-538-913-1     | Sequence 1, Appli  |
| 2          | 592   | 100.0 | 113    | 22 | US-09-822-698A-1    | Sequence 1, Appli  |
| 3          | 592   | 100.0 | 220    | 22 | US-09-822-698A-24   | Sequence 24, Appli |
| 4          | 592   | 100.0 | 381    | 19 | US-09-538-913-5     | Sequence 5, Appli  |
| 5          | 592   | 100.0 | 381    | 22 | US-09-822-698A-5    | Sequence 5, Appli  |
| 6          | 534   | 90.2  | 262    | 1  | PCR-US01-19110-2081 | Sequence 2081, Ap  |
| 7          | 534   | 90.2  | 262    | 22 | US-09-880-748-2081  | Sequence 2081, Ap  |

## RESULT 1

```

RESOLUTION 1
US-09-538-913-1
/ Sequence 1, Application US/09538913
/ GENERAL INFORMATION:
/ APPLICANT: Hooenboom, Hendricus R.J.M.
/ APPLICANT: Henderikx, Paula
/ TITLE OF INVENTION: MUCIN-1 SPECIFIC BIND
/ TITLE OF INVENTION: THEROF
/ FILE REFERENCE: seqlist DYX-15
/ CURRENT APPLICATION NUMBER: US/09/538,913
/ CURRENT FILING DATE: 2000-03-30
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 113
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-538-913-1

```

Query Match 100.0%; Score 592; DB 19; Length 113;

|                       |              |                    |               |             |
|-----------------------|--------------|--------------------|---------------|-------------|
| Query Match           | 100.0%;      | Score 392;         | DB 19;        | Length 113; |
| Best Local Similarity | 100.0%;      | Pred. No. 8.1e-50; |               |             |
| Matches 113;          | Conservative | 0;                 | Mismatches 0; | Indels 0;   |
| Gaps                  | 0;           |                    |               |             |

QY 1 EIVLTQSP<sup>LS</sup>LPVTPGEPASISCRSSQ<sup>LL</sup>HSNGYTYLDWY<sup>LQ</sup>KPGQSP<sup>OLLI</sup>YSGSHRA 60

|  |     |   |                                                                  |    |
|--|-----|---|------------------------------------------------------------------|----|
|  | QY  | 1 | EIVLIQSPFLSEUFAVFGEFASISCRSSQSLLHSNGTIIIDWILQAAPGGSFQUILLIISGRRA | 60 |
|  |     |   |                                                                  |    |
|  |     |   |                                                                  |    |
|  |     |   |                                                                  |    |
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|  |     |   |                                                                  |    |
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|  | Dbb | 1 | EIVLTQSPISLPVTPGEPASISCRRSSQSLLHNSGYTYLDWLQKPGQSPALLIYSGRRA      | 60 |

QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGYYCMQGLQSPFTFGPGTKVDIKR 113

|    |                                                        |     |
|----|--------------------------------------------------------|-----|
| 57 | CGVDFATSGVSVGGIGCTATKTSKREKEDGVLLCMQDQGFETFGQAINVDIAKR | 113 |
| 58 |                                                        |     |
| 59 |                                                        |     |
| 60 |                                                        |     |
| 61 | SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYVCMQGLQSPFTFGPGTKVVDIKR | 113 |
| 62 |                                                        |     |

```
RESULT 2
US-09-822-698A-1
; Sequence 1, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 1
; LENGTH: 113
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: light chain variable region of the MUC1-specific
; OTHER INFORMATION: binding domain of PH1 Fab antibody
US-09-822-698A-1
Query Match 100.0%; Score 592; DB 22; Length 113;
Best Local Similarity 100.0%; Pred. No. 8.1e-50;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 60
Db 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 60
Qy 61 SGVPDRFSGVSGTDFTLRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGVSGTDFTLRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
RESULT 3
US-09-822-698A-24
; Sequence 24, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 24
; LENGTH: 220
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: immunoglobulin kappa light chain of MUC1-specific PH1-IgG1
US-09-822-698A-24
Query Match 100.0%; Score 592; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.8e-49;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 60
Db 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 60
Qy 61 SGVPDRFSGVSGTDFTLRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGVSGTDFTLRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
```

```
RESULT 4
US-09-538-913-5
; Sequence 5, Application US/09538913
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Paula
; TITLE OF INVENTION: MUCIN-1 SPECIFIC BINDING MEMBERS AND METHODS OF USE
; FILE REFERENCE: seqlist DYX-15
; CURRENT APPLICATION NUMBER: US/09/538,913
; CURRENT FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: amino acid
; OTHER INFORMATION: sequence for b1vPHI-IL-2 immunocytokine fusion
; OTHER INFORMATION: protein
; OTHER INFORMATION: protein
US-09-538-913-5
Query Match 100.0%; Score 592; DB 19; Length 381;
Best Local Similarity 100.0%; Pred. No. 3.3e-49;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 60
Db 127 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 186
Qy 61 SGVPDRFSGVSGTDFTLRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 187 SGVPDRFSGVSGTDFTLRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 239
RESULT 5
US-09-822-698A-5
; Sequence 5, Application US/09822698A
; GENERAL INFORMATION:
; APPLICANT: Hoogenboom, Hendricus R.J.M.
; APPLICANT: Henderikx, Maria P.G.
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof
; FILE REFERENCE: DYX-015.1 US
; CURRENT APPLICATION NUMBER: US/09/822,698A
; CURRENT FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: US 09/538,913
; PRIOR FILING DATE: 2000-03-30
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Microsoft Word
; SEQ ID NO 5
; LENGTH: 381
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: MUC1-specific immunocytokine b1vPHI-IL-2
US-09-822-698A-5
Query Match 100.0%; Score 592; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 3.3e-49;
Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 60
Db 127 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 186
Qy 61 SGVPDRFSGVSGTDFTLRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 113
Db 187 SGVPDRFSGVSGTDFTLRISRVAEADVGVYCMQGLQSPFTFGPGTKVDIKR 239
RESULT 6
PCT-US01-19110-2081
```

```
; Sequence 2081, Application PC/TUS0119110
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523PCT
; CURRENT APPLICATION NUMBER: PCT/US01/19110
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US01-19110-2081

Query Match 90.2%; Score 534; DB 1; Length 262;
Best Local Similarity 90.3%; Pred. No. 1e-43;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPOLLIIYSGSHRA 60
DB 150 EIVMTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPOLLIIYSGSRA 209

QY 61 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYVCMQGLQSPFTFGPGTKVDIKR 113
DB 210 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYVCMQALQPTPLTFGGTKVEIKR 262

RESULT 7
US-09-880-748-2081
; Sequence 2081, Application US/09880748
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2081
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2081

Query Match 90.2%; Score 534; DB 22; Length 262;
Best Local Similarity 90.3%; Pred. No. 1e-43;
Matches 102; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPOLLIIYSGSHRA 60
DB 150 EIVMTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPOLLIIYSGSRA 209
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```
QY 61 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYVCMQGLQSPFTFGPGTKVDIKR 113
DB 210 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYVCMQALQPTPLTFGGTKVEIKR 262

RESULT 8
US-09-490-070-15
; Sequence 15, Application US/09490070
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/025,769
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 113 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-490-070-15

Query Match 89.9%; Score 532; DB 18; Length 113;
Best Local Similarity 88.5%; Pred. No. 6e-44;
Matches 100; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPOLLIIYSGSHRA 60
DB 1 DIVMTQSPVLSPLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGQSPOLLIIYSGSRA 60

QY 61 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYVCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFSGSVSGTDTFLIRSRVEADVGYYVCMQALQPTPLTFGGTKVEIKR 113

RESULT 9
US-08-700-737-8
; Sequence 8, Application US/08700737
; GENERAL INFORMATION:
; APPLICANT: Ponath, Paul D.
; APPLICANT: Ringler, Douglas J.
; APPLICANT: Jones, S. Farran
; APPLICANT: Newman, Walter
```





```

RESULT 13
US-08-331-396-49
; Sequence 49, Application US/08331396
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira
; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Byungkook
; TITLE OF INVENTION: HUMANIZED TUMOR-SPECIFIC ANTIBODY
; TITLE OF INVENTION: FRAGMENTS, FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 50
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourie and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,396
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM GM607 VL region"
US-08-331-396-49

Query Match 88.28; Score 522; DB 7; Length 112;
Best Local Similarity 89.3%; Pred. No. 5.6e-43;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60

QY 1 EIVLTQSPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60

QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEADVGVYICMQGLQSPFTFGPGTKVDIK 112
Db 61 SGVPDRFSGSVSGTDFTLRISRVEAEADVGVYICMQGLQSPFTFGPGTKVDIK 112

RESULT 14
US-08-331-396A-49
; Sequence 49, Application US/08331396A
; GENERAL INFORMATION:
; APPLICANT: PASTAN, Ira H.

```

```

; APPLICANT: BENHAR, Itai
; APPLICANT: PADLAN, Eduardo A.
; APPLICANT: JUNG, Sun-Hee
; APPLICANT: LEE, Byungkook
; TITLE OF INVENTION: TUMOR-SPECIFIC ANTIBODY FRAGMENTS,
; TITLE OF INVENTION: FUSION PROTEINS, AND USES THEREOF
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: Stewart Street Tower, One Market Plaza
; CITY: San Francisco
; STATE: California
; COUNTRY: US
; ZIP: 94105-1493
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,396A
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-126-1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM GM607 VL
; OTHER INFORMATION: region"
US-08-331-396A-49

Query Match 88.28; Score 522; DB 7; Length 112;
Best Local Similarity 89.3%; Pred. No. 5.6e-43;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSPLSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60

QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEADVGVYICMQGLQSPFTFGPGTKVDIK 112
Db 61 SGVPDRFSGSVSGTDFTLRISRVEAEADVGVYICMQGLQSPFTFGPGTKVDIK 112

RESULT 15
US-08-331-396C-49
; Sequence 49, Application US/08331396C
; GENERAL INFORMATION:
; APPLICANT: Pastan, Ira
; APPLICANT: Benhar, Itai
; APPLICANT: Padlan, Eduardo A.
; APPLICANT: Jung, Sun-Hee
; APPLICANT: Lee, Byungkook
; TITLE OF INVENTION: Humanized Tumor-Specific Antibody Fragments,

```

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; TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,396C
; FILING DATE: 28-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/767,331
; FILING DATE: 30-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/596,289
; FILING DATE: 12-OCT-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 015280-126130US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 49:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..112
; OTHER INFORMATION: /note= "Human IgM antibody GM607
; OTHER INFORMATION: Variable Light chain (V-L)"
US-08-331-396C-49

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Query Match 88.2%; Score 522; DB 7; Length 112;
Best Local Similarity 89.3%; Pred. No. 5.6e-43;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 EIVLTQSPVLSPLVPTGCEPASISCRSSQSLHNSGYLYLDWYLOKPGOSPOLLIYSGSHRA 60
Db 1 DIVMTQSPVLSPLVPTGCEPASISCRSSQSLHNSGYLYLDWYLOKPGOSPOLLIYSGSHRA 60

Qy 61 SGVPDRFSGSVGCTDFTLRISVEAEADVGVVYCMQGLQSPFTFGPTGKVDIK 112
Db 61 SGVPDRFSGSVGCTDFTLRISVEAEADVGVVYCMQGLQSPFTFGPTGKVDIK 112

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Search completed: October 9, 2002, 19:19:26  
Job time : 45.537 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:11:10 ; Search time 14.9898 Seconds

(without alignments)  
2085.589 Million cell updates/sec

Title: US-09-822-698a-1

Perfect score: 592

Sequence: 1 EIVLTQSPVLPVTPGEPAS.....MQGLQSPFTFGPCTKVDIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1006125 seqs, 276659714 residues

Total number of hits satisfying chosen parameters: 1006125

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*
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- 7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description          |
|------------|-------|---------------|--------|-------|----------------------|
| 1          | 540   | 91.2          | 114    | 5     | US-09-791-537-86326  |
| 2          | 533   | 90.0          | 136    | 5     | US-09-791-537-71827  |
| 3          | 533   | 90.0          | 137    | 5     | US-09-791-537-56427  |
| 4          | 531   | 89.7          | 114    | 5     | US-09-791-537-86001  |
| 5          | 529   | 89.4          | 116    | 5     | US-09-791-537-43479  |
| 6          | 529   | 89.4          | 117    | 5     | US-09-791-537-48291  |
| 7          | 529   | 89.4          | 118    | 5     | US-09-791-537-129360 |
| 8          | 529   | 89.4          | 135    | 5     | US-09-791-537-12279  |
| 9          | 529   | 89.4          | 135    | 5     | US-09-791-537-123428 |
| 10         | 528   | 89.2          | 112    | 5     | US-09-791-537-21285  |
| 11         | 527   | 89.0          | 114    | 5     | US-09-791-537-137519 |
| 12         | 527   | 89.0          | 117    | 5     | US-09-791-537-107503 |
| 13         | 526   | 88.9          | 113    | 5     | US-09-791-537-59499  |
| 14         | 524   | 88.5          | 125    | 6     | US-10-010-942B-6     |
| 15         | 524   | 88.5          | 132    | 5     | US-09-791-537-78289  |
| 16         | 523   | 88.3          | 118    | 5     | US-09-791-537-54839  |
| 17         | 522   | 88.2          | 112    | 5     | US-09-791-537-21281  |
| 18         | 522   | 88.2          | 112    | 5     | US-09-791-537-110202 |
| 19         | 522   | 88.0          | 125    | 5     | US-09-791-537-26052  |
| 20         | 521   | 88.0          | 112    | 5     | US-09-791-537-34978  |
| 21         | 521   | 88.0          | 113    | 5     | US-09-791-537-64225  |
| 22         | 520.5 | 87.9          | 115    | 5     | US-09-791-537-137518 |
| 23         | 520   | 87.8          | 112    | 5     | US-09-791-537-110195 |
| 24         | 516   | 87.2          | 113    | 5     | US-09-791-537-106796 |
| 25         | 513   | 86.7          | 239    | 5     | US-09-992-600A-8     |
| 26         | 511.5 | 86.4          | 114    | 5     | US-09-791-537-64706  |

ALIGNMENTS

RESULT 1

US-09-791-537-86326  
; Sequence 86326, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 86326  
; LENGTH: 114  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-86326

Query Match 91.2%; Score 540; DB 5; Length 114;  
Best Local Similarity 91.2%; Pred. No. 5.7e-34;  
Matches 103; Conservative 5; Mismatches 5; Indels 0; Gaps 0;  
QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60  
Db 1 DIVMTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSNRA 60  
QY 61 SGVPDRSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTFGPCTKVDIKR 113  
Db 61 SGVPDRSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTFGPCTKVDIKR 113

RESULT 2

US-09-791-537-71827  
; Sequence 71827, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 71827  
; LENGTH: 136

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-71827

Query Match 90.0%; Score 533; DB 5; Length 136;
Best Local Similarity 89.4%; Pred. No. 2.3e-33;
Matches 101; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPQLLIYSGSHRA 60
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Db 21 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGSQPQLLIYLSNRA 80
 :||:||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 SGVPDRFSGVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
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Db 81 SGVPDRFSGSGTDFTLKISRVEAEDGVVYCMQALQTPWTFGGTKVEIKR 133
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RESULT 3
US-09-791-537-56427
; Sequence 56427, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56427
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-56427

Query Match 90.0%; Score 533; DB 5; Length 137;
Best Local Similarity 89.4%; Pred. No. 2.3e-33;
Matches 101; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPQLLIYSGSHRA 60
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Db 21 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGSQPQLLIYLSNRA 80
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QY 61 SGVPDRFSGVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
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Db 81 SGVPDRFSGSGTDFTLKISRVEAEDGVVYCMQALQTPWTFGGTKVEIKR 133
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RESULT 4
US-09-791-537-86001
; Sequence 86001, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 86001
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-86001

Query Match 89.7%; Score 531; DB 5; Length 114;
Best Local Similarity 89.4%; Pred. No. 2.7e-33;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
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QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPQLLIYSGSHRA 60
 :||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGSQPQLLIYLSNRA 60
 :||:||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 SGVPDRFSGVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 SGVPDRFSGSGTDFTLKISRVEAEDGVVYCMQALQTPWTFGGTKVEIKR 113
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-09-791-537-43479
; Sequence 43479, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 43479
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-43479

Query Match 89.4%; Score 529; DB 5; Length 116;
Best Local Similarity 89.4%; Pred. No. 3.9e-33;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPQLLIYSGSHRA 60
 :||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 4 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGSQPQLLIYLSNRA 63
 :||:||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 SGVPDRFSGVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
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Db 64 SGVPDRFSGSGTDFTLKISRVEAEDGVVYCMQALQTPWTFGGTKVEIKR 116
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RESULT 6
US-09-791-537-48291
; Sequence 48291, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 48291
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-48291

Query Match 89.4%; Score 529; DB 5; Length 117;
Best Local Similarity 89.4%; Pred. No. 4e-33;
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPQLLIYSGSHRA 60
 :||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 5 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYNYLDWYLOKPGSQPQLLIYLSNRA 64
 :||:||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 SGVPDRFSGVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 65 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 117

## RESULT 7

US-09-791-537-129360

; Sequence 129360, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 129360

; LENGTH: 118

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-129360

Query Match 89.4%; Score 529; DB 5; Length 118;

Best Local Similarity 89.4%; Pred. No. 4e-33;

Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYSGSHRA 60

Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYLSNRA 60

QY 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 113

Db 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 113

## RESULT 8

US-09-791-537-12279

; Sequence 12279, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 12279

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-12279

Query Match 89.4%; Score 529; DB 5; Length 135;

Best Local Similarity 89.4%; Pred. No. 4.5e-33;

Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYSGSHRA 60

Db 14 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYLSNRA 73

QY 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 113

Db 74 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 126

## RESULT 9

US-09-791-537-123428

; Sequence 123428, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 123428

; LENGTH: 135

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-123428

Query Match 89.4%; Score 529; DB 5; Length 135;

Best Local Similarity 89.4%; Pred. No. 4.5e-33;

Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYSGSHRA 60

Db 14 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYLSNRA 73

QY 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 113

Db 74 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 126

## RESULT 10

US-09-791-537-21285

; Sequence 21285, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537

; CURRENT FILING DATE: 2001-02-22

; NUMBER OF SEQ ID NOS: 153055

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 21285

; LENGTH: 112

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-791-537-21285

Query Match 89.2%; Score 528; DB 5; Length 112;

Best Local Similarity 89.3%; Pred. No. 4.6e-33;

Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYSGSHRA 60

Db 1 DIVMTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYLSNRA 60

QY 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 112

Db 61 SGVPRFSGSGGDTFTLKISRVEADVGVYCMQALQTPQTGGQTKVEIKR 112

## RESULT 11

US-09-791-537-137519

; Sequence 137519, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.

; APPLICANT: Debe, Derek

; APPLICANT: Danzer, Joseph

; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS

; TITLE OF INVENTION: METHODS OF USE THEREOF

; FILE REFERENCE: 261/210

; CURRENT APPLICATION NUMBER: US/09/791,537



```

Query Match 88.5%; Score 524; DB 5; Length 132;
Best Local Similarity 89.3%; Pred. No. 1.1e-32;
Matches 100; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 21 DIVMTQSPVLPVTPGEPASISCRSSQSLHLSNGYTYLDWYLOKPGQSPQLLIYLSNRA 80
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SGVPDRFGSGVSGTDFTLIRISRVEADVGYYCMQGLQSPPTFGPGTKVDIK 112
 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 81 SGVPDRFGSGVSGTDFTLIRISRVEADVGYYCMQGLQSPPTFGPGTKVKEIK 132

```

Search completed: October 9, 2002, 19:21:22  
 Job time : 14.9898 secs





GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:07:45 ; Search time 6.05357 Seconds  
(without alignments)  
1793.668 Million cell updates/sec

Title: US-09-822-698a-1

Perfect score: 592  
Sequence: 1 EIVLTQSPSLPVTGPGEAS.....MQGLQSPFTFGPTKVDIKR 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 533   | 90.0        | 136    | 2 S40357 | Ig kappa chain V-J |
| 2          | 529   | 89.4        | 135    | 2 S40342 | Ig kappa chain - h |
| 3          | 528   | 89.2        | 112    | 2 S58207 | Ig light chain V r |
| 4          | 527   | 89.0        | 117    | 1 K2HUGM | Ig kappa chain pre |
| 5          | 524   | 88.5        | 132    | 2 S26882 | Ig kappa chain V r |
| 6          | 522   | 88.2        | 112    | 2 S58206 | Ig light chain V r |
| 7          | 522   | 88.2        | 125    | 2 S40356 | Ig kappa chain - h |
| 8          | 507.5 | 85.7        | 126    | 2 S40339 | Ig kappa chain - h |
| 9          | 505   | 85.3        | 121    | 2 S40371 | Ig kappa chain - h |
| 10         | 500   | 84.5        | 113    | 1 K2HUTW | Ig kappa chain V-J |
| 11         | 494   | 83.4        | 131    | 2 S40372 | Ig kappa chain V-I |
| 12         | 484   | 81.8        | 124    | 2 S03876 | Ig kappa chain V-I |
| 13         | 478.5 | 80.8        | 112    | 1 K2HUML | Ig kappa chain V-I |
| 14         | 478   | 80.7        | 123    | 2 S40319 | Ig kappa chain V-I |
| 15         | 473.5 | 80.0        | 130    | 2 S40321 | Ig kappa chain - h |
| 16         | 467.5 | 79.0        | 115    | 1 K2HUCM | Ig kappa chain V-I |
| 17         | 467   | 78.9        | 100    | 2 S24681 | Ig kappa chain - h |
| 18         | 457   | 77.2        | 113    | 2 PL0203 | anti-DNA autoantib |
| 19         | 457   | 77.2        | 114    | 2 S40375 | Ig kappa chain - h |
| 20         | 455   | 76.9        | 113    | 1 K2HUCR | Ig kappa chain V-I |
| 21         | 452.5 | 76.4        | 114    | 2 S40340 | Ig kappa chain V-J |
| 22         | 449   | 75.8        | 131    | 2 B39276 | Ig light chain pre |
| 23         | 447   | 75.5        | 142    | 2 S22902 | Ig kappa chain V r |
| 24         | 447   | 75.5        | 219    | 2 S52028 | Ig kappa chain - m |
| 25         | 446   | 75.3        | 133    | 2 S23230 | Ig kappa chain pre |
| 26         | 445.5 | 75.3        | 127    | 2 S40323 | Ig kappa chain - h |
| 27         | 445   | 75.2        | 114    | 2 A32967 | Ig kappa chain V-I |
| 28         | 445   | 75.2        | 133    | 2 S40324 | Ig kappa chain V r |
| 29         | 444   | 75.0        | 112    | 2 A31807 | Ig kappa chain V r |

30 444 75.0 131 2 B30577 Ig kappa chain pre  
31 444 75.0 133 1 K2HURP Ig kappa chain pre  
32 444 75.0 219 2 PC4203 Ig kappa chain (no  
33 443 74.8 112 2 I26317 Ig kappa chain V r  
34 443 74.8 118 2 PT0359 Ig kappa chain V r  
35 443 74.8 197 2 S29593 Ig kappa chain (WM  
36 442.5 74.7 126 2 S40341 Ig kappa chain - h  
37 442 74.7 112 2 G26317 Ig kappa chain V r  
38 442 74.7 112 2 S38719 Ig light chain V r  
39 442 74.7 115 2 S38715 Ig kappa chain V r  
40 442 74.7 122 2 S40338 Ig kappa chain - h  
41 441 74.5 112 2 A26317 Ig kappa chain V r  
42 441 74.5 112 2 F27887 Ig kappa chain V r  
43 441 74.5 112 2 F26317 Ig kappa chain V r  
44 441 74.5 113 2 B41940 Ig light chain V r  
45 441 74.5 126 2 S40312 Ig kappa chain - h

ALIGNMENTS

RESULT 1  
S40357  
Ig kappa chain V-J-C region - human  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40357  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891  
A:Accession: S40357  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-136 <KLE>  
A:Cross-references: EMBL:X72467  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 90.0%; Score 533; DB 2; Length 136;  
Best Local Similarity 89.4%; Pred. No. 6.8e-42; Mismatches 5; Indels 0; Gaps 0;  
Matches 101; Conservative 7;

QY 1 EIVLTQSPSLPVTGPGEASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYSGSHRA 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 21 DIVMTQSPSLPVTGPGEASISCRSSQSLHNSGYTYLDWYLOKPGSQPLLIIYSGNRA 80  
QY 61 SCVPPDRFSGSVSGTDFTLRISRVEADGVYVYCMQGLQSPFTFGPTKVDIKR 113  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 81 SCVPPDRFSGSVSGTDFTLRISRVEADGVYVYCMQGLQSPFTFGPTKVDIKR 133

RESULT 2  
S40342  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C:Accession: S40342  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A:Reference number: S40312; MUID:94080891  
A:Accession: S40342  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-135 <KLE>  
A:Cross-references: EMBL:X72452; NID:9441372; PID:9441373  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 89.4%; Score 529; DB 2; Length 135;

Best Local Similarity 89.4%; Pred. No. 1.6e-41;  
Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGSQPLLIIYSGSRA 60  
:::|||||  
Db 14 DIVMTQSPLSPVTPGEPASISCRSSQSLHNSGYNYLDWYLQKPGSQPLLIIYLSNRA 73  
:  
  
QY 61 SGVPDRFSGSVGTDTFLRISRVEADGVYYCMQGLOSPTFGTGKVDIR 113  
|||  
Db 74 SGVPDRFSGSGTDTFLKRISRVEADVYYICMQALQTPTFGGTKVKIEIR 126  
|||

RESULT 3  
S58207  
Ig light chain V region anti-F(ab')2 - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 13-Jan-1996 #sequence\_revision 19-Apr-1996 #text\_change 21-Jan-2000  
R:Accession: S58207  
C:Welshof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; DoebeI, S.; Breiting,  
submitted to the EMBL Data Library, July 1995  
A:Description: Characterization of heavy and light chain immunoglobulin variable region  
A:Reference number: S58206  
A:Accession: S58207  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-112 <RES>  
C:Cross-references: EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PID:g929643  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMX>

Query Watch 89.2% Score 528 DB 2 Length 112;  
Best Local Similarity 89.3%; Pred. No. 1.6e-41;  
Matches 100; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGSQPLLIIYSGSRA 60  
:::|||||  
Db 1 DIVMTQSPLSPVTPGEPASISCRSSQSLHNSGYNYLDWYLQKPGSQPLLIIYLSNRA 60  
:  
  
QY 61 SGVPDRFSGSVGTDTFLRISRVEADGVYYCMQGLOSPTFGTGKVDIR 112  
|||  
Db 61 SGVPDRFSGSGTDTFLKRISRVEADVYYICMQALQTPTFGGTKVKIEIR 112  
|||

RESULT 4  
K2HUGM  
Ig kappa chain precursor V-II region (GM607) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 16-Jul-1999  
C:Accession: A01889; B24452  
R:Klobeck, H.G.; Solomon, A.; Zachau, H.G.  
Nature 309, 73-76, 1984  
A>Title: Contribution of human V-kappaII germ-line genes to light-chain diversity.  
A:Reference number: A01889; MUID:84191506  
A:Accession: A01889  
A:Molecule type: mRNA  
A:Residues: 1-117 <KLO>  
A>Note: The sequence was determined from the differentiated gene  
C:Genetics:  
A:Gene: GDB:IGKV2  
A:Cross-references: GDB:I36265  
A:Map position: 2p12-zp12  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger complexes.  
C:Superfamily: Immunoglobulin V region; Immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>  
F:5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>  
F:20-99/Domain: immunoglobulin homology <IMX>  
F:27-97/Disulfide bonds: #status predicted

Query Watch 89.0% Score 527 DB 1 Length 117;  
Best Local Similarity 89.4%; Pred. No. 2e-41;

Db 61 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIK 112  
|||||

## RESULT 7

S40356  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
A:Accession: S40356  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
C:Keywords: heterotetramer; immunoglobulin  
A:Reference number: S40312; MUID:94080891  
A:Accession: S40356  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-125 <KLE>  
A:Cross-references: EMBL:X72466; NID:g441400; PID:CAA51134.1; PID:g441401  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:25-104/Domain: immunoglobulin homology <IMM>

Query Match 88.2%; Score 522; DB 2; Length 125;  
Best Local Similarity 88.5%; Pred. No. 6.3e-41;  
Matches 100; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60  
:|||||  
Db 10 DIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSRA 69  
:|||||

QY 61 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 113  
|||||

Db 70 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 122  
|||||

## RESULT 8

S40339  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
A:Accession: S40339  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
C:Keywords: heterotetramer; immunoglobulin  
A:Reference number: S40312; MUID:94080891  
A:Accession: S40339  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-126 <KLE>  
A:Cross-references: EMBL:X72449; NID:g441366; PID:CAA51117.1; PID:g441367  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:31-110/Domain: immunoglobulin homology <IMM>

Query Match 85.7%; Score 507.5; DB 2; Length 126;  
Best Local Similarity 87.5%; Pred. No. 1.3e-39;  
Matches 98; Conservative 7; Mismatches 6; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60  
:|||||

Db 16 DIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSRA 75  
:|||||

QY 61 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 112  
|||||

Db 76 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 126  
|||||

## RESULT 9

S40371  
Ig kappa chain - human  
C:Species: Homo sapiens (man)  
C>Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40371  
R:Klein, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3271, 1993  
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.  
C:Reference number: S40312; MUID:94080891  
A:Accession: S40371  
A:Status: preliminary; translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-121 <KLE>  
A:Cross-references: EMBL:X72481; NID:g441430; PID:CAA51149.1; PID:g441431  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:13-92/Domain: immunoglobulin homology <IMM>

Query Match 85.3%; Score 505; DB 2; Length 121;  
Best Local Similarity 87.3%; Pred. No. 2.2e-39;  
Matches 96; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 4 LTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRASGV 63  
:|||||  
Db 1 MTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRASGV 60  
:|||||

QY 64 PDPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 113  
|||||

Db 61 PDPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 110  
|||||

## RESULT 10

K2HUTW  
Ig kappa chain V-II region (Tew) - human (tentative sequence)  
C:Species: Homo sapiens (man)  
C>Date: 24-Apr-1984 #sequence\_revision 24-Apr-1984 #text\_change 31-Mar-2000  
A:Accession: A90370; A92764; A01888  
R:Putnam, F.W.; Whitley Jr., E.J.; Paul, C.; Davidson, J.N.  
Biochemistry 12, 3763-3780, 1973  
A:Title: Amino acid sequence of a kappa Bence Jones protein from a case of primary am  
A:Reference number: A90370; MUID:74148480  
A:Contents: Bence Jones protein Tew  
A:Accession: A90370  
A:Molecule type: protein  
A:Residues: 1-113 <PUT>  
A:Note: This protein was isolated from the urine of a patient with plasma cell dyscra  
A:Note: the C region of this chain has the Inv (1,2) marker  
R:Terry, W.D.; Page, D.L.; Kimura, S.; Isobe, T.; Osserman, E.F.; Glennier, G.G.  
J. Clin. Invest. 52, 1276-1281, 1973  
A:Title: Structural identity of Bence Jones and amyloid fibril proteins in a patient  
A:Reference number: A92764; MUID:73166638  
A:Contents: amyloid protein Tew  
A:Accession: A92764  
A:Molecule type: protein  
A:Residues: 1-27 <TER>  
A:Note: the major amyloid protein appears to be identical with the Bence Jones protei  
C:Genetics:  
A:Gene: GDB:IGKV2  
A:Cross-references: GDB:136265  
A:Map position: 2p12-2p12  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light ( chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: amyloid; heterotetramer; immunoglobulin  
F:16-95/Domain: immunoglobulin homology <IMM>  
F:23-93/Disulfide bonds: #status predicted

Query Match 84.5%; Score 500; DB 1; Length 113;  
Best Local Similarity 82.3%; Pred. No. 5.8e-39;  
Matches 93; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60  
:|||||

Db 1 DIVMTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYALSNA 60  
:|||||

QY 61 SGVPRFSGSGGDTFLKISRVEADVGYTCMQALQPLTFGGGTKEIKR 113  
|||||

```
Db 61 SGVPDRFSGSGTDTFTLKISRVEAEDGIVYCMZALQAPITFGQGTLEIKR 113
RESULT 11
S40372
Ig kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40372
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40372
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-131 <KLE>
A:Cross-references: EMBL:X72482; NID:g441432; PIDN:CAA51150.1; PID:g441433
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 83.4%; Score 494; DB 2; Length 131;
Best Local Similarity 83.8%; Pred. No. 2.4e-38;
Matches 93; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLISGSHRA 60
Db 21 DIVVTQSPISLPVTPGEPASISCRSSQSLHNSGHNHNYLDWYLQKPGQSPOLLISGSTR 80
QY 61 SGVPDRFSGSGTDTFTLKISRVEAEDGIVYCMQGLQSPFTFGPGTKVDIKR 111
Db 81 SGVPDRFSGSGTDTFTLKISRVEAEDGIVYCMQPLQTPFTFGQGTLEIKR 131
RESULT 12
S03876
Ig kappa chain V-II region (Inc) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S03876
R:Perri, G.; Stopponi, M.; Tadarola, P.; Bellotti, V.; Merlini, G.
Biochim. Biophys. Acta 995, 103-108, 1989
A:Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.
A:Reference number: S03876; MUID:89194238
A:Accession: S03876
A:Molecule type: protein
A:Residues: 1-124 <PER>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 81.8%; Score 484; DB 2; Length 124;
Best Local Similarity 82.3%; Pred. No. 1.9e-37;
Matches 93; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLISGSHRA 60
Db 1 DIVLTQSPISLPVTPGEPASISCRSSQSLHNSGDNWYLDWYLQKPGSQPIVIVLGSNRA 60
QY 61 SGVPDRFSGSGTDTFTLKISRVEAEDGIVYCMQGLQSPFTFGPGTKVDIKR 113
Db 61 SGVPDFTFSGSGTDTFTLLISSVGAEDGVYVCMQALQTPWTFGGQTKVGIRK 113
RESULT 13
K2HDM1
Ig kappa chain V-II region (Mil) - human (tentative sequence)
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 31-Mar-2000
C:Accession: A01887
R:Dreyer, W.J.; Gray, W.R.; Hood, L.
Cold Spring Harb. Symp. Quant. Biol. 32, 353-367, 1967
A:Title: The genetic, molecular, and cellular basis of antibody formation: some facts
A:Reference number: A01887
A:Accession: A01887
A:Molecule type: protein
A:Residues: 1-112 <DRE>
A:Note: the C region of this chain has the Inv (3) marker
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGKV2
A:Cross-references: GDB:I36265
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F;16-94/Domain: immunoglobulin homology <IMM>
F;23-92/Disulfide bonds: #status predicted

Query Match 80.8%; Score 478.5; DB 1; Length 112;
Best Local Similarity 78.8%; Pred. No. 5.4e-37;
Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLISGSHRA 60
Db 1 DIVLTQSPISLPVTPGEPASISCRSSQSLHNSG-BYLDWYLZKPGSPZLLIYLSNRA 59
QY 61 SGVPDRFSGSGTDTFTLKISRVEAEDGVYVCMQGLQSPFTFGPGTKVDIKR 113
Db 60 SGVPDRFSGSGTDTFTLKISRVAZBVGIVYCMQALQTPFTFGGTNVEIKR 112
RESULT 14
S40319
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40319
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40319
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <KLE>
A:Cross-references: EMBL:X72429; NID:g441326; PIDN:CAA51097.1; PID:g441327
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;26-105/Domain: immunoglobulin homology <IMM>

Query Match 80.7%; Score 478; DB 2; Length 123;
Best Local Similarity 90.0%; Pred. No. 6.6e-37;
Matches 90; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 EIVLTQSPISLPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLISGSHRA 60
Db 11 DIVVTQSPISLPVTPGEPASISCRSSQSLHNSGVDWYLDWYLQKPGQSPOLLISGSHRA 70
QY 61 SGVPDRFSGSGTDTFTLKISRVEAEDGVYVCMQGLQSP 100
Db 71 SGVPDRFSGSGTDTFTLKISRVEAEDGVYVCMQALQTP 110
RESULT 15
S40321
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40321
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
```





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:04:54 ; Search time 3.45918 Seconds  
(without alignments)  
1264.839 Million cell updates/sec

Title: US-09-822-698A-1

Perfect score: 592

Sequence: 1 EIVLTQSPSLPVTGPGEPA.....MQGLQSPFTFGPTKVDIKR 113

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match % | Length | ID           | Description         |
|------------|-------|---------------|--------|--------------|---------------------|
| 1          | 527   | 89.0          | 117    | 1 KV2E_HUMAN | P06309 homo sapien  |
| 2          | 500   | 84.5          | 113    | 1 KV2D_HUMAN | P01617 homo sapien  |
| 3          | 478.5 | 80.8          | 112    | 1 KV2C_HUMAN | P01616 homo sapien  |
| 4          | 467.5 | 79.0          | 115    | 1 KV2A_HUMAN | P01614 homo sapien  |
| 5          | 455   | 76.9          | 113    | 1 KV2B_HUMAN | P01615 homo sapien  |
| 6          | 444   | 75.0          | 133    | 1 KV2F_HUMAN | P06310 homo sapien  |
| 7          | 432   | 73.0          | 113    | 1 KV2E_MOUSE | P03976 mus musculus |
| 8          | 429   | 72.5          | 113    | 1 KV2G_MOUSE | P01631 mus musculus |
| 9          | 423   | 71.5          | 113    | 1 KV2F_MOUSE | P01630 mus musculus |
| 10         | 402   | 67.9          | 112    | 1 KV2D_MOUSE | P01629 mus musculus |
| 11         | 394.5 | 66.6          | 108    | 1 KV1_CANFA  | P01618 canis famill |
| 12         | 394   | 66.6          | 113    | 1 KV2C_MOUSE | P01628 mus musculus |
| 13         | 387   | 65.4          | 112    | 1 KV2A_MOUSE | P01626 mus musculus |
| 14         | 370   | 62.5          | 129    | 1 KV3L_HUMAN | P18135 homo sapien  |
| 15         | 369   | 62.3          | 129    | 1 KV3M_HUMAN | P18136 homo sapien  |
| 16         | 368.5 | 62.2          | 114    | 1 KV4A_HUMAN | P01625 homo sapien  |
| 17         | 366.5 | 61.9          | 134    | 1 KV4B_HUMAN | P06314 homo sapien  |
| 18         | 366   | 61.8          | 109    | 1 KV3B_HUMAN | P01620 homo sapien  |
| 19         | 366   | 61.8          | 109    | 1 KV3D_HUMAN | P01621 homo sapien  |
| 20         | 362   | 61.1          | 120    | 1 KV2B_MOUSE | P01627 mus musculus |
| 21         | 357   | 60.3          | 109    | 1 KV2C_HUMAN | P01623 homo sapien  |
| 22         | 357   | 60.3          | 109    | 1 KV3G_HUMAN | P04206 homo sapien  |
| 23         | 354   | 59.8          | 133    | 1 KV4B_HUMAN | P06313 homo sapien  |
| 24         | 351   | 59.3          | 108    | 1 KV3A_HUMAN | P01619 homo sapien  |
| 25         | 349.5 | 59.0          | 128    | 1 KV3K_HUMAN | P06311 homo sapien  |
| 26         | 343.5 | 58.0          | 111    | 1 KV3M_MOUSE | P01665 mus musculus |
| 27         | 340.5 | 57.5          | 111    | 1 KV3L_MOUSE | P01664 mus musculus |
| 28         | 340   | 57.4          | 109    | 1 KV3F_HUMAN | P01624 homo sapien  |
| 29         | 338.5 | 57.2          | 111    | 1 KV3O_MOUSE | P01667 mus musculus |
| 30         | 338.5 | 57.2          | 111    | 1 KV3U_MOUSE | P01673 mus musculus |
| 31         | 338   | 57.1          | 129    | 1 KV3H_HUMAN | P04207 homo sapien  |
| 32         | 336.5 | 56.8          | 111    | 1 KV3S_MOUSE | P01671 mus musculus |
| 33         | 335.5 | 56.7          | 111    | 1 KV3N_MOUSE | P01666 mus musculus |

## RESULT 1

KV2E\_HUMAN  
ID KV2E\_HUMAN STANDARD; PRT; 117 AA.  
AC P06309;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-JAN-1988 (Rel. 06, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region GM607 precursor (Fragment).  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84191506; PubMed=6325927;  
RA Klobbeck H.G., Solomon A., Zachau H.G.;  
RT "Contribution of human V kappa II germ-line genes to light-chain diversity."  
RL Nature 309:73-76(1984).  
CC -----  
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CC -----  
DR EMBL: Z00009; ; NOT\_ANNOTATED\_CDS.  
DR PIR: A01889; K2HUGM.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig; 1.  
DR SMART: SM00406; Igv; 1.  
KW Immunoglobulin V region; Signal.  
FT NON\_TER 1 1  
FT SIGNAL <1 4  
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.  
FT DOMAIN 5 27 FRAMEWORK-1.  
FT DOMAIN 28 43 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 44 58 FRAMEWORK-2.  
FT DOMAIN 59 65 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 66 97 FRAMEWORK-3.  
FT DOMAIN 98 106 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 107 116 FRAMEWORK-4.  
FT DISULFID 27 97 BY SIMILARITY.  
FT NON\_TER 117 117  
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;

Query Match 89.0%; Score 527; DB 1; Length 117;

Best Local Similarity 89.4%; Pred. No. 2e-46;

Matches 101; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTGPGEPAISCRSSQLLHNSGYTYLDWYLOKPCQSPQLLIYSGSRA 60

:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

DB 5 DIYMTQSPSLPVTGPGEPAISCRSSQLLHNSGYNYLDWYLOKPCQSPQLLIYLSGNA 64

|            |            |
|------------|------------|
| KV2C_HUMAN |            |
| ID         | KV2C_HUMAN |
| AC         | P01616;    |
| STANDARD;  | PRT;       |
|            | 112 AA.    |



PIR; A01885; K2HUCM.  
DR InterPro: IPR003006; Ig\_MHC.  
DR Pfam: PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Bence-Jones protein.  
FT DISULFID 24 95  
FT NON\_TER 115 115  
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 79.0%; Score 467.5; DB 1; Length 115;  
Best Local Similarity 79.8%; Pred. No. 1.9e-40;  
Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 0;

QY 1 EIVLTQSPLSLPVTGPEPASISCRSSQLLSHS-NGYTYLDWYLKPGQSPQLLIYSGSRR 59  
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 2 DVVMTQSPFLPVTGLGPASIQCRSSQSLVSYBEGTYLWLYLKAGQSPQLLIYLSYRD 61

QY 60 ASGVDPFRSGSVGTDFTLIRSRVEADVGYYCMOGLQSPFTFGPTKVDIKR 113  
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 62 ASGVDPFRSGSVGTDFTLIRSRVEADVGYYCMOGLQSPFTFGPTKVDIKR 113

RESULT 5  
KV2B\_HUMAN STANDARD; PRT; 113 AA.  
AC P01615;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region FR.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=6253627; PubMed=821524;  
RX Riesen W.F., Jaton J.-C.;  
RA "Variable region sequence of the light chain from a Waldenstrom's IgM  
with specificity for phosphorylcholine."  
RT Biochemistry 15:3829-3833(1976).  
RL -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.  
PIR; A01885; K2HURP.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT SIGNAL 1 20  
FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.  
FT DOMAIN 21 43 FRAMEWORK-1.  
FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.  
FT DOMAIN 60 74 FRAMEWORK-2.  
FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.  
FT DOMAIN 82 113 FRAMEWORK-3.  
FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.  
FT DOMAIN 123 133 FRAMEWORK-4.  
FT DISULFID 43 113 BY SIMILARITY.  
FT NON\_TER 133 133  
SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 75.0%; Score 444; DB 1; Length 133;  
Best Local Similarity 75.2%; Pred. No. 5.3e-38;  
Matches 85; Conservative 15; Mismatches 13; Indels 0; Gaps 0;

QY 1 EIVLTQSPLSLPVTGPEPASISCRSSQSLLSHNGYTYLDWYLKPGQSPQLLIYSGSRR 60  
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 21 DVVMTQSPFLPVTGLGPASIQCRSSQSLVSYDGNNTLNWFQQRPGSPRLIYKVSRRD 80

QY 61 SGVPDRFSGSGTDFTLIRSRVEADVGYYCMOGLQSPFTFGPTKVDIKR 113  
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :  
Db 81 SGVPDRFSGSGTDFTLIRSRVEADVGYYCMOGLQSPFTFGPTKVDIKR 133

RESULT 7  
KV2E\_MOUSE STANDARD; PRT; 113 AA.  
AC P03976;  
DT 23-OCT-1986 (Rel. 02, Created)  
DT 23-OCT-1986 (Rel. 02, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region 17S29.1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC TRISUJE-Hybridoma;
RA MEDLINE=85128968; PubMed=6441768;
RX Abersold R., Herbst H., Grutter T., Chang J.Y., Braun D.G.;
RT "Murine V kappa 25 and V kappa 27 amino-acid sequences of C57Bl/6
RT origin: monoclonal antibodies 17529.1 and 22S25.1 specific for the
RT group A-streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 365:1375-1383(1984).
CC -I- MISCELLANEOUS: ANTI-STREPTOCOCCAL GROUP A CARBOHYDRATE ANTIBODY.
DR PIR; A01912; KVM517.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12390 MW; 4593797046F8DB33 CRC64;

Query Match 73.0%; Score 432; DB 1; Length 113;
Best Local Similarity 75.2%; Pred. No. 7.le-37; Indels 0; Gaps 0;
Matches 85; Conservative 10; Mismatches 18;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGSPQLLIYSGSHRA 60
DB 1 DIVMTQAVSNPVLGTASISCRSSKSLHNSGITYLYWYLQKPGSPQLLIYQMSNLA 60
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFSSGSGTDFTLRISRVEAEDGVVYCAHNLPLPYTFGGGKLEIKR 113

RESULT 8
KV2G_MOUSE STANDARD; PRT; 113 AA.
ID KV2G_MOUSE
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoozobenzene isothiocyanate technique
RT for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).
CC -I- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KVM57S.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 71.5%; Score 423; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 5.7e-36;
Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGSPQLLIYSGSHRA 60
DB 1 DIVMTQAPSAVLPVTPGESVSISSCRSSKSLHNSGNTLYWYFLQRPQCPQLLIYMSNLA 60
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFSSGSGTDFTLRISRVEAEDGVVYCMQQRPEYPTFGGKLEIKR 113
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FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 72.5%; Score 429; DB 1; Length 113;
Best Local Similarity 72.6%; Pred. No. 1.4e-36;
Matches 82; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGSPQLLIYSGSHRA 60
DB 1 DVVMTQTPLSLPVSLGDOASISCRSSQSLVHSNGTYLYNWYLQKAGSPKLLIYKVSNRF 60
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFSGSGTDFTLKISRVEAEDGIYFCSTQTHVPTFGGKLEIKR 113

RESULT 9
KV2F_MOUSE STANDARD; PRT; 113 AA.
ID KV2F_MOUSE
AC P01630;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-II region 7S34.1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=83256427; PubMed=6409088;
RA Chang J.-Y., Herbst H., Abersold R., Braun D.G.;
RT "A new isotype sequence (V kappa 27) of the variable region of kappa-
RT light chains from a mouse hybridoma-derived anti-(streptococcal group
RT A polysaccharide) antibody containing an additional cysteine residue.
RT Application of the dimethylaminoozobenzene isothiocyanate technique
RT for the isolation of peptides.";
RL Biochem. J. 211:173-180(1983).
CC -I- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR; A01913; KVM57S.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;

Query Match 71.5%; Score 423; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 5.7e-36;
Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps 0;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHNSGYTYLDWYLQKPGSPQLLIYSGSHRA 60
DB 1 DIVMTQAPSAVLPVTPGESVSISSCRSSKSLHNSGNTLYWYFLQRPQCPQLLIYMSNLA 60
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
DB 61 SGVPDRFSSGSGTDFTLRISRVEAEDGVVYCMQQRPEYPTFGGKLEIKR 113
```

CC CHAINS.  
CC -!- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF  
CC THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.  
CC PIR; A01907; K2DGM.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 34  
FT DOMAIN 25 49  
FT DOMAIN 35 49  
FT DOMAIN 50 56  
FT DOMAIN 57 88  
FT DOMAIN 89 97  
FT DOMAIN 98 107  
FT DISULFID 23 88  
FT NON\_TER 108 108  
FT SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;  
Query Match 66.6%; Score 394.5; DB 1; Length 108;  
Best Local Similarity 69.0%; Pred. No. 4e-33;  
Matches 78; Conservative 13; Mismatches 17; Indels 5; Gaps 1;  
QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHNSGTYVLDWYLOKPCQSPQLLIYSGSHRA 60  
:||:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||  
DB 1 DIVMTQTPLESLVSGEPASISCRSSQSNL-----DYLNNWYLOKAGQSPRLPEQDSQRA 55  
:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||  
QY 61 SGVPDFRFGSGGDTFTLRISRVRAEDVGVYVCMQGLQSPFTGPGTKVDIKR 113  
:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||  
DB 56 SGVPDFRFGSGGDTFTLRIGRVEADAGIYCMQRSFYPTFGQGRLEVR 108  
:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:||||| 1:|||||  
RESULT 12  
KV2C\_MOUSE  
ID KV2C\_MOUSE STANDARD; PRT; 113 AA.  
AC P01628;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region MOPC 511.  
DE OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=81052016; PubMed=6776396;  
RA Appella E.;  
RT "Amino acid sequence of the light chain variable region of M511, a  
RT phosphorylcholine-binding murine myeloma protein.";  
RT Mol. Immunol. 17:711-718(1980).  
RL CC  
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS PHOSPHORYLCHOLINE.  
CC PIR; A01910; KVM551.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 45 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON\_TER 113 113  
FT SEQUENCE 113 AA; 12496 MW; EBF0DC4DA2BD3450 CRC64;  
Query Match 66.6%; Score 394; DB 1; Length 113;  
Best Local Similarity 69.0%; Pred. No. 4.7e-33;

Matches 78; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EIVLTQSPLSVPTGEPASISCRSSOSLLHSNGTYLDWYLKQPQSPQLLIYSGSHRA 60  
: : : : | | | | | | | | | | : : : : | | | | | | | | | |  
Db 1 DIVITQELSNTVSGESVSISCRSSKSLLYKDGTKVLNWFLOPQQSPQLLIYLMSTRA 60

Qy 61 SGVPDRFGSGVSGTDFTLIRISRVAEADVGVYICMGOGLSFPETFGPKTKVDIKR 113  
| | | | | | | | | | | | | | | | | | | | : : | | | | | : : | |  
Db 61 SGVSDRFSGSGGTDTLEISKRAEDVGVIYCQQLVEYPLTFEGAGTKLELR 113

RESULT 13  
KV2A\_MOUSE STANDARD; PRT; 112 AA.  
ID KV2A\_MOUSE AC P01626;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-II region MOPC 167.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=79000273; PubMed=99160;  
RA Rudikoff S.; Potter W.;  
RT "kappa Chain variable region from MI67, a phosphorylcholine binding myeloma protein.";  
RL Biochemistry 17:2703-2707(1978).  
CC -I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN HAS ALSO BEEN DETERMINED.  
CC PTR: A01908; KMS16.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_V.  
DR Pfam: PF00047; Ig\_1.  
DR SMART; SM00406; Igv; 1.  
KW Immunoglobulin v region.  
FT DOMAIN 1 23  
FT FT 24 39  
FT DOMAIN 24 39  
FT FT 40 54  
FT DOMAIN 40 54  
FT FT 55 61  
FT DOMAIN 55 61  
FT FT 62 93  
FT DOMAIN 62 93  
FT FT 94 102  
FT DOMAIN 94 102  
FT FT 103 112  
FT DISULFID 23 93  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 12349 MW; A58EDEFD640A9726 CRC64;  
  
Query Match 65.4%; Score 387; DB 1; Length 112;  
Best Local Similarity 68.8%; Pred No. 2.4e-32;  
Matches 77; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EIVLTQSPLSVPTGEPASISCRSSOSLLHSNGTYLDWYLKQPQSPQLLIYSGSHRA 60  
: : : : | | | | | | | | | | : : : : | | | | | | | | | |  
Db 1 DIVITQELSNTVSGESVSISCRSSKSLLYKDGTKVLNWFLOPQQSPQLLIYLMSTRA 60

Qy 61 SGVPDRFGSGVSGTDFTLIRISRVAEADVGVYICMGOGLSFPETFGPKTKVDIK 112  
| | | | | | | | | | | | | | | | | | | | : : | | | | | : : | |  
Db 61 SGVSDRFSGSGRTDTLEISKRAEDVGVIYCQQLVEYPLTFEGAGTKLEK 112

RESULT 14  
KV3L\_HUMAN STANDARD; PRT; 129 AA.  
ID KV3L\_HUMAN AC P18135;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region HAH precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

```
DR Pfam: PF00047; ig: 1.
DR SMART: SM00406; Igv: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2BB74D6 CRC64;

Query Match 62.3%; Score 369; DB 1; Length 129;
Best Local Similarity 65.5%; Pred No. 1.8e-30;
Matches 74; Conservative 14; Mismatches 21; Indels 4; Gaps 1;

QY 1 EIVLTQSPVLSPTGPGEASISCRSSQSLHSHNGYTYLDWYLOKPGSPQLLIYSGSHRA 60
Db 21 EIVLTQSPGTLSPGGERATLSRASQSVSS---YLAWYQOKPGQAPRLLIYGASSRA 76

QY 61 SGVPDRFSGSVGCTDFTLRISRVEREDGVYVCMQGLQSPFTFGPGTKVDIKR 113
Db 77 TGIPDRFSGSGCTDFTLRISRLRLEPXFDAFYVYCCQYQYGSPPWTFGGQTKVEIKR 129

Search completed: October 9, 2002, 19:11:04
Job time : 4.45918 secs
```



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:05:30 ; Search time 9.65689 seconds  
(without alignments)  
2024.299 Million cell updates/sec

Title: us-09-822-698a-1  
Perfect score: 592  
Sequence: 1 EIVLTQSPLSLPVTGPAS.....MGLQSPFTFGTKVDIKR 113

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222.

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phase:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rviris:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID        | Description        |
|------------|-------|-------------|--------|-----------|--------------------|
| 1          | 457   | 77.2        | 238    | 11 Q99M37 | Q99M37 mus musculu |
| 2          | 428.5 | 72.4        | 114    | 4 Q9UL80  | Q9UL80 homo sapien |
| 3          | 406   | 68.6        | 104    | 11 Q9UL82 | Q9UL82 mus musculu |
| 4          | 373   | 63.0        | 109    | 4 Q9UL78  | Q9UL78 homo sapien |
| 5          | 369   | 62.3        | 109    | 4 Q9UL86  | Q9UL86 homo sapien |
| 6          | 351.5 | 59.4        | 108    | 4 Q9UL83  | Q9UL83 homo sapien |
| 7          | 340.5 | 57.5        | 111    | 11 Q920E9 | Q920E9 mus musculu |
| 8          | 325.5 | 55.0        | 107    | 11 Q9ER29 | Q9ER29 mus musculu |
| 9          | 322   | 54.4        | 107    | 4 Q9UL81  | Q9UL81 homo sapien |
| 10         | 322   | 54.4        | 109    | 4 Q9UL85  | Q9UL85 homo sapien |
| 11         | 316.5 | 53.5        | 108    | 4 Q9UL77  | Q9UL77 homo sapien |
| 12         | 313   | 52.9        | 106    | 5 Q9UL10  | Q9UL10 schistosoma |
| 13         | 309.5 | 52.3        | 108    | 4 Q9UL79  | Q9UL79 homo sapien |
| 14         | 308   | 52.0        | 107    | 4 Q96SA9  | Q96SA9 homo sapien |
| 15         | 306.5 | 51.8        | 108    | 4 Q9UL70  | Q9UL70 homo sapien |
| 16         | 301.5 | 50.9        | 214    | 11 Q9RIA5 | Q9RIA5 mus musculu |

|    |       |      |     |           |                    |
|----|-------|------|-----|-----------|--------------------|
| 17 | 296.5 | 50.1 | 298 | 11 Q9QYF0 | Q9QYF0 mus musculu |
| 18 | 293.5 | 49.6 | 109 | 11 Q920E6 | Q920E6 mus musculu |
| 19 | 289.5 | 48.9 | 211 | 11 Q9IXL0 | Q9IXL0 mus musculu |
| 20 | 288.5 | 48.7 | 116 | 4 Q96PF6  | Q96PF6 homo sapien |
| 21 | 286   | 48.3 | 235 | 11 Q9IWL2 | Q9IWL2 mus musculu |
| 22 | 284.5 | 48.1 | 103 | 11 Q9JL80 | Q9JL80 mus musculu |
| 23 | 283.5 | 47.9 | 99  | 11 Q9JL74 | Q9JL74 mus musculu |
| 24 | 282.5 | 47.7 | 234 | 11 Q9LWF8 | Q9LWF8 mus musculu |
| 25 | 276.5 | 46.7 | 101 | 11 Q9JL78 | Q9JL78 mus musculu |
| 26 | 270.5 | 45.7 | 233 | 11 Q9LWS9 | Q9LWS9 mus musculu |
| 27 | 265.5 | 44.8 | 97  | 11 Q9UL76 | Q9UL76 mus musculu |
| 28 | 255.5 | 43.2 | 127 | 11 Q925S9 | Q925S9 mus musculu |
| 29 | 249.5 | 42.1 | 109 | 6 Q9N0W5  | Q9N0W5 oryctolagus |
| 30 | 240.5 | 40.6 | 107 | 11 Q9JL84 | Q9JL84 mus musculu |
| 31 | 223.5 | 37.8 | 236 | 4 Q96E61  | Q96E61 homo sapien |
| 32 | 223   | 37.7 | 108 | 4 Q96SB0  | Q96SB0 homo sapien |
| 33 | 222   | 37.5 | 241 | 11 Q92LA6 | Q92LA6 mus musculu |
| 34 | 213.5 | 36.1 | 107 | 4 Q9UL82  | Q9UL82 homo sapien |
| 35 | 211.5 | 35.7 | 218 | 11 Q925S1 | Q925S1 mus musculu |
| 36 | 202.5 | 34.2 | 112 | 4 Q96JDI  | Q96JDI homo sapien |
| 37 | 201   | 34.0 | 107 | 4 Q9NSD6  | Q9NSD6 homo sapien |
| 38 | 198   | 33.4 | 116 | 4 Q96JD0  | Q96JD0 homo sapien |
| 39 | 197   | 33.3 | 112 | 4 Q96JD2  | Q96JD2 homo sapien |
| 40 | 185   | 31.2 | 235 | 11 Q99M11 | Q99M11 mus musculu |
| 41 | 182.5 | 30.8 | 130 | 4 Q9NP29  | Q9NP29 homo sapien |
| 42 | 181   | 30.6 | 233 | 4 Q96I69  | Q96I69 homo sapien |
| 43 | 169   | 28.5 | 233 | 11 Q9IV32 | Q9IV32 m adult mal |
| 44 | 164   | 27.7 | 109 | 11 Q9ET13 | Q9ET13 mus musculu |
| 45 | 151.5 | 25.6 | 154 | 11 Q91XK2 | Q91XK2 mus musculu |

ALIGNMENTS

RESULT 1

Q99M37 Q99M37 PRELIMINARY; PRT; 238 AA.  
AC Q99M37;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 26.3 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS  
RC TISSUE.;  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; BC02035; AAH02035.1; -;  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR003599; Iq.  
DR InterPro; IPR003597; Iq.cl.  
DR InterPro; IPR003600; Iq.cl.  
DR InterPro; IPR003006; Iq\_MHC.  
DR InterPro; IPR003596; Iq\_v.  
DR Pfam; PF00047; Iq; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IG1; 1.  
DR SMART; SM00406; IG; 1.  
DR SMART; SM00410; IG; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.  
SQ SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;

Query Match 77.2%; Score 457; DB 11; Length 238;  
Best Local Similarity 75.2%; Pred. No. 7.3e-44;  
Matches 85; Conservative 16; Mismatches 12; Indels 0; Gaps 0;

Qy 1 EIVLTQSPLSLPVTGPASISCRSSQSLHNSNGYIYLDWYLOKPGQSPQLLIYSGSHRA 60

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Db 20 DVVMTOTPLSLPVSLGQASISCRSSQSIHVSNTYLVLEWYLOKPGSPKLLIYKVSNR 79
QY 61 SGVPDRFSGSGTDTLRLISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
Db 80 SGVPDRFSGSGTDTLRLISRVEAEDGVVYCFQGSHPYTFGSGTKLEIKR 132

RESULT 2
Q9JL80 PRELIMINARY; PRT; 114 AA.
AC Q9JL80.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035034; RAD56270.1; -.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 114
SQ SEQUENCE 114 AA; 12775 MW; 070F31E210D1CB01 CRC64;

Query Match 72.4%; Score 428.5; DB 4; Length 114;
Best Local Similarity 73.7%; Pred. No. 4.9e-41;
Matches 84; Conservative 15; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGTYLVLYWYLOKPGSPOLLIIYSGSHRA 60
Db 1 DVVMTQSPSLPVTPVRQSPASISCRSSQSPVSDGNTYLVNWFQRPQSPRLIIYKVSNRD 60

QY 61 SGVPDRFSGSGTDTLRLISRVEAEDGVVYCMQGLQ-SPFTFGPGTKVDIKR 113
Db 61 SGVPDRFSGSGTDTLRLISRVEAEDGVVYCMQGHPPWTFGGTKVEIKR 114

RESULT 3
Q9JL82 PRELIMINARY; PRT; 104 AA.
AC Q9JL82.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C;
RX MEDLINE=20448942; PubMed=10992488;
RA Walkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
with cardiac myosin.";
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RL Infect. Immun. 68:5803-5808(2000).
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBD5F0AAIAE CRC64;

Query Match 68.6%; Score 406; DB 11; Length 104;
Best Local Similarity 75.0%; Pred. No. 1.6e-38;
Matches 78; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 9 LSLPVTTPGEPASISCRSSQSLHSGTYLVLYWYLOKPGSPOLLIIYSGSHRAGVDPDRFS 68
Db 1 LSLPVSILGQASISCRSSQSLVHTNGNTYLHWYLOKPGSPKLLIYKVSNRFGVDPDRFS 60

QY 69 GSVSGTDTLRLISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIK 112
Db 61 GSGSGTDTLRLISRVEAEDLGVIYFCSTHVPYTFGGTKLEIK 104

RESULT 4
Q9JL78 PRELIMINARY; PRT; 109 AA.
AC Q9JL78.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; RAD56272.1; -.
DR HSSP; P80362; IWTU.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 63.0%; Score 373; DB 4; Length 109;
Best Local Similarity 66.4%; Pred. No. 9.4e-35;
Matches 75; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGTYLVLYWYLOKPGSPOLLIIYSGSHRA 60
Db 1 EIVLTQSPGTLISLPGERATLSCRASQSVSSS----YLAWYQQKRPQAPRLIIYGASSRA 56

QY 61 SGVPDRFSGSGTDTLRLISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKR 113
Db 57 TGIPDRFSGSGTDTLRLISLEPEDCAVYVCQYGSPLTFGGGTKEIKR 109

RESULT 5
Q9JL86 PRELIMINARY; PRT; 109 AA.
ID Q9JL86
AC Q9JL86;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
```





|                                                                              |         |                                                                        |    |
|------------------------------------------------------------------------------|---------|------------------------------------------------------------------------|----|
| Chen P., Deng J.B., Wang Z.L., Han H., Yao L.B., Su C.Z.;                    | Q9UL85; | 01-MAY-2000 (TREMBLrel. 13, Created)                                   | AC |
| Submitted (MAY-2000) to the EMBL/GenBank/DBDJB databases.                    | DT      | 01-MAY-2000 (TREMBLrel. 13, Last sequence update)                      | DT |
| EMBL; AF262753; AAG23804.1; -                                                | DR      | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)                    | DR |
| HSSP; P80362; 1WTL.                                                          | DR      | MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION (FRAGMENT). | DE |
| InterPro; IPR003599; Ig.                                                     | DR      | Homo sapiens (Human).                                                  | OS |
| InterPro; IPR003006; Ig_MHC.                                                 | DR      | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      | OC |
| InterPro; IPR003596; Ig_v.                                                   | DR      | Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.              | OC |
| Pfam; PF00047; Ig; 1.                                                        | DR      | NCBI_TaxID=9606;                                                       | OX |
| SMART; SM00409; Ig; 1.                                                       | DR      | [1]                                                                    | RN |
| SMART; SM00406; Ig; 1.                                                       | DR      | SEQUENCE FROM N.A.                                                     | RP |
| NON_TER 107 107                                                              | FT      | MEDLINE=98277139; PubMed=9614934;                                      | RX |
| SEQUENCE 107 AA; 11784 MW; 2B15EBA6604A26C3 CRC64;                           | SEQ     | Query Match 55.0%; Score 325.5; DB 11; Length 107;                     |    |
|                                                                              |         | Best Local Similarity 58.9%; Pred. No. 2.3e-29;                        |    |
|                                                                              |         | Matches 63; Conservative 18; Mismatches 25; Indels 1; Gaps 1;          |    |
| QY 4 LTOSPLSLPVTGPEPASISCRSSQSLHNSGY-TYLDWYLRKPGSPQLLIYSGSHRASG 62           |         |                                                                        |    |
| Db 1 MTQSPSLAWSVGKVTMSCKSSQVLSNNTQKNYLAWYKRPQSPPELLIYFASTRSSG 60             |         |                                                                        |    |
| QY 63 VPDREFGSGVSGTDFTLIRSRVEADGVYVCMQGLQSPFTFGPKVDIKR 109                   |         |                                                                        |    |
| Db 61 VPDREFGSGVSGTDFTLIRSRVEADGVYVCMQGLQSPFTFGPKVDIKR 107                   |         |                                                                        |    |
| RESULT 9                                                                     |         |                                                                        |    |
| Q9UL81                                                                       |         |                                                                        |    |
| ID Q9UL81 PRELIMINARY; PRT; 107 AA.                                          |         |                                                                        |    |
| AC Q9UL81;                                                                   |         |                                                                        |    |
| DT 01-MAY-2000 (TREMBLrel. 13, Created)                                      |         |                                                                        |    |
| DR 01-MAY-2000 (TREMBLrel. 13, Last sequence update)                         |         |                                                                        |    |
| DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)                       |         |                                                                        |    |
| DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION (FRAGMENT).    |         |                                                                        |    |
| OS Homo sapiens (Human).                                                     |         |                                                                        |    |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;         |         |                                                                        |    |
| OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.                 |         |                                                                        |    |
| OX NCBI_TaxID=9606;                                                          |         |                                                                        |    |
| RN [1]                                                                       |         |                                                                        |    |
| RN SEQUENCE FROM N.A.                                                        |         |                                                                        |    |
| RX MEDLINE=98277139; PubMed=9614934;                                         |         |                                                                        |    |
| RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,               |         |                                                                        |    |
| RA Young D.C.;                                                               |         |                                                                        |    |
| RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."; |         |                                                                        |    |
| RL Clin. Immunol. Immunopathol. 87:184-192(1998).                            |         |                                                                        |    |
| DR EMBL; AF035033; AAD56269.1; -                                             |         |                                                                        |    |
| DR HSSP; P01607; 1REI.                                                       |         |                                                                        |    |
| DR InterPro; IPR003006; Ig_MHC.                                              |         |                                                                        |    |
| DR InterPro; IPR003596; Ig_v.                                                |         |                                                                        |    |
| DR Pfam; PF00047; Ig; 1.                                                     |         |                                                                        |    |
| DR SMART; SM00406; Ig; 1.                                                    |         |                                                                        |    |
| DR SMART; SM00409; Ig; 1.                                                    |         |                                                                        |    |
| DR NON_TER 1 107                                                             |         |                                                                        |    |
| FT NON_TER 107 107                                                           |         |                                                                        |    |
| SEQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;                       |         |                                                                        |    |
| Query Match 54.4%; Score 322; DB 4; Length 107;                              |         |                                                                        |    |
| Best Local Similarity 59.3%; Pred. No. 5.7e-29;                              |         |                                                                        |    |
| Matches 67; Conservative 15; Mismatches 25; Indels 6; Gaps 3;                |         |                                                                        |    |
| QY 1 EIVLTOSPLSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLRKPGSPQLLIYSGSHRA 60           |         |                                                                        |    |
| Db 1 DIQMTQSPSLASVSGDRVITCRASQSI--SN--YLNWYQKRPKAPNLLIYAASISIQ 55            |         |                                                                        |    |
| QY 61 SGVDFRFGSGVSGTDFTLIRSRVEADGVYVCMQGLQSPFTFGPKVDIKR 113                  |         |                                                                        |    |
| Db 56 SGVDFRFGSGVSGTDFTLIRSRVEADGVYVCMQGLQSPFTFGPKVDIKR 107                  |         |                                                                        |    |
| RESULT 10                                                                    |         |                                                                        |    |
| Q9UL85                                                                       |         |                                                                        |    |
| ID Q9UL85 PRELIMINARY; PRT; 109 AA.                                          |         |                                                                        |    |
| AC Q9UL85;                                                                   |         |                                                                        |    |
| DT 01-MAY-2000 (TREMBLrel. 13, Created)                                      |         |                                                                        |    |
| DR 01-MAY-2000 (TREMBLrel. 13, Last sequence update)                         |         |                                                                        |    |
| DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)                       |         |                                                                        |    |
| DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION (FRAGMENT).    |         |                                                                        |    |
| OS Homo sapiens (Human).                                                     |         |                                                                        |    |
| OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;         |         |                                                                        |    |
| OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.                 |         |                                                                        |    |
| OX NCBI_TaxID=9606;                                                          |         |                                                                        |    |
| RN [1]                                                                       |         |                                                                        |    |
| RN SEQUENCE FROM N.A.                                                        |         |                                                                        |    |
| RX MEDLINE=98277139; PubMed=9614934;                                         |         |                                                                        |    |
| RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,               |         |                                                                        |    |
| RA Young D.C.;                                                               |         |                                                                        |    |
| RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."; |         |                                                                        |    |
| RL Clin. Immunol. Immunopathol. 87:184-192(1998).                            |         |                                                                        |    |
| DR EMBL; AF035033; AAD56269.1; -                                             |         |                                                                        |    |
| DR HSSP; P01607; 1REI.                                                       |         |                                                                        |    |
| DR InterPro; IPR003006; Ig_MHC.                                              |         |                                                                        |    |
| DR InterPro; IPR003596; Ig_v.                                                |         |                                                                        |    |
| DR Pfam; PF00047; Ig; 1.                                                     |         |                                                                        |    |
| DR SMART; SM00406; Ig; 1.                                                    |         |                                                                        |    |
| DR SMART; SM00409; Ig; 1.                                                    |         |                                                                        |    |
| DR NON_TER 1 109                                                             |         |                                                                        |    |
| FT NON_TER 109 109                                                           |         |                                                                        |    |
|                                                                              |         |                                                                        |    |

```
Best Local Similarity 54.9%; Pred. No. 2.4e-28;
Matches 62; Conservative 18; Mismatches 28; Indels 5; Gaps 1;

QY 1 EIVLTQSPSLPVTGPPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 :|:||||| :|: :|:||||| :|:||||| :|:||||| :|:||||| :|:||||| :|:|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSI-----SSYLNWYQKPGKAPNLLIYAASLQ 55

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 56 SGVPSRFSGSGGTDFTLTISSLPQEDFATYYCQYSYISWTGEGTKVEIKR 108

RESULT 12
Q9U410 PRELIMINARY; PRT; 106 AA.
ID Q9U410;
AC Q9U410;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MONOCLONAL ANTI-IDIOTYPIC ANTIBODY NP30 IMMUNOGLOBULIN LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP SEQUENCE FROM N.A.
RA Song X.T., Feng Z.Q., Qiu Z.N., Li Y.Q., Huang H.L., Guan X.H.;
RT "Amplification, cloning and sequence analysis of the light chain
RT variable region gene of monoclonal anti-idiotypic antibody NP30 of
RT Schistosoma japonicum.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF207620; AAF19434.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 1
SQ SEQUENCE 106 AA; 11478 MW; F20F544426BAE63E CRC64;

Query Match 52.9%; Score 313; DB 5; Length 106;
Best Local Similarity 54.5%; Pred. No. 6e-28;
Matches 61; Conservative 18; Mismatches 27; Indels 6; Gaps 1;

QY 1 EIVLTQSPSLPVTGPPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 |:||||| :|:||||| :|:||||| :|:||||| :|:||||| :|:||||| :|:|||||
Db 1 ENLTSQPAIMASPGKVTMTCSASSV-----SIVYWLQKPGSSPRLLIYDTSNLA 54

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 112
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 55 SGVPSRFSGSGGTSLTISRWEADATYYCQQTWSYPTFGSGTKLEK 106

RESULT 13
Q9UL79 PRELIMINARY; PRT; 108 AA.
ID Q9UL79;
AC Q9UL79;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
```

```
"Myosin-reactive autoantibodies in rheumatic carditis and normal
fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035035; AAD56271.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Igv; 1.
DR NON_TER 1
FT NON_TER 108
SQ SEQUENCE 108 AA; 11787 MW; DB5845F19724FB4E CRC64;

Query Match 52.3%; Score 309.5; DB 4; Length 108;
Best Local Similarity 55.8%; Pred. No. 1.5e-27;
Matches 63; Conservative 15; Mismatches 30; Indels 5; Gaps 1;

QY 1 EIVLTQSPSLPVTGPPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 :|:||||| :|: :|:||||| :|:||||| :|:||||| :|:||||| :|:|||||
Db 1 DIVMTQSPSLLSASTGDRVTISCRMSQI-----SSYLAWYQKPGKAPPELLIYAASLQ 55

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 56 SGVPSRFSGSGGTDFTLTISLQSDPFIATYYCQYSYFPPTFGGQTKVEIKR 108

RESULT 14
Q96SA9 PRELIMINARY; PRT; 107 AA.
ID Q96SA9;
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN KAPPA LIGHT CHAIN
DE VARIABLE REGION (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=98375893; PubMed=97112075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR NON_TER 1
FT NON_TER 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 52.0%; Score 308; DB 4; Length 107;
Best Local Similarity 55.8%; Pred. No. 2.2e-27;
Matches 63; Conservative 17; Mismatches 27; Indels 6; Gaps 2;

QY 1 EIVLTQSPSLPVTGPPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
 :|:||||| :|: :|:||||| :|:||||| :|:||||| :|:||||| :|:|||||
Db 1 DIQMTQSPSSLSASVGRVTITCRASQSI-----SSYLNWYQKPGKAPKLLIYAASLQ 55

QY 61 SGVPDRFSGSVSGTDFTLIRSRVEADVGYYCMQGLQSPFTFGPGTKVDIKR 113
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 56 SGVPSRFSGSGGTDFTLTISSLPQEDFATYYCQQS-YSTLTGGGQTKVEIKR 107

RESULT 15
Q9UL70 PRELIMINARY; PRT; 108 AA.
ID Q9UL70;
AC Q9UL70;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
```

```
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035044; AAD56280.1; -.
DR HSSP: P01607; 1RET.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 108
FT NON_TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCCA37 CRC64;

Query Match 51.8%; Score 306.5; DB 4; Length 108;
Best Local Similarity 55.8%; Pred. NO. 3.3e-27;
Matches 63; Conservative 17; Mismatches 28; Indels 5; Gaps 2;

QY 1 EIVLTQSPISLPVTPCEPASISCRSSQSLHNSGYTLDWYLQKPGQSPOLLIIYSGSHRA 60
Db 1 DIQMTQSPSSLSASVGDRVTITCRASQGI--SN---YLANWQKPKGVKSLIYAASLTQ 55

QY 61 SGVPRFSGSVSGTDFTLRISRVEADVGYYCMQGLQSPFTFGPTKVDIKR 113
Db 56 SGVPSRFSGSGCTDFTLTISLQPEDVATYYCQKYNAPRTFGPTKLEIKR 108
```

Search completed: October 9, 2002, 19:12:24  
Job time : 10.6569 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:12:30 ; Search time 48.3214 Seconds  
(without alignments)  
1036.689 Million cell updates/sec

Title: US-09-822-698a-26

Perfect score: 451

Sequence: 1 QVQLVSGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPGK 451

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000.

Post-processing: Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

|  | 1:                                                | 2:                                                | 3:                                                | 4:                                                | 5:                                                | 6:                                                | 7:                                                | 8:                                                | 9:                                                | 10:                                               | 11:                                               | 12:                                               | 13:                                               | 14:                                               | 15:                                               | 16:                                               | 17:                                               | 18:                                               | 19:                                               | 20:                                               | 21:                                               | 22:                                               |
|--|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|---------------------------------------------------|
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|  | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                | Humanised HMFg-1 h                                |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 451   | 100.0       | 451    | 22 | AAU0745     |
| 2          | 343   | 76.1        | 461    | 22 | AAU0745     |
| 3          | 342   | 75.8        | 449    | 14 | AAU0745     |
| 4          | 342   | 75.8        | 449    | 17 | AAU0745     |
| 5          | 342   | 75.8        | 449    | 19 | AAU0745     |
| 6          | 342   | 75.8        | 581    | 22 | AAU0745     |
| 7          | 342   | 75.8        | 581    | 22 | AAU0745     |
| 8          | 342   | 75.8        | 731    | 22 | AAU0745     |
| 9          | 342   | 75.8        | 741    | 22 | AAU0745     |
| 10         | 341   | 75.6        | 475    | 22 | AAU0745     |
| 11         | 341   | 75.6        | 476    | 14 | AAU0745     |

|    |     |      |     |    |         |                    |
|----|-----|------|-----|----|---------|--------------------|
| 12 | 341 | 75.6 | 481 | 13 | AAU0745 | Sequence of antio  |
| 13 | 341 | 75.6 | 729 | 22 | AAU0745 | Humanised HMFg-1 h |
| 14 | 341 | 75.6 | 730 | 22 | AAU0745 | Humanised HMFg-1 h |
| 15 | 340 | 75.4 | 730 | 22 | AAU0745 | Humanised HMFg-1 h |
| 16 | 340 | 75.4 | 740 | 22 | AAU0745 | Humanised HMFg-1 h |
| 17 | 340 | 75.4 | 961 | 21 | AAU0745 | Humanised HMFg-1 h |
| 18 | 338 | 74.9 | 371 | 10 | AAU0745 | Sequence of the li |
| 19 | 336 | 74.5 | 465 | 22 | AAU0745 | Humanised 323/A3 ( |
| 20 | 336 | 74.5 | 467 | 13 | AAU0745 | Reshaped CD4 antib |
| 21 | 336 | 74.5 | 467 | 13 | AAU0745 | Reshaped CD4 antib |
| 22 | 336 | 74.5 | 470 | 13 | AAU0745 | Reshaped CAMPATH-1 |
| 23 | 335 | 74.3 | 461 | 14 | AAU0745 | Anti-HIV-1 recombi |
| 24 | 335 | 74.3 | 464 | 22 | AAU0745 | Humanised 323/A3 ( |
| 25 | 335 | 74.3 | 475 | 13 | AAU0745 | Heavy chain of 3D6 |
| 26 | 335 | 74.3 | 476 | 20 | AAU0745 | Monoclonal antibod |
| 27 | 334 | 74.1 | 582 | 22 | AAU0745 | Ganglioside GD3 sp |
| 28 | 334 | 74.1 | 582 | 22 | AAU0745 | Ganglioside GD3 sp |
| 29 | 333 | 73.8 | 473 | 22 | AAU0745 | Human type antihum |
| 30 | 333 | 73.8 | 473 | 22 | AAU0745 | Human type antihum |
| 31 | 333 | 73.8 | 473 | 22 | AAU0745 | Human type antihum |
| 32 | 333 | 73.8 | 473 | 22 | AAU0745 | Human type antihum |
| 33 | 330 | 73.2 | 330 | 22 | AAU0745 | Zcytor 10::Igg gam |
| 34 | 330 | 73.2 | 351 | 14 | AAU0745 | Human kappa immuno |
| 35 | 330 | 73.2 | 447 | 20 | AAU0745 | Human IgG1 chain C |
| 36 | 330 | 73.2 | 452 | 20 | AAU0745 | Heavy chain sequen |
| 37 | 330 | 73.2 | 534 | 13 | AAU0745 | Sequence of CD4-Ig |
| 38 | 330 | 73.2 | 547 | 22 | AAU0745 | Human IL-20RA-Ig g |
| 39 | 330 | 73.2 | 571 | 22 | AAU0745 | Human IL-20RA/Igmu |
| 40 | 330 | 73.2 | 571 | 22 | AAU0745 | Human IL-20RA-Ig g |
| 41 | 330 | 73.2 | 595 | 20 | AAU0745 | Anti-5T4 single ch |
| 42 | 330 | 73.2 | 652 | 19 | AAU0745 | Heavy chain of hMA |
| 43 | 330 | 73.2 | 690 | 21 | AAU0745 | Human IL-6R-alpha- |
| 44 | 330 | 73.2 | 729 | 10 | AAU0745 | Sequence encoded b |
| 45 | 330 | 73.2 | 729 | 21 | AAU0745 | CD4-Ig fusion prot |

# ALIGNMENTS

|          |                                                                         |                                     |
|----------|-------------------------------------------------------------------------|-------------------------------------|
| RESULT 1 | AAE12715                                                                | AAE12715 standard; Protein; 451 AA. |
| ID       | AAE12715                                                                | AAE12715 standard; Protein; 451 AA. |
| XX       | AAE12715                                                                |                                     |
| AC       | AAE12715                                                                |                                     |
| XX       | AAE12715                                                                |                                     |
| DT       | 04-JAN-2002                                                             | (first entry)                       |
| XX       | 04-JAN-2002                                                             |                                     |
| DE       | Human recombinant immunoglobulin (Ig) heavy chain region.               |                                     |
| XX       | Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;        |                                     |
| KW       | heavy chain region; cancer; breast; lung; ovary; bladder;               |                                     |
| KW       | cytostatic; therapy; immunoglobulin; Ig.                                |                                     |
| OS       | Homo sapiens.                                                           |                                     |
| PN       | WO200175110-A2.                                                         |                                     |
| XX       | WO200175110-A2.                                                         |                                     |
| PD       | 11-OCT-2001.                                                            |                                     |
| XX       | 11-OCT-2001.                                                            |                                     |
| PF       | 30-MAR-2001; 2001WO-US10589.                                            |                                     |
| XX       | 30-MAR-2001; 2001WO-US10589.                                            |                                     |
| PR       | 30-MAR-2000; 2000US-0538913.                                            |                                     |
| XX       | 30-MAR-2000; 2000US-0538913.                                            |                                     |
| PA       | (DYAX-) DYAX CORP.                                                      |                                     |
| XX       | (DYAX-) DYAX CORP.                                                      |                                     |
| PI       | Hoogenboom HRJM, Henderikx MPG;                                         |                                     |
| XX       | Hoogenboom HRJM, Henderikx MPG;                                         |                                     |
| DR       | WPI; 2001-626437/72.                                                    |                                     |
| XX       | WPI; 2001-626437/72.                                                    |                                     |
| DR       | N-PSDB; AAD20745.                                                       |                                     |
| XX       | N-PSDB; AAD20745.                                                       |                                     |
| PT       | Novel isolated tumor-associated antigen mucin-1-specific binding member |                                     |
| PT       | for diagnosing and treating cancer, comprises mucin-1 binding domain or |                                     |
| PT       | its portion for binding to an epitope of the protein core of mucin-1    |                                     |



```
|||||
Db 359 EQVYTLPPSRDELTKNOVSLTCLVKGYPSDIAVEWESNGQPNKYKTPPVLDSDGSF 418
QY 409 FLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 451
Db 419 FLYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 461

RESULT 3
AAR43339
ID AAR43339 standard; Protein; 449 AA.
XX
AC AAR43339;
XX
DT 29-NOV-1993 (first entry)
XX
DE Completely humanised C4G1 Ig heavy chain.
XX
KW Immunoglobulin; H-chain; platelet membrane glycoprotein; GPIIb/IIIb;
KW monoclonal antibody; platelet agglutination; humanised antibody.
XX
OS Synthetic.
XX
PN WO9313133-A.
XX
PD 08-JUL-1993.
XX
PF 15-DEC-1992; 92WO-JP01630.
XX
PR 20-DEC-1991; 91US-0812111.
PR 09-JUN-1992; 92US-0895952.
PR 11-SEP-1992; 92US-0944159.
XX
(PROT-) PROTEIN DESIGN LABS INC.
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
PI Co MS, Tso JY;
XX
DR WPI; 1993-227275/28.
XX
Compn. contg. immunoglobulin specific for the GP-IIb and -IIIa
PT protein - for treating disorders related to vascular thrombosis
PS Claim 26; Fig 5C; 54pp; Japanese.
XX
This is the sequence of the humanised C4G1 immunoglobulin heavy
CC chain fragment. See AAR43338 for the light chain sequence. The
CC antibody is specific for the platelet membrane glycoprotein
CC GPIIb/IIIa and inhibits platelet agglutination. The Ig is thus
CC useful in the treatment of thrombosis.
XX
SQ Sequence 449 AA;
Query Match 75.8%; Score 342; DB 14; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.5e-245;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 110 YNQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNLSGALTS 169
Db 108 YNQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNLSGALTS 167
QY 170 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHT 229
Db 168 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHT 227
QY 230 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
Db 228 CPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 287
QY 290 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPRE 349
Db 288 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPRE 347
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QY 350 PQVYTLPPSRDELTKNOVSLTCLVKGYPSDIAVEWESNGQPNKYKTPPVLDSDGSF 409
Db 348 PQVYTLPPSRDELTKNOVSLTCLVKGYPSDIAVEWESNGQPNKYKTPPVLDSDGSF 407
QY 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 451
Db 408 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTKSLSPGK 449

RESULT 4
AAR49816
ID AAR49816 standard; Protein; 449 AA.
XX
AC AAR49816;
XX
DT 24-SEP-1998 (first entry)
XX
DE Amino acid sequence of the humanised antibody C4G1 heavy chain.
XX
KW Humanised antibody C4G1; heavy chain; humanised; immunoglobulin; Ig;
KW mouse C4G1; antibody; inhibition; antigen; cardiovascular disease;
KW thromboembolic disorder; cancer; acute myocardial infarction;
KW unstable angina; stroke; transient ischemic episode; pulmonary embolism;
KW deep vein thrombosis; extracorporeal cardiopulmonary circulation.
XX
OS Chimeric - Mus sp.
OS Chimeric - Homo sapiens.
XX
PN US5777085-A.
XX
PD 07-JUL-1998.
XX
PF 17-MAY-1995; 95US-0458516.
XX
PR 03-MAY-1993; 93US-0059159.
PR 20-DEC-1991; 91US-0812111.
PR 09-JUN-1992; 92US-0895952.
PR 11-SEP-1992; 92US-0944159.
XX
(PROT-) PROTEIN DESIGN LABS INC.
XX
PI Co MS, Tso JY;
XX
DR WPI; 1998-398136/34.
XX
New humanised immunoglobulin which binds GPIIb/IIIa - derived from
PT mouse C4G1 antibody, used for inhibiting platelet aggregation for
PT treating cardiovascular and thromboembolic disorders.
XX
Claim 4; Fig 5D; 35pp; English.
XX
This is the amino acid sequence of the humanised antibody C4G1 heavy
CC chain, used in the method of the invention involving the creation
CC of a humanised immunoglobulin (Ig) derived from the mouse C4G1 antibody.
CC The humanised Ig is capable of binding to GPIIb/IIIa and inhibiting
CC platelet aggregation and also the releasing reaction of platelets. The
CC Ig can be used for treating cardiovascular diseases and thromboembolic
CC disorders, e.g. acute myocardial infarction, unstable angina, stroke,
CC transient ischemic episodes, deep vein thrombosis and pulmonary embolism,
CC extracorporeal cardiopulmonary circulation. The Ig can also be used in
CC diagnosing the presence and location of a thrombus, or certain types of
CC cancer cells which develop GPIIb/IIIa on their surfaces, for the
CC detection of GPIIb/IIIa antigens or for isolating platelets.
XX
SQ Sequence 449 AA;
Query Match 75.8%; Score 342; DB 19; Length 449;
Best Local Similarity 100.0%; Pred. No. 1.5e-245;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 110 YNQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNLSGALTS 169
Db 108 YNQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVWSNLSGALTS 167
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QY 170 GVHTFPAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHT 229  
DB 168 GVHTFPAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHT 227  
QY 230 CPPCPAPELLGGPSVFLPPPKDFTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289  
DB 228 CPPCPAPELLGGPSVFLPPPKDFTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 287  
QY 290 NAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE 349  
DB 288 NAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE 347  
QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF 409  
DB 348 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF 407  
QY 410 LYSKLVDRKSRWQOGNPFSCSYMHEALHNHYTQKSLSLSPGK 451  
DB 408 LYSKLVDRKSRWQOGNPFSCSYMHEALHNHYTQKSLSLSPGK 449

RESULT 5  
AAR93553 standard; Protein; 475 AA.  
XX  
AC AAR93553;  
XX  
DT 20-AUG-1996 (first entry)  
XX  
DE Monoclonal antibody DNA heavy chain against 65 kD hCMV antigen.

XX  
XX Polymerase chain reaction; primer; amplify; PCR; light chain; MAB;  
KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.  
XX  
XX Synthetic.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT /note= "Signal peptide"  
FT Protein 20..475  
FT /note= "Mature heavy chain"

XX JP08038178-A.  
XX  
XX 13-FEB-1996.  
XX  
XX 20-FEB-1995; 95JP-0030742.  
XX  
XX 18-FEB-1994; 94JP-0021628.  
XX  
XX (NISN ) NISSHINBO IND INC.  
XX (TANA/) TANAKA H.  
XX  
XX WPI; 1996-154852/16.  
XX N-PSDB; AAT18059.  
XX  
XX Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -  
PT produced by primer amplification, used in the diagnosis of hCMV  
PT infection

XX  
XX Claim 4; Page 16-18; 22pp; Japanese.  
XX  
XX The sequences given in AAR93553-54 represent the heavy and light chains  
CC respectively of a monoclonal antibody against a 65 kD antigen of human  
CC cytomegalovirus (hCMV). The DNA's encoding these sequences were  
CC amplified using the sequences given in AAT18040-58. The monoclonal  
CC antibody may be used in the diagnosis of hCMV.  
XX  
XX Sequence 475 AA;

Query Match 75.8%; Score 342; DB 17; Length 475;  
Best Local Similarity 100.0%; Pred. No. 1.6e-245;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 110 YMQGQTLTVTSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPVTVSWNSGALTS 169  
DB 134 YMQGQTLTVTSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPPVTVSWNSGALTS 193  
QY 170 GVHTFPAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHT 229  
DB 194 GVHTFPAVLQSSGLYSLSSVWTPVSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHT 253  
QY 230 CPPCPAPELLGGPSVFLPPPKDFTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289  
DB 254 CPPCPAPELLGGPSVFLPPPKDFTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 313  
QY 290 NAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE 349  
DB 314 NAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPRE 373  
QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF 409  
DB 374 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF 433  
QY 410 LYSKLVDRKSRWQOGNPFSCSYMHEALHNHYTQKSLSLSPGK 451  
DB 434 LYSKLVDRKSRWQOGNPFSCSYMHEALHNHYTQKSLSLSPGK 475

RESULT 6  
AAB81972 standard; Protein; 581 AA.  
XX  
AC AAB81972;  
XX  
DT 03-JUL-2001 (first entry)  
XX  
DE Ganglioside GD2 specific antibody related protein SEQ ID NO: 31.  
XX  
XX Ganglioside; GD2; complementation determining region; CDR; antibody;  
KW mouse; cancer.  
XX  
XX Synthetic.  
XX  
XX WO200123573-A1.  
XX  
XX 05-APR-2001.  
XX  
XX 29-SEP-2000; 2000WO-JP06773.  
XX  
XX 30-SEP-1999; 99JP-0278290.  
XX  
XX (KYOW ) KYOWA HAKKO KOGYO KK.  
XX  
XX Hanai N, Shitara K, Nakamura K, Niwa R;  
XX  
XX WPI; 2001-266163/27.  
XX  
XX Human type complementation-determining domain transplanted antibody and  
PT derivatives against ganglioside GD2, useful in diagnosis and therapy of  
PT e.g. tumours, has low antigenicity, little side effects but potent  
PT activity in cancer -

XX  
XX Example 3; Page 111-114; 123pp; Japanese.  
XX  
XX The present invention describes an antibody, which can react specifically  
CC with ganglioside GD2, and is transplanted with a human type  
CC complementation-determining domain (CDR), or its fragments. The antibody  
CC and its derivatives are useful in diagnosis and therapy of tumours,  
CC particularly cancer diagnosis. The present sequence is a protein  
CC used in the exemplification of the invention.  
XX  
XX Sequence 581 AA;

Query Match 75.8%; Score 342; DB 22; Length 581;



|                                                                                                                                                                                                                                                                             |  |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
| Best Local Similarity 100.0%; Pred. No. 1.9e-245;<br>Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                                           |  |
| QY 110 YWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 169                                                                                                                                                                                                     |  |
| DB 107 YWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 166                                                                                                                                                                                                     |  |
| QY 170 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHT 229                                                                                                                                                                                                      |  |
| DB 167 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHT 226                                                                                                                                                                                                      |  |
| QY 230 CPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289                                                                                                                                                                                                      |  |
| DB 227 CPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 286                                                                                                                                                                                                      |  |
| QY 290 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349                                                                                                                                                                                                      |  |
| DB 287 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 346                                                                                                                                                                                                      |  |
| QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 409                                                                                                                                                                                                     |  |
| DB 347 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 406                                                                                                                                                                                                     |  |
| QY 410 LYSKLTVDKSRWQOGNVFSCSVMHREALHNYTQKSLSPGK 451                                                                                                                                                                                                                         |  |
| DB 407 LYSKLTVDKSRWQOGNVFSCSVMHREALHNYTQKSLSPGK 448                                                                                                                                                                                                                         |  |
| RESULT 7                                                                                                                                                                                                                                                                    |  |
| AAB83156                                                                                                                                                                                                                                                                    |  |
| ID AAB83156 standard; protein; 583 AA.                                                                                                                                                                                                                                      |  |
| XX AC AAB83156;                                                                                                                                                                                                                                                             |  |
| XX DT 02-JUL-2001 (first entry)                                                                                                                                                                                                                                             |  |
| DE Ganglioside GM2 antibody-related protein #1.                                                                                                                                                                                                                             |  |
| XX KW Ganglioside; GM2; antibody; cytostatic; cytotoxic; cancer.                                                                                                                                                                                                            |  |
| XX OS Unidentified.                                                                                                                                                                                                                                                         |  |
| XX PN WO200123431-A1.                                                                                                                                                                                                                                                       |  |
| XX PD 05-APR-2001.                                                                                                                                                                                                                                                          |  |
| XX PF 29-SEP-2000; 2000WO-JP06775.                                                                                                                                                                                                                                          |  |
| XX PR 30-SEP-1999; 99JP-0278292.                                                                                                                                                                                                                                            |  |
| XX PA (KYOW ) KYOWA HAKKO KOGYO KK.                                                                                                                                                                                                                                         |  |
| XX PI Hanai N, Nakamura K, Niwa R;                                                                                                                                                                                                                                          |  |
| XX DR WPI; 2001-266142/27.                                                                                                                                                                                                                                                  |  |
| XX PT Monoclonal antibodies against ganglioside GM2 combined with drugs, radioisotopes or proteins for treatment and diagnosis of cancer -                                                                                                                                  |  |
| XX PS Claim 43; Page 61-65; 80pp; Japanese.                                                                                                                                                                                                                                 |  |
| XX CC The present invention relates to derivatives of an antibody against ganglioside GM2. The antibody may be a monoclonal antibody or its fragments. The antibody is combined with a radioactive isotope, protein or small drug in the treatment and diagnosis of cancer. |  |
| XX SQ Sequence 583 AA;                                                                                                                                                                                                                                                      |  |
| Query Match 75.8%; Score 342; DB 22; Length 583;                                                                                                                                                                                                                            |  |
| Best Local Similarity 100.0%; Pred. No. 1.9e-245;<br>Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                                           |  |
| QY 110 YWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 169                                                                                                                                                                                                     |  |

|                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |  |
|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|--|
| Best Local Similarity 100.0%; Pred. No. 1.9e-245;<br>Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;                                                                                                                                                                                                                                                                                                                                                   |  |
| DB 109 YWQGGTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTS 168                                                                                                                                                                                                                                                                                                                                                                                             |  |
| QY 170 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHT 229                                                                                                                                                                                                                                                                                                                                                                                              |  |
| DB 169 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHT 228                                                                                                                                                                                                                                                                                                                                                                                              |  |
| QY 230 CPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289                                                                                                                                                                                                                                                                                                                                                                                              |  |
| DB 229 CPCPAPELLGGPSVFLFPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 288                                                                                                                                                                                                                                                                                                                                                                                              |  |
| QY 290 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349                                                                                                                                                                                                                                                                                                                                                                                              |  |
| DB 289 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 348                                                                                                                                                                                                                                                                                                                                                                                              |  |
| QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 409                                                                                                                                                                                                                                                                                                                                                                                             |  |
| DB 349 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFF 408                                                                                                                                                                                                                                                                                                                                                                                             |  |
| QY 410 LYSKLTVDKSRWQOGNVFSCSVMHREALHNYTQKSLSPGK 451                                                                                                                                                                                                                                                                                                                                                                                                                 |  |
| DB 409 LYSKLTVDKSRWQOGNVFSCSVMHREALHNYTQKSLSPGK 450                                                                                                                                                                                                                                                                                                                                                                                                                 |  |
| RESULT 8                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| AAM52156                                                                                                                                                                                                                                                                                                                                                                                                                                                            |  |
| ID AAM52156 standard; Protein; 731 AA.                                                                                                                                                                                                                                                                                                                                                                                                                              |  |
| XX AC AAM52156;                                                                                                                                                                                                                                                                                                                                                                                                                                                     |  |
| XX DT 05-FEB-2002 (first entry)                                                                                                                                                                                                                                                                                                                                                                                                                                     |  |
| XX DE Humanised HMFG-1 heavy chain/DNase I fusion protein 1.                                                                                                                                                                                                                                                                                                                                                                                                        |  |
| XX KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1; cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.                                                                                                                                                                                                                                                                                                                    |  |
| XX OS Homo sapiens.                                                                                                                                                                                                                                                                                                                                                                                                                                                 |  |
| XX OS Synthetic.                                                                                                                                                                                                                                                                                                                                                                                                                                                    |  |
| XX PN WO200174905-A1.                                                                                                                                                                                                                                                                                                                                                                                                                                               |  |
| XX PD 11-OCT-2001.                                                                                                                                                                                                                                                                                                                                                                                                                                                  |  |
| XX PF 26-MAR-2001; 2001WO-GB01324.                                                                                                                                                                                                                                                                                                                                                                                                                                  |  |
| XX PR 03-APR-2000; 2000GB-0008049.                                                                                                                                                                                                                                                                                                                                                                                                                                  |  |
| XX PR 02-OCT-2000; 2000US-237159P.                                                                                                                                                                                                                                                                                                                                                                                                                                  |  |
| XX PA (ANTI-) ANTISOMA RES LTD.                                                                                                                                                                                                                                                                                                                                                                                                                                     |  |
| XX PI Young RJ;                                                                                                                                                                                                                                                                                                                                                                                                                                                     |  |
| XX DR WPI; 2001-662969/76.                                                                                                                                                                                                                                                                                                                                                                                                                                          |  |
| XX PT Novel compound used to treat cancer has target cell-specific portion comprising humanised monoclonal antibody having specificity for polymorphic epithelial mucin, and cytotoxic portion having endonucleolytic activity -                                                                                                                                                                                                                                    |  |
| XX PS Claim 20; Figure 7; 176pp; English.                                                                                                                                                                                                                                                                                                                                                                                                                           |  |
| XX CC The invention relates to a compound which comprises a target cell-specific portion, comprising an humanised monoclonal antibody, having specificity for polymorphic epithelial mucin (PEM) or its antigen binding fragment and a cytotoxic portion having endonucleolytic activity, exemplified by AAM52156 and encoded by ABA02682-ABA02728. The compound has cytostatic activity useful for treating cancer and acting as a potential inducer of apoptosis. |  |
| XX SQ Sequence 731 AA;                                                                                                                                                                                                                                                                                                                                                                                                                                              |  |
| Query Match 75.8%; Score 342; DB 22; Length 731;                                                                                                                                                                                                                                                                                                                                                                                                                    |  |

|          | Best Local Similarity                    | 100.0%;                                  | Pred. No. 2.2e-245;           |         |            |      |
|----------|------------------------------------------|------------------------------------------|-------------------------------|---------|------------|------|
|          | Matches                                  | 342;                                     | Conservative                  | 0;      | Mismatches | 0;   |
|          |                                          |                                          |                               |         | Indels     | Gaps |
| Qy       | 110                                      | YWQGGTLVTYSSASTKPGSVFPLAPSSKTS           | SGTGAALGCLVKDYPEPVTYVSN       | SGALTS  | 169        |      |
| Db       | 126                                      | YWQGGTLVTYSSASTKPGSVFPLAPSSKTS           | SGTGAALGCLVKDYPEPVTYVSN       | SGALTS  | 185        |      |
| Qy       | 170                                      | GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQ          | YICNVNHHKPSNTKVDKKVEPKSCDKTHT | 229     |            |      |
| Db       | 186                                      | GVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQ          | YICNVNHHKPSNTKVDKKVEPKSCDKTHT | 245     |            |      |
| Qy       | 230                                      | CPPCPAPELLGGPSVFLFPPKPKDILMISRT          | PEVTCVVVDVSHEDPEVKFNWYDGV     | EVH 289 |            |      |
| Db       | 246                                      | CPPCPAPELLGGPSVFLFPPKPKDILMISRT          | PEVTCVVVDVSHEDPEVKFNWYDGV     | EVH 305 |            |      |
| Qy       | 290                                      | NAKTKPREEQNYSTYRVVSVLTVLHQDWLNG          | KEYCKKVSNNKALPAPIEKTISKAKGQPR | 349     |            |      |
| Db       | 306                                      | NAKTKPREEQNYSTYRVVSVLTVLHQDWLNG          | KEYCKKVSNNKALPAPIEKTISKAKGQPR | 365     |            |      |
| Qy       | 350                                      | PQVYTLPPSDELTKNOVSLTLCKVGFYPSDIA         | VEWESNGOPENNYKITTPVPLDSDGSFF  | 409     |            |      |
| Db       | 366                                      | PQVYTLPPSDELTKNOVSLTLCKVGFYPSDIA         | VEWESNGOPENNYKITTPVPLDSDGSFF  | 425     |            |      |
| Qy       | 410                                      | LYSKLTVDKSRWQOGNVSFCSVNH                 | EALHNHYTKLSLSPGK              | 451     |            |      |
| Db       | 426                                      | LYSKLTVDKSRWQOGNVSFCSVNH                 | EALHNHYTKLSLSPGK              | 467     |            |      |
| RESULT 9 |                                          |                                          |                               |         |            |      |
| AAM52159 |                                          |                                          |                               |         |            |      |
| ID       | AAM52159                                 | standard;                                | Protein;                      | 741     | AA.        |      |
| XX       |                                          |                                          |                               |         |            |      |
| AC       | AAM52159;                                |                                          |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| DT       | 05-FEB-2002                              | (first entry)                            |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| DE       | Humanised HMFG-1                         | heavy chain/DNase I fusion protein 4.    |                               |         |            |      |
| DE       |                                          |                                          |                               |         |            |      |
| KW       | Humanised monoclonal antibody;           | polymorphic epithelial mucin; PEM1;      |                               |         |            |      |
| KW       | cytotoxic; endonuclease; DNase I;        | human; cytostatic; cancer; apoptosis.    |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| OS       | Homo sapiens.                            |                                          |                               |         |            |      |
| OS       | Synthetic.                               |                                          |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| PN       | W0200174905-A1.                          |                                          |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| PD       | 11-OCT-2001.                             |                                          |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| PF       | 26-MAR-2001;                             | 2001WO-GB01324.                          |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| PR       | 03-APR-2000;                             | 2000GB-0008049.                          |                               |         |            |      |
| PR       | 02-OCT-2000;                             | 2000US-237159P.                          |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| XX       | {ANTI-}                                  | ANTISOMA RES LTD.                        |                               |         |            |      |
| PA       |                                          |                                          |                               |         |            |      |
| PI       | Young RJ;                                |                                          |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| DR       | WPI;                                     | 2001-662969/76.                          |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| PT       | Novel compound used to treat cancer      | has target cell-specific portion         |                               |         |            |      |
| PT       | comprising humanised monoclonal antibody | having specificity for                   |                               |         |            |      |
| PT       | polymorphic epithelial mucin, and        | cytotoxic portion having                 |                               |         |            |      |
| XX       | endonucleolytic activity -               |                                          |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| PS       | Claim 20; Figure 10;                     | 176pp; English.                          |                               |         |            |      |
| XX       |                                          |                                          |                               |         |            |      |
| CC       | The invention relates to a compound      | which comprises a target                 |                               |         |            |      |
| CC       | cell-specific portion, comprising        | an humanised monoclonal antibody,        |                               |         |            |      |
| CC       | having specificity for polymorphic       | epithelial mucin (PEM) or its antigen    |                               |         |            |      |
| CC       | binding fragment and a cytotoxic         | portion having endonucleolytic activity, |                               |         |            |      |
| CC       | exemplified by AAM52154-AAM52168         | and encoded by ABA02682-ABA02728. The    |                               |         |            |      |
| CC       | compound has cytostatic activity         | useful for treating cancer and acting as |                               |         |            |      |
| CC       | a potential inducer of apoptosis.        |                                          |                               |         |            |      |

CC with expression of CD81, or CD81. This substance is especially an  
CC antibody with affinity towards HCV E2/NS1 protein, containing amino  
CC acid sequences based on the complementarity determining region (CDR) 1,  
CC CDR2 and CDR3 of the H and L chain variable regions. The antibody  
CC inhibits the viral envelope glycoprotein. It is also a CD81 inhibitor.  
CC The antibodies and drugs are used for treatment and/or prevention of  
CC hepatitis C, or for diagnosis of hepatitis C.

XX  
SQ Sequence 475 AA;

Query Match 75.6%; Score 341; DB 22; Length 475;  
Best Local Similarity 100.0%; Pred. No. 8.9e-245;  
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 WQGGTLVTSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170  
Db 135 WQGGTLVTSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 194

QY 171 VHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNPKSNTKVDKKVEPKSCDKTHTC 230  
Db 195 VHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNPKSNTKVDKKVEPKSCDKTHTC 254

QY 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
Db 255 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 314

QY 291 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 315 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 374

QY 351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 410  
Db 375 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 434

QY 411 YSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451  
Db 435 YSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 475

RESULT 11  
ID AAR31023  
AC AAR31023;  
XX  
XX  
DT 19-MAY-1993 (first entry)  
XX  
DE Antibody D heavy chain.  
XX  
KW Heavy; light; chain; antibody; D; monoclonal; peripheral; blood;  
KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;  
KW murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.  
XX  
OS Synthetic.  
XX  
FH Location/Qualifiers  
FT Peptide  
FT 1..19 /note= "Signal peptide"  
FT Region 20..49  
FT /label= FR1  
FT Region 50..54  
FT /label= CDR1  
FT Region 55..68  
FT /label= FR2  
FT Region 69..84  
FT /label= CDR2  
FT Region 85..113  
FT /label= FR3  
FT Region 114..121  
FT /label= CDR3  
FT Region 122..132  
FT /label= FR4  
FT Region 133..241  
FT Domain

FT Region /label= CH1  
FT 242..262  
FT /label= HINGE  
FT Domain 263..379  
FT /label= CH2  
FT Domain 380..497  
FT /label= CH3  
XX  
PN EP523949-A.  
XX  
XX 20-JAN-1993.  
XX  
PF 14-JUL-1992; 92EP-0306420.  
XX  
PR 15-JUL-1991; 91GB-0015284.  
PR 01-AUG-1991; 91GB-0016594.  
PR 23-MAR-1992; 92GB-0006284.  
XX  
PA (WELL ) WELLCOME FOUND LTD.  
XX  
XX Crowe JS, Lewis AP;  
XX  
DR WPI; 1993-019951/03.  
DR N-PSDB; AAQ35099.  
XX  
XX Prodn. of recombinant primate antibodies - useful for treating  
PT infections caused by hepatitis A, B and C, herpes,  
PT cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,  
PT arthritis etc.  
XX  
PS Disclosure; Fig 2; 35pp; English.  
XX  
XX The sequences given in AAR31023-24 represent the heavy and light chains  
CC of Antibody D respectively. Antibody D is a monoclonal antibody which  
CC was derived from peripheral blood lymphocytes from a hepatitis A virus  
CC (HAV) sero positive patient. Antibody D is closely related in nature  
CC to murine antibody B5B3. Total RNA was isolated from antibody D  
CC expressing cells and polyadenylated RNA was extracted. These polyA  
CC RNA's were used to prepare a cDNA library which was screened for human  
CC kappa light (L) chains and two positive clones were detected.  
CC Further heavy (H) chain clones were also isolated.  
XX  
SQ Sequence 476 AA;

Query Match 75.6%; Score 341; DB 14; Length 476;  
Best Local Similarity 100.0%; Pred. No. 8.9e-245;  
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 WQGGTLVTSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170  
Db 136 WQGGTLVTSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 195

QY 171 VHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNPKSNTKVDKKVEPKSCDKTHTC 230  
Db 196 VHTFPAVLQSSGLYSLSSVTPVPSSSLGTQTYICNVNPKSNTKVDKKVEPKSCDKTHTC 255

QY 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
Db 256 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 315

QY 291 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 316 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 375

QY 351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 410  
Db 376 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 435

QY 411 YSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451  
Db 436 YSKLTVDKSRWQGNVFSCSVNHEALHNHYTQKSLSLSPGK 476



```

SQ Sequence 729 AA;
Query Match 75.6%; Score 341; DB 22; Length 729;
Best Local Similarity 100.0%; Pred. No. 1.2e-244;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 YMGQGLTVTVSSASTKGFVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNGALTS 169
DB 126 YMGQGLTVTVSSASTKGFVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNGALTS 185
QY 170 GVHTFPAVLQSSGLYSLSSVTVSPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 229
DB 186 GVHTFPAVLQSSGLYSLSSVTVSPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 245
QY 230 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
DB 246 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305
QY 290 NAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPRE 349
DB 306 NAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPRE 365
QY 350 POVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF 409
DB 426 LYSKLTVDKSRWQOGNVPFSCSVNHEALHNHYTQKSLSLSPG 466

RESULT 14
AAM52161
ID AAM52161 standard; Protein; 739 AA.
XX
AC AAM52161;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 6.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
OS Homo sapiens.
XX Synthetic.
XX WO200174905-A1.
XX
XX 11-OCT-2001.
XX
XX 26-MAR-2001; 2001WO-GB01324.
XX
XX 03-APR-2000; 2000GB-0008049.
XX 02-OCT-2000; 2000US-237159P.
XX
XX {ANTI-} ANTISOMA RES LTD.
XX
XX Young RJ;
XX
XX WPI; 2001-662969/76.
XX
XX Novel compound used to treat cancer has target cell-specific portion
XX comprising humanised monoclonal antibody having specificity for
XX polymorphic epithelial mucin, and cytotoxic portion having
XX endonucleolytic activity.
XX
XX Claim 20; Figure 12; 176pp; English.
XX
XX The invention relates to a compound which comprises a target
XX cell-specific portion, comprising an humanised monoclonal antibody,
XX having specificity for polymorphic epithelial mucin (PEM) or its antigen
XX binding fragment and a cytotoxic portion having endonucleolytic activity.
XX

CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The
CC compound has cytostatic activity useful for treating cancer and acting as
CC a potential inducer of apoptosis.
XX
SQ Sequence 739 AA;
Query Match 75.6%; Score 341; DB 22; Length 739;
Best Local Similarity 100.0%; Pred. No. 1.2e-244;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 YMGQGLTVTVSSASTKGFVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNGALTS 169
DB 126 YMGQGLTVTVSSASTKGFVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNNGALTS 185
QY 170 GVHTFPAVLQSSGLYSLSSVTVSPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 229
DB 186 GVHTFPAVLQSSGLYSLSSVTVSPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 245
QY 230 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
DB 246 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305
QY 290 NAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPRE 349
DB 306 NAKTRPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGPRE 365
QY 350 POVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF 409
DB 366 POVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF 425
QY 410 LYSKLTVDKSRWQOGNVPFSCSVNHEALHNHYTQKSLSLSPG 450
DB 426 LYSKLTVDKSRWQOGNVPFSCSVNHEALHNHYTQKSLSLSPG 466

RESULT 15
AAM52157
ID AAM52157 standard; Protein; 730 AA.
XX
AC AAM52157;
XX
DT 05-FEB-2002 (first entry)
XX
DE Humanised HMFG-1 heavy chain/DNase I fusion protein 2.
XX
KW Humanised monoclonal antibody; polymorphic epithelial mucin; PEM1;
KW cytotoxic; endonuclease; DNase I; human; cytostatic; cancer; apoptosis.
OS Homo sapiens.
XX Synthetic.
XX WO200174905-A1.
XX
XX 11-OCT-2001.
XX
XX 26-MAR-2001; 2001WO-GB01324.
XX
XX 03-APR-2000; 2000GB-0008049.
XX 02-OCT-2000; 2000US-237159P.
XX
XX {ANTI-} ANTISOMA RES LTD.
XX
XX Young RJ;
XX
XX WPI; 2001-662969/76.
XX
XX Novel compound used to treat cancer has target cell-specific portion
XX comprising humanised monoclonal antibody having specificity for
XX polymorphic epithelial mucin, and cytotoxic portion having
XX endonucleolytic activity.
XX
XX Claim 20; Figure 8; 176pp; English.
XX
```

CC The invention relates to a compound which comprises a target  
CC cell-specific portion, comprising an humanised monoclonal antibody,  
CC having specificity for polymorphic epithelial mucin (PEM) or its antigen  
CC binding fragment and a cytotoxic portion having endonucleolytic activity,  
CC exemplified by AAM52154-AAM52168 and encoded by ABA02682-ABA02728. The  
CC compound has cytostatic activity useful for treating cancer and acting as  
CC a potential inducer of apoptosis.

|    |                           |                                                                    |
|----|---------------------------|--------------------------------------------------------------------|
| XX | Sequence                  | 730 AA;                                                            |
| SQ | Query Match               | 75.4%; Score 340; DB 22; Length 730;                               |
|    | Best Local Similarity     | 100.0%; Pred. NO. 6.8e-244;                                        |
|    | Matches 340; Conservative | 0; Mismatches 0; Indels 0; Gaps 0;                                 |
| Qy | 110                       | YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTS 169     |
| Db | 126                       | YWGQGTLLTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWNSGALTS 185     |
| Qy | 170                       | GVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHT 229 |
| Db | 186                       | GVHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHT 245 |
| Qy | 230                       | CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 289    |
| Db | 246                       | CPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 305    |
| Qy | 290                       | NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPTEKTIISKAKGQPRE 349  |
| Db | 306                       | NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPLEKTIISKAKGQPRE 365  |
| Qy | 350                       | PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF 409   |
| Db | 366                       | PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFF 425   |
| Qy | 410                       | LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 449                       |
| Db | 426                       | LYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 465                       |

Search completed: October 9, 2002, 19:23:02  
Job time : 50.3214 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:21:30 ; Search time 18.4082 Seconds  
(without alignments)  
598.427 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

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Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 2442594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA.\*

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- 2: /cgn2\_6/ptodata/2/iaa/5B.COMB.pep.\*
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- 4: /cgn2\_6/ptodata/2/iaa/6B.COMB.pep.\*
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- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description       |
|------------|-------|-------------|--------|-------|-------------------|
| 1          | 343   | 76.1        | 446    | 3     | US-08-397-411-7   |
| 2          | 342   | 75.8        | 449    | 1     | US-08-458-516-13  |
| 3          | 341   | 75.6        | 476    | 2     | US-08-378-939-10  |
| 4          | 338   | 74.9        | 371    | 1     | US-08-236-311-7   |
| 5          | 338   | 74.9        | 371    | 3     | US-08-457-918-7   |
| 6          | 283   | 62.7        | 459    | 1     | US-08-157-101A-7  |
| 7          | 251   | 55.7        | 449    | 4     | US-08-679-397-2   |
| 8          | 249   | 55.2        | 451    | 2     | US-08-887-352B-14 |
| 9          | 249   | 55.2        | 451    | 2     | US-08-887-352B-16 |
| 10         | 249   | 55.2        | 451    | 2     | US-08-887-352B-18 |
| 11         | 249   | 55.2        | 451    | 3     | US-08-466-151-65  |
| 12         | 249   | 55.2        | 451    | 4     | US-09-109-207C-14 |
| 13         | 249   | 55.2        | 451    | 4     | US-09-109-207C-16 |
| 14         | 249   | 55.2        | 451    | 4     | US-09-109-207C-18 |
| 15         | 249   | 55.2        | 451    | 4     | US-09-282-505-2   |
| 16         | 249   | 55.2        | 451    | 4     | US-09-034-255-2   |
| 17         | 249   | 55.2        | 451    | 4     | US-09-296-005-14  |
| 18         | 249   | 55.2        | 451    | 4     | US-09-296-005-16  |
| 19         | 249   | 55.2        | 451    | 4     | US-09-296-005-18  |
| 20         | 249   | 55.2        | 452    | 3     | US-09-027-449-71  |
| 21         | 249   | 55.2        | 452    | 4     | US-09-026-985-71  |
| 22         | 243   | 53.9        | 454    | 2     | US-07-934-373C-22 |
| 23         | 243   | 53.9        | 454    | 3     | US-08-437-642B-22 |
| 24         | 243   | 53.9        | 454    | 5     | PCT-US93-07832-22 |
| 25         | 243   | 53.9        | 467    | 4     | US-09-049-672A-8  |
| 26         | 236   | 52.3        | 442    | 5     | PCT-US96-10043-9  |
| 27         | 235   | 52.1        | 453    | 3     | US-08-466-151-8   |

ALIGNMENTS

RESULT 1

US-08-397-411-7  
; Sequence 7, Application US/08397411  
; Patent No. 6129914  
; GENERAL INFORMATION:  
; APPLICANT: Weiner, George  
; APPLICANT: Gingrich, Roger  
; APPLICANT: Link, Brian  
; APPLICANT: Tso, J. Yun  
; TITLE OF INVENTION: Bisppecific Antibody Effective to Treat  
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
; NUMBER OF SEQUENCES: 14  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/397,411  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: A24  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/859,583  
; FILING DATE: 27-MAR-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 011823-004901  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 446 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-397-411-7

Query Match 76.1%; Score 343; DB 3; Length 446;  
Best Local Similarity 100.0%; Pred. No. 4.6e-238;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 8, Appli  
Sequence 4, Appli  
Sequence 12, Appli  
Sequence 8, Appli  
Sequence 50, Appli  
Sequence 2, Appli  
Sequence 11, Appli  
Sequence 22, Appli  
Sequence 3, Appli  
Sequence 12, Appli  
Sequence 14, Appli  
Sequence 11, Appli  
Sequence 33, Appli  
Sequence 33, Appli  
Sequence 6, Appli  
Sequence 43, Appli

QY 109 DYWGQGLTVTSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWGALT 168  
 Db 104 DYWGQGLTVTSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWGALT 163  
 QY 169 SGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDKTH 228  
 Db 164 SGVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDKTH 223  
 QY 229 TCPPAPPELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 288  
 Db 224 TCPPAPPELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 283  
 QY 289 HNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 348  
 Db 284 HNAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 343  
 QY 349 EPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVWESNGQPENNYKTTPPVLDSDGSF 408  
 Db 344 EPQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVWESNGQPENNYKTTPPVLDSDGSF 403  
 QY 409 FLYSKLTVDKSRWQOGNVCSCVMHEALHNHYTQKSLSLSPGK 451  
 Db 404 FLYSKLTVDKSRWQOGNVCSCVMHEALHNHYTQKSLSLSPGK 446

RESULT 2

US-08-458-516-13  
 ; Sequence 13, Application US/08458516  
 ; Patent No. 5777085  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Co. Man Sung  
 ; APPLICANT: Tso, J. Yun  
 ; TITLE OF INVENTION: Humanized Antibodies Reactive with  
 ; TITLE OF INVENTION: GPIIb/IIIa  
 ; NUMBER OF SEQUENCES: 23  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: William M. Smith  
 ; STREET: One Market Plaza, Steuart Tower, Suite 2000  
 ; CITY: San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94105  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/458,516  
 ; FILING DATE:  
 ; CLASSIFICATION: 424  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/059,159  
 ; FILING DATE: 03-MAY-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Smith, William M.  
 ; REGISTRATION NUMBER: 30,223  
 ; REFERENCE/DOCKET NUMBER: 11823-37-3  
 ; TELEPHONE: 415-326-2400  
 ; TELEFAX: 415-326-2422  
 ; INFORMATION FOR SEQ ID NO: 13:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 449 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-458-516-13

-Query Match 75.8%; Score 342; DB 1; Length 449;  
 Best Local Similarity 100.0%; Pred. No. 2.4e-237;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 110 YWGQGLTVTSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWGALT 169  
 Db 108 YWGQGLTVTSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWGALT 167  
 QY 170 GVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDKTH 229  
 Db 168 GVHTFPAVLQSSGLYSLSVVTVPSSSLGTQTYICNVNHRKPSNTKVDKVPKSCDKTH 227  
 QY 230 CPPAPPELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 289  
 Db 228 CPPAPPELLGGPSVFLPAPSKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEV 287  
 QY 290 NAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 349  
 Db 288 NAKTPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKGQPR 347  
 QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVWESNGQPENNYKTTPPVLDSDGSF 409  
 Db 348 PQVYTLPPSRDELTKNQVSLTCLVKGYFSPDIAVWESNGQPENNYKTTPPVLDSDGSF 407  
 QY 410 LYSKLTVDKSRWQOGNVCSCVMHEALHNHYTQKSLSLSPGK 451  
 Db 408 LYSKLTVDKSRWQOGNVCSCVMHEALHNHYTQKSLSLSPGK 449

RESULT 3

US-08-378-939-10  
 ; Sequence 10, Application US/08378939  
 ; Patent No. 5876961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CROME, JAMES SCOTT  
 ; APPLICANT: LEWIS, ALAN PETER  
 ; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
 ; NUMBER OF SEQUENCES: 46  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
 ; STREET: 555 THIRTEENTH ST. N.W.  
 ; CITY: WASHINGTON  
 ; STATE: D. C.  
 ; COUNTRY: U.S.  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/378,939  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/952640  
 ; FILING DATE: 01-DEC-1992  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: ERNST, BARBARA G.  
 ; REGISTRATION NUMBER: 30,377  
 ; REFERENCE/DOCKET NUMBER: 1808-118  
 ; TELEPHONE: (202) 783-6040  
 ; TELEFAX: (202) 783-6031  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 476 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-378-939-10

Query Match 75.6%; Score 341; DB 2; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-236;  
 Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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QY 111 WGGTLVTVSSASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSQ 170
 |||
Db 136 WGGTLVTVSSASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSQ 195
 |||
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTC 230
 |||
Db 196 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTC 255
 |||
QY 231 PCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
 |||
Db 256 PCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 315
 |||
QY 291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKTIISKAKGQPREP 350
 |||
Db 316 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKTIISKAKGQPREP 375
 |||
QY 351 QYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPPVLDSDGSPFL 410
 |||
Db 376 QYVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPPVLDSDGSPFL 435
 |||
QY 411 YSKLAVDKSRWQOGNVFSCSVMHREALHNYHTQKLSLSLSPGK 451
 |||
Db 436 YSKLAVDKSRWQOGNVFSCSVMHREALHNYHTQKLSLSLSPGK 476
 |||

RESULT 4
US-08-236-311-7
; Sequence 7, Application US/08236311
; Patent No. 5365335
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/236,311
; FILING DATE: 02-MAY-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: 444P1C2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1896
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-236-311-7

Query Match 74.98; Score 338; DB 1; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.5e-234;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GTLVTVSSASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSQVHT 173
 |||
Db 34 GTLVTVSSASTKPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNGALTSQVHT 93
 |||
QY 174 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPC 233
 |||
Db 94 FPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCPC 153
 |||
QY 234 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAT 293
 |||
Db 154 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAT 213
 |||
QY 294 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKTIISKAKGQPREPOVY 353
 |||
Db 214 KPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPAEKTIISKAKGQPREPOVY 273
 |||
QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPPVLDSDGSPFLYSK 413
 |||
Db 274 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGOPENNYKTTTPPVLDSDGSPFLYSK 333
 |||
QY 414 LTVDKSRWQOGNVFSCSVMHREALHNYHTQKLSLSLSPGK 451
 |||
Db 334 LTVDKSRWQOGNVFSCSVMHREALHNYHTQKLSLSLSPGK 371
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RESULT 5
US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; TITLE OF INVENTION: Adheson Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
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; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.
; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444PIC3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-457-918-7

Query Match 74.9%; Score 338; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.5e-234;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GTLVTSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSVGH 173
Db 34 GTLVTSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSVGH 93
QY 174 FPAVLOSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCP 233
Db 94 FPAVLOSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKHTCP 153
QY 234 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 293
Db 154 PAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 213
QY 294 KPPEQYNTSTYRVSVTLVTLHQLDMLNGKEYCKVSNKALPAPIEKTSISKAGOP 353
Db 214 KPPEQYNTSTYRVSVTLVTLHQLDMLNGKEYCKVSNKALPAPIEKTSISKAGOP 273
QY 354 TLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTPPVLDSDGSF 413
Db 274 TLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTPPVLDSDGSF 333
QY 414 LTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
Db 334 LTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 371

RESULT 6
; Sequence 7, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NORIO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HES ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
```

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; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 459 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-157-101A-7

Query Match 62.7%; Score 283; DB 1; Length 459;
Best Local Similarity 100.0%; Pred. No. 3.6e-195;
Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 169 SGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDK 228
Db 177 SGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDK 236
QY 229 TCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG 288
Db 237 TCPPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDG 296
QY 289 HNAKTKPREEQNSTYRVSVTLVTLHQLDMLNGKEYCKVSNKALPAPIEKTSISKAGOP 348
Db 297 HNAKTKPREEQNSTYRVSVTLVTLHQLDMLNGKEYCKVSNKALPAPIEKTSISKAGOP 356
QY 349 EPQYVITLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTPPVLDSDGSF 408
Db 357 EPQYVITLPPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTPPVLDSDGSF 416
QY 409 FLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
Db 417 FLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 459

RESULT 7
; Sequence 2, Application US/09679397
; Patent No. 6339142
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; APPLICANT: BLANK, GREG S.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: PL241R1D2
; CURRENT APPLICATION NUMBER: US/09/679,397
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: US 09/304,465
; PRIOR FILING DATE: 1999-05-03
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PPT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-09-679-397-2

Query Match 55.7%; Score 251; DB 4; Length 449;
Best Local Similarity 100.0%; Pred. No. 2.7e-172;
Matches 251; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 DYGOGTILVTWSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALT 168
; FILING DATE: 05-APR-1994
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Db 108 DYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPPTVSWNSGALT 167  
QY 169 SGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTH 228  
Db 168 SGVHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTH 227  
QY 229 TCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 288  
Db 228 TCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV 287  
QY 289 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 348  
Db 288 HNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 347  
QY 349 EPQVTLPPSR 359  
Db 348 EPQVTLPPSR 358  
RESULT 8  
US-08-887-352B-14  
; Sequence 14, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe  
; TITLE OF INVENTION: Improved Anti-Ige Antibodies and Method of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-14  
Query Match 55.2%; Score 249; DB 2; Length 451;  
Best Local Similarity 100.0%; Pred. No. 7.2e-171;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 111 WQGTTLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPPTVSWNSGALTSG 170  
Db 111 WQGTTLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPPTVSWNSGALTSG 170  
QY 171 VHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTHTC 230  
Db 171 VHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTHTC 230  
QY 231 PCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
Db 231 PCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290

QY 291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
QY 351 QVYTLPPSR 359  
Db 351 QVYTLPPSR 359  
RESULT 9  
US-08-887-352B-16  
; Sequence 16, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardiou, John Lowe  
; TITLE OF INVENTION: Improved Anti-Ige Antibodies and Method of  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-16  
Query Match 55.2%; Score 249; DB 2; Length 451;  
Best Local Similarity 100.0%; Pred. No. 7.2e-171;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 111 WQGTTLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPPTVSWNSGALTSG 170  
Db 111 WQGTTLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPPTVSWNSGALTSG 170  
QY 171 VHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTHTC 230  
Db 171 VHTFPAVLQSSGLYSLSSVTVVPSSSLGTQTYICNVNHHKPSNTKYVDKKVEPKSCDKTHTC 230  
QY 231 PCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
Db 231 PCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
QY 291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 291 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
QY 351 QVYTLPPSR 359  
Db 351 QVYTLPPSR 359

## RESULT 10

US-08-887-352B-18  
; Sequence 18, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 18:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-887-352B-18

Query Match 55.2%; Score 249; DB 2; Length 451;

Best Local Similarity 100.0%; Pred. No. 7.2e-171;

Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 WGQGLTVTVSSASTKGSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170  
Db 111 WGQGLTVTVSSASTKGSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170  
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTC 230  
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTC 230  
QY 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHN 290  
Db 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHN 290  
QY 291 AKTKPREQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 291 AKTKPREQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
QY 351 QVYTLPPSR 359  
Db 351 QVYTLPPSR 359

## RESULT 11

US-08-466-151-65  
; Sequence 65, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants

; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,151  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/466163  
; FILING DATE: 06-Jun-1995  
; APPLICATION NUMBER: 08/405617  
; FILING DATE: 15-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/185899  
; FILING DATE: 26-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/879495  
; FILING DATE: 07-MAY-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/744768  
; FILING DATE: 14-AUG-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig G.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P07182C1D1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 65:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-466-151-65

Query Match 55.2%; Score 249; DB 3; Length 451;

Best Local Similarity 100.0%; Pred. No. 7.2e-171;

Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 WGQGLTVTVSSASTKGSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170  
Db 111 WGQGLTVTVSSASTKGSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170  
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTC 230  
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTC 230  
QY 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHN 290  
Db 231 PPCPAPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHN 290  
QY 291 AKTKPREQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 291 AKTKPREQYNSTYRVVSVLTVLHQDLNKGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
QY 351 QVYTLPPSR 359  
Db 351 QVYTLPPSR 359

## RESULT 12

US-09-109-207C-14  
; Sequence 14, Application US/09109207C

; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 14  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-451  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-109-207C-14

Query Match 55.2%; Score 249; DB 4; Length 451;  
Best Local Similarity 100.0%; Pred. No. 7.2e-171;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 111 WGGGTLVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170  
Db 111 WGGGTLVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170  
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTC 230  
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTC 230  
QY 231 PCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
Db 231 PCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
QY 291 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 291 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
QY 351 QVYTLPPSR 359  
Db 351 QVYTLPPSR 359

RESULT 13  
US-09-109-207C-16  
; Sequence 16, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 16  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-451  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-109-207C-16

Query Match 55.2%; Score 249; DB 4; Length 451;  
Best Local Similarity 100.0%; Pred. No. 7.2e-171;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 111 WGGGTLVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170

Db 111 WGGGTLVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170  
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTC 230  
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTC 230  
QY 231 PCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
Db 231 PCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
QY 291 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 291 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
QY 351 QVYTLPPSR 359  
Db 351 QVYTLPPSR 359

RESULT 14  
US-09-109-207C-18  
; Sequence 18, Application US/09109207C  
; Patent No. 6172213  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptide  
; FILE REFERENCE: P1123R1  
; CURRENT APPLICATION NUMBER: US/09/109,207C  
; CURRENT FILING DATE: 1998-06-30  
; PRIOR APPLICATION NUMBER: US 60/051,554  
; PRIOR FILING DATE: 1997-07-03  
; NUMBER OF SEQ ID NOS: 44  
; SEQ ID NO 18  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; NAME/KEY: Artificial  
; LOCATION: 1-451  
; OTHER INFORMATION: Heavy chain sequence derived from MAE11  
US-09-109-207C-18

Query Match 55.2%; Score 249; DB 4; Length 451;  
Best Local Similarity 100.0%; Pred. No. 7.2e-171;  
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 111 WGGGTLVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170  
Db 111 WGGGTLVTVSSASTKGPVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSG 170  
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTC 230  
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTC 230  
QY 231 PCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
Db 231 PCPCAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290  
QY 291 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
Db 291 AKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
QY 351 QVYTLPPSR 359  
Db 351 QVYTLPPSR 359

RESULT 15  
US-09-282-505-2  
; Sequence 2, Application US/09282505A  
; Patent No. 6194551  
; GENERAL INFORMATION:

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; APPLICANT: Esho Ekinaduse Idusogie et al.
; TITLE OF INVENTION: Polypeptide Variants
; FILE REFERENCE: P1266R1
; CURRENT APPLICATION NUMBER: US/09/282,505A
; CURRENT FILING DATE: 1999-03-31
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-451
; OTHER INFORMATION: Sequence is completely synthesized
; Patent No. 6194551
US-09-282-505-2

Query Match 55.2%; Score 249; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 7.2e-171; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 WQQTGLTVTSASTKGPSPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170
Db 111 WQQTGLTVTSASTKGPSPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170

Qy 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHTC 230
Db 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKKVEPKSCDKTHTC 230

Qy 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
Db 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290

Qy 291 AKTKPREQYNSTYRVYSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350
Db 291 AKTKPREQYNSTYRVYSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350

Qy 351 QVYTLPPSR 359
Db 351 QVYTLPPSR 359

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:23:10 ; Search time 177,179 Seconds  
(without alignments)  
895,951 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

Sequence: 1 QVQLVQSGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPCK 451

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 3502263 seqs, 351980561 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

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Post-processing: Listing first 45 summaries

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24: /cgn2\_6/ptodata/2/paa/US100\_COMB.pep.\*  
25: /cgn2\_6/ptodata/2/paa/US101\_COMB.pep.\*  
26: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length DB | ID | Description       |
|------------|-------|-------------|-----------|----|-------------------|
| 1          | 451   | 100.0       | 451       | 22 | US-09-822-698A-26 |
| 2          | 343   | 76.1        | 446       | 20 | US-09-618-380-7   |
| 3          | 343   | 76.1        | 494       | 21 | US-09-760-479-636 |
| 4          | 342   | 75.8        | 449       | 3  | US-07-944-159-23  |
| 5          | 342   | 75.8        | 731       | 22 | US-09-825-012-46  |
| 6          | 342   | 75.8        | 741       | 22 | US-09-825-012-55  |
| 7          | 341   | 75.6        | 481       | 21 | US-09-760-479-644 |

|    |     |      |      |    |                   |                   |
|----|-----|------|------|----|-------------------|-------------------|
| 8  | 341 | 75.6 | 729  | 22 | US-09-825-012-52  | Sequence 52, Appl |
| 9  | 340 | 75.6 | 739  | 22 | US-09-825-012-61  | Sequence 61, Appl |
| 10 | 340 | 75.4 | 730  | 22 | US-09-825-012-49  | Sequence 49, Appl |
| 11 | 340 | 75.4 | 740  | 22 | US-09-825-012-58  | Sequence 58, Appl |
| 12 | 338 | 74.9 | 371  | 3  | US-07-885-959-7   | Sequence 7, Appl  |
| 13 | 338 | 74.9 | 371  | 16 | US-09-275-310-7   | Sequence 7, Appl  |
| 14 | 338 | 74.9 | 430  | 21 | US-09-760-479-715 | Sequence 715, App |
| 15 | 336 | 74.5 | 467  | 4  | US-08-030-175-41  | Sequence 41, Appl |
| 16 | 336 | 74.5 | 467  | 4  | US-08-030-175-42  | Sequence 42, Appl |
| 17 | 336 | 74.5 | 480  | 21 | US-09-760-479-637 | Sequence 637, App |
| 18 | 335 | 74.3 | 447  | 21 | US-09-760-479-623 | Sequence 623, App |
| 19 | 335 | 74.3 | 475  | 7  | US-08-309-530-4   | Sequence 4, Appl  |
| 20 | 335 | 74.3 | 476  | 15 | US-09-111-286-3   | Sequence 3, Appl  |
| 21 | 335 | 74.3 | 476  | 26 | US-60-051-945-3   | Sequence 3, Appl  |
| 22 | 335 | 74.3 | 499  | 21 | US-09-760-479-645 | Sequence 645, App |
| 23 | 334 | 74.1 | 663  | 1  | PCT-US01-32140-32 | Sequence 32, Appl |
| 24 | 334 | 74.1 | 4852 | 1  | PCT-US01-32140-33 | Sequence 33, Appl |
| 25 | 333 | 73.8 | 474  | 21 | US-09-760-479-655 | Sequence 655, App |
| 26 | 330 | 73.2 | 330  | 19 | US-09-569-343-29  | Sequence 29, Appl |
| 27 | 330 | 73.2 | 330  | 19 | US-09-569-343A-29 | Sequence 29, Appl |
| 28 | 330 | 73.2 | 330  | 22 | US-09-892-949-38  | Sequence 38, Appl |
| 29 | 330 | 73.2 | 379  | 4  | US-08-057-292-3   | Sequence 3, Appl  |
| 30 | 330 | 73.2 | 447  | 16 | US-09-256-156-1   | Sequence 1, Appl  |
| 31 | 330 | 73.2 | 473  | 21 | US-09-760-479-578 | Sequence 578, App |
| 32 | 330 | 73.2 | 541  | 1  | PCT-US02-07214-32 | Sequence 32, Appl |
| 33 | 330 | 73.2 | 547  | 21 | US-09-746-359A-54 | Sequence 54, Appl |
| 34 | 330 | 73.2 | 547  | 23 | US-09-951-268-40  | Sequence 40, Appl |
| 35 | 330 | 73.2 | 558  | 1  | PCT-US02-07214-31 | Sequence 31, Appl |
| 36 | 330 | 73.2 | 567  | 19 | US-09-543-320-16  | Sequence 16, Appl |
| 37 | 330 | 73.2 | 567  | 22 | US-09-825-561A-16 | Sequence 16, Appl |
| 38 | 330 | 73.2 | 571  | 21 | US-09-746-359A-53 | Sequence 53, Appl |
| 39 | 330 | 73.2 | 571  | 23 | US-09-951-268-30  | Sequence 30, Appl |
| 40 | 330 | 73.2 | 951  | 9  | US-08-563-105-8   | Sequence 8, Appl  |
| 41 | 330 | 73.2 | 951  | 15 | US-09-177-009-8   | Sequence 9, Appl  |
| 42 | 330 | 73.2 | 951  | 17 | US-09-313-942-9   | Sequence 9, Appl  |
| 43 | 326 | 72.3 | 470  | 16 | US-09-238-741-4   | Sequence 4, Appl  |
| 44 | 319 | 70.7 | 470  | 15 | US-09-107-223A-2  | Sequence 2, Appl  |
| 45 | 283 | 62.7 | 459  | 5  | US-08-157-101-7   | Sequence 7, Appl  |

#### ALIGNMENTS

RESULT 1  
US-09-822-698A-26  
; Sequence 26, Application US/09822698A  
; GENERAL INFORMATION:  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Henderikx, Maria P.G.  
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
; FILE REFERENCE: DX-015.1 US  
; CURRENT APPLICATION NUMBER: US/09/822,698A  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/538,913  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 26  
; LENGTH: 451  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1  
US-09-822-698A-26

Query Match 100.0%; Score 451; DB 22; Length 451;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRAQAPKGLVWSGISGGSTYY 60  
Db 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRAQAPKGLVWSGISGGSTYY 60

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Db 61 ADSVKGRFTTISRNSKNTLYQWNSLRADTAVYYCAKHTGGVWDPIDWGGGTLTVTS 120
QY 121 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQS 180
Db 121 SASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALTSGVHTFPAVLQS 180
QY 181 SGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTHHTCCPPCPAPPELLG 240
Db 181 SGLYSLSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTHHTCCPPCPAPPELLG 240
QY 241 GPSVFLPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
Db 241 GPSVFLPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQY 300
QY 301 NSTYRVSVSLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360
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QY 361 ELTNQVSLTCLVKGFPSPDIATVWESNGOPENNYKTPPVLDSDGSFELYSKLTVDKSR 420
Db 361 ELTNQVSLTCLVKGFPSPDIATVWESNGOPENNYKTPPVLDSDGSFELYSKLTVDKSR 420
QY 421 WOQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451
Db 421 WOQGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

RESULT 2
US-09-618-380-7
; Sequence 7, Application US/09618380
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; Gingrich, Roger
; Link, Brian
; Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/618,380
; FILING DATE: 18-Jul-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/397,411
; FILING DATE: 1995-03-01
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
```

```
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-618-380-7
Query Match 76.1%; Score 343; DB 20; Length 446;
Best Local Similarity 100.0%; Pred. No. 9.7e-311;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 DYWGQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALT 168
Db 104 DYWGQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALT 163
QY 169 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTH 228
Db 164 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTH 223
QY 229 TCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEV 288
Db 224 TCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEV 283
QY 289 HNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 348
Db 284 HNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 343
QY 349 EPQVYITLPPSRDELTKNQVSLTCLVKGYFSPDIAVWESNGOPENNYKTPPVLDSDGSF 408
Db 344 EPQVYITLPPSRDELTKNQVSLTCLVKGYFSPDIAVWESNGOPENNYKTPPVLDSDGSF 403
QY 409 FLYSKLTVDKSRWQQGNVSCSVNHEALHNHYTQKSLSLSPGK 451
Db 404 FLYSKLTVDKSRWQQGNVSCSVNHEALHNHYTQKSLSLSPGK 446

RESULT 3
US-09-760-479-636
; Sequence 636, Application US/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253
; CURRENT APPLICATION NUMBER: US/09/760,479
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 946
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 636
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-479-636
Query Match 76.1%; Score 343; DB 21; Length 494;
Best Local Similarity 100.0%; Pred. No. 1.1e-310;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 109 DYWGQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALT 168
Db 152 DYWGQGTTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVYSNWSGALT 211
QY 169 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTH 228
Db 212 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKKEPKSCDKTH 271
QY 229 TCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEV 288
Db 272 TCPPCPAPPELLGGPSVFLFPPPKPKDTLMISRPETVCVVVDVSHEDPEVKFNWYVDGVEV 331
QY 289 HNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 348
Db 332 HNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPR 391
QY 349 EPQVYITLPPSRDELTKNQVSLTCLVKGYFSPDIAVWESNGOPENNYKTPPVLDSDGSF 408
Db 392 EPQVYITLPPSRDELTKNQVSLTCLVKGYFSPDIAVWESNGOPENNYKTPPVLDSDGSF 451
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QY 409 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 451  
|||||  
Db 452 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 494  
|||||  
RESULT 4  
US-07-944-159-23  
; Sequence 23, Application US/07944159  
; GENERAL INFORMATION:  
; APPLICANT: Co, Man Sung  
; APPLICANT: Iso, J. Yun  
; TITLE OF INVENTION: Humanized Antibodies Reactive with  
; TITLE OF INVENTION: GP1b/IIIA  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: William M. Smith  
; STREET: One Market Plaza, Steuart Tower, Suite 2000  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/944,159  
; FILING DATE: 19920911  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 11823-37-2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-326-2400  
; TELEFAX: 415-326-2422  
; INFORMATION FOR SEQ ID NO: 23:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 449 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-07-944-159-23  
Query Match 75.8%; Score 342; DB 3; Length 449;  
Best Local Similarity 100.0%; Pred. No. 8.4e-310; Mismatches 0; Indels 0; Gaps 0;  
Matches 342; Conservative 0;  
QY 110 YMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKLYKDYFPPEPTVSNWNGALTS 169  
|||||  
Db 108 YMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKLYKDYFPPEPTVSNWNGALTS 167  
|||||  
QY 170 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHY 229  
|||||  
Db 168 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHY 227  
|||||  
QY 230 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 289  
Db 228 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 287  
|||||  
QY 290 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQPRE 349  
Db 288 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQPRE 347  
|||||  
QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 409  
Db 348 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 407  
|||||  
QY 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 451  
|||||

Db 408 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 449  
RESULT 5  
US-09-825-012-46  
; Sequence 46, Application US/09825012  
; GENERAL INFORMATION:  
; APPLICANT: Young, Robert  
; TITLE OF INVENTION: Compounds for Targeting  
; FILE REFERENCE: 43191-256808  
; CURRENT APPLICATION NUMBER: US/09/825,012  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/237,159  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: GB 0008049.9  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 46  
; LENGTH: 731  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanised HMFG1 heavy chain - Dnaase I fusion  
US-09-825-012-46  
Query Match 75.8%; Score 342; DB 22; Length 731;  
Best Local Similarity 100.0%; Pred. No. 1.3e-309;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 110 YMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKLYKDYFPPEPTVSNWNGALTS 169  
|||||  
Db 126 YMGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKLYKDYFPPEPTVSNWNGALTS 185  
|||||  
QY 170 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHY 229  
|||||  
Db 186 GVHTFPAVLQSSGLYSLSSVTVFSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHY 245  
|||||  
QY 230 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 289  
Db 246 CPPCPAPELGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVDGVEVH 305  
|||||  
QY 290 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQPRE 349  
Db 306 NAKTKPREQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETKISKAKGQPRE 365  
|||||  
QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 409  
Db 366 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 425  
|||||  
QY 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 451  
|||||  
Db 426 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 467  
|||||  
RESULT 6  
US-09-825-012-55  
; Sequence 55, Application US/09825012  
; GENERAL INFORMATION:  
; APPLICANT: Young, Robert  
; TITLE OF INVENTION: Compounds for Targeting  
; FILE REFERENCE: 43191-256808  
; CURRENT APPLICATION NUMBER: US/09/825,012  
; CURRENT FILING DATE: 2001-04-03  
; PRIOR APPLICATION NUMBER: US 60/237,159  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: GB 0008049.9  
; PRIOR FILING DATE: 2000-04-03  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 55  
; LENGTH: 741  
; TYPE: PRT

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFGL heavy chain - DNase I fusion
US-09-825-012-55

Query Match 75.8%; Score 342; DB 22; Length 741;
Best Local Similarity 100.0%; Pred. No. 1.3e-309;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 YWGGTLTVSSASTKGPVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTS 169
Db 126 YWGGTLTVSSASTKGPVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTS 185
Qy 170 GVHTFPAVLOSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 229
Db 186 GVHTFPAVLOSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 245
Qy 230 CPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
Db 246 CPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305
Qy 290 NAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPRE 349
Db 306 NAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPRE 365
Qy 350 POVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF 409
Db 366 POVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF 425
Qy 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 451
Db 426 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 467

RESULT 7
US-09-760-479-644
; Sequence 644, Application US/09760479
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT253
; CURRENT APPLICATION NUMBER: US/09/760,479
; CURRENT FILING DATE: 2001-01-16
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 946
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 644
; LENGTH: 481
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-760-479-644

Query Match 75.6%; Score 341; DB 21; Length 481;
Best Local Similarity 100.0%; Pred. No. 7.6e-309;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 WGQGTLLTVSSASTKGPVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTS 170
Db 141 WGQGTLLTVSSASTKGPVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTS 200
Qy 171 VHTFPAVLOSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTC 230
Db 201 VHTFPAVLOSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTC 260
Qy 231 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 290
Db 261 PPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN 320
Qy 291 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 350
Db 321 AKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 380
Qy 351 QVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 410
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Db 381 QVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFL 440
Qy 411 YSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 451
Db 441 YSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPGK 481

RESULT 8
US-09-825-012-52
; Sequence 52, Application US/09825012
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 729
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFGL heavy chain - DNase I fusion
US-09-825-012-52

Query Match 75.6%; Score 341; DB 22; Length 729;
Best Local Similarity 100.0%; Pred. No. 1.1e-308;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 YWGGTLTVSSASTKGPVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTS 169
Db 126 YWGGTLTVSSASTKGPVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTS 185
Qy 170 GVHTFPAVLOSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 229
Db 186 GVHTFPAVLOSSGLYSLSSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 245
Qy 230 CPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
Db 246 CPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305
Qy 290 NAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPRE 349
Db 306 NAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPRE 365
Qy 350 POVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF 409
Db 366 POVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFF 425
Qy 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPG 450
Db 426 LYSKLTVDKSRWQGNVFCSCVMHEALHNNHYTQKLSLSLSPG 466

RESULT 9
US-09-825-012-61
; Sequence 61, Application US/09825012
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
```

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; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 739
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFg1 heavy chain - DNase I fusion
US-09-825-012-61

Query Match
Best Local Similarity 75.6%; Score 341; DB 22; Length 739;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 YMQGGLTVTVSSASTKGPSVFLPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 169
DB 126 YMQGGLTVTVSSASTKGPSVFLPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 185

QY 170 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 229
DB 186 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 245

QY 230 CPPCPAPPELLGGPSVFLFPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
DB 246 CPPCPAPPELLGGPSVFLFPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305

QY 290 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349
DB 306 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 365

QY 350 PQVYTLPPSRDELTKNOVSLTCLVKGYFSDIAVEENSGQPENNYKTTTPVLDSDGSFF 409
DB 366 PQVYTLPPSRDELTKNOVSLTCLVKGYFSDIAVEENSGQPENNYKTTTPVLDSDGSFF 425

QY 410 LYSKLTVDKSRWQGNFVSCSVHHEALHNHYTQKSLSLSPG 450
DB 426 LYSKLTVDKSRWQGNFVSCSVHHEALHNHYTQKSLSLSPG 466

RESULT 10
US-09-825-012-49
; Sequence 49, Application US/09825012
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 730
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFg1 heavy chain - DNase I fusion
US-09-825-012-49

Query Match
Best Local Similarity 75.4%; Score 340; DB 22; Length 730;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 YMQGGLTVTVSSASTKGPSVFLPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 169
DB 126 YMQGGLTVTVSSASTKGPSVFLPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 185

QY 170 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 229
DB 186 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 245

QY 230 CPPCPAPPELLGGPSVFLFPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
DB 246 CPPCPAPPELLGGPSVFLFPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305

QY 290 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349
DB 306 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 365

QY 350 PQVYTLPPSRDELTKNOVSLTCLVKGYFSDIAVEENSGQPENNYKTTTPVLDSDGSFF 409
DB 366 PQVYTLPPSRDELTKNOVSLTCLVKGYFSDIAVEENSGQPENNYKTTTPVLDSDGSFF 425

QY 410 LYSKLTVDKSRWQGNFVSCSVHHEALHNHYTQKSLSLSPG 450
DB 186 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 245
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QY 230 CPPCPAPPELLGGPSVFLFPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
DB 246 CPPCPAPPELLGGPSVFLFPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305

QY 290 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349
DB 306 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 365

QY 350 PQVYTLPPSRDELTKNOVSLTCLVKGYFSDIAVEENSGQPENNYKTTTPVLDSDGSFF 409
DB 366 PQVYTLPPSRDELTKNOVSLTCLVKGYFSDIAVEENSGQPENNYKTTTPVLDSDGSFF 425

QY 410 LYSKLTVDKSRWQGNFVSCSVHHEALHNHYTQKSLSLSPG 449
DB 426 LYSKLTVDKSRWQGNFVSCSVHHEALHNHYTQKSLSLSPG 465

RESULT 11
US-09-825-012-58
; Sequence 58, Application US/09825012
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 740
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFg1 heavy chain - DNase I fusion
US-09-825-012-58

Query Match
Best Local Similarity 75.4%; Score 340; DB 22; Length 740;
Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 YMQGGLTVTVSSASTKGPSVFLPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 169
DB 126 YMQGGLTVTVSSASTKGPSVFLPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 185

QY 170 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 229
DB 186 GVHTFPAVLQSSGLYSLSVVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHT 245

QY 230 CPPCPAPPELLGGPSVFLFPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 289
DB 246 CPPCPAPPELLGGPSVFLFPPPKDQTLMIKRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 305

QY 290 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 349
DB 306 NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE 365

QY 350 PQVYTLPPSRDELTKNOVSLTCLVKGYFSDIAVEENSGQPENNYKTTTPVLDSDGSFF 409
DB 366 PQVYTLPPSRDELTKNOVSLTCLVKGYFSDIAVEENSGQPENNYKTTTPVLDSDGSFF 425

QY 410 LYSKLTVDKSRWQGNFVSCSVHHEALHNHYTQKSLSLSPG 449
DB 426 LYSKLTVDKSRWQGNFVSCSVHHEALHNHYTQKSLSLSPG 465

RESULT 12
US-07-885-959-7
; Sequence 7, Application US/07885959
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QY 234 PAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293  
DB 154 PAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 213  
QY 294 KPREEQNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPLEKTIISKAKGPPEQVY 353  
DB 214 KPREEQNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPLEKTIISKAKGPPEQVY 273  
QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGDSFELYSK 413  
DB 274 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGDSFELYSK 333  
QY 414 LTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 451  
DB 334 LTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 371

## RESULT 14

US-09-760-479-715  
; Sequence 715, Application US/09760479  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT253  
; CURRENT APPLICATION NUMBER: US/09/760,479  
; Prior application data removed - refer to PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 946  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 715  
; LENGTH: 430  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-760-479-715

Query Match 74.9%; Score 338; DB 21; Length 430;  
Best Local Similarity 100.0%; Pred. No. 4.4e-306;  
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 114 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 173  
DB 93 GTLVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHT 152  
QY 174 FPAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHPKSNTRKVDKVEPKSCDKTHTCPPC 233  
DB 153 FPAVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHPKSNTRKVDKVEPKSCDKTHTCPPC 212  
QY 234 PAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293  
DB 213 PAPELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 272  
QY 294 KPREEQNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPLEKTIISKAKGPPEQVY 353  
DB 273 KPREEQNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPLEKTIISKAKGPPEQVY 332  
QY 354 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGDSFELYSK 413  
DB 333 TLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGDSFELYSK 392  
QY 414 LTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 451  
DB 393 LTVDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 430

## RESULT 15

US-08-030-175-41  
; Sequence 41, Application US/08030175  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Scott D.  
; APPLICANT: Clark, Michael R.  
; APPLICANT: Cobbold, Stephen P.  
; APPLICANT: Waldmann, Herman  
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION

; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.  
; STREET: 555 13TH ST., NW Suite 701 East  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: U.S.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 Kb storage  
; COMPUTER: IBM AT compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
; SOFTWARE: WordPerfect 5.0 (Dos Text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/030,175  
; FILING DATE: 17-MAY-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01578  
; FILING DATE: 13-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ernst, Barbara G.  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1768-113  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)783-6040  
; TELEFAX: (202)783-6031  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 467 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-030-175-41

Query Match 74.5%; Score 336; DB 4; Length 467;  
Best Local Similarity 100.0%; Pred. No. 3.4e-304;  
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 175  
DB 132 LVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 191  
QY 176 AVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHPKSNTRKVDKVEPKSCDKTHTCPPCPA 235  
DB 192 AVLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHPKSNTRKVDKVEPKSCDKTHTCPPCPA 251  
QY 236 PELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 295  
DB 252 PELLGGPSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 311  
QY 296 REEQYNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPLEKTIISKAKGPPEQVYTL 355  
DB 312 REEQYNSTYRVSVLVTLVHODWLNKGEYKCKVSNKALPAPLEKTIISKAKGPPEQVYTL 371  
QY 356 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGDSFELYSKLT 415  
DB 372 PPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNPKTTPPVLDSGDSFELYSKLT 431  
QY 416 VDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 451  
DB 432 VDKSRWQGNVFCSCVWHEALHNHYTQKSLSLSPGK 467

Search completed: October 9, 2002, 19:32:01  
Job time : 179.179 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:23:45 ; Search time 59.8265 Seconds  
(without alignments)  
2085.589 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

Sequence: 1 QVQLVQSGGGLVOPGGSLRL.....MHEALHNHYTKSLSPGK 451

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1006125 seqs, 276659714 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1006125

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*  
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2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description          |
|------------|-------|-------------|--------|-------|----------------------|
| 1          | 343   | 76.1        | 442    | 1     | PCT-US02-21323-12    |
| 2          | 343   | 76.1        | 442    | 1     | PCT-US02-21323-21    |
| 3          | 343   | 76.1        | 442    | 1     | PCT-US02-21324-12    |
| 4          | 343   | 76.1        | 442    | 1     | PCT-US02-21324-21    |
| 5          | 343   | 76.1        | 442    | 1     | PCT-US02-26321-12    |
| 6          | 343   | 76.1        | 442    | 1     | PCT-US02-26321-16    |
| 7          | 343   | 76.1        | 449    | 1     | PCT-US02-11853-12    |
| 8          | 343   | 76.1        | 453    | 1     | PCT-US02-11854A-12   |
| 9          | 343   | 76.1        | 468    | 1     | PCT-US02-11853-20    |
| 10         | 343   | 76.1        | 472    | 1     | PCT-US02-11854A-20   |
| 11         | 343   | 76.1        | 494    | 6     | US-10-206-008-636    |
| 12         | 342   | 75.6        | 450    | 1     | PCT-US02-21281-18    |
| 13         | 341   | 75.6        | 448    | 1     | PCT-US01-27352-2     |
| 14         | 341   | 75.6        | 473    | 5     | US-09-791-537-118977 |
| 15         | 341   | 75.6        | 476    | 5     | US-09-791-537-104528 |
| 16         | 341   | 75.6        | 481    | 6     | US-10-206-008-644    |
| 17         | 338   | 74.9        | 371    | 6     | US-10-097-044A-7     |
| 18         | 338   | 74.9        | 430    | 6     | US-10-206-008-715    |
| 19         | 338   | 74.9        | 430    | 6     | US-10-211-364-1052   |
| 20         | 336   | 74.5        | 465    | 6     | US-10-031-355-5      |
| 21         | 336   | 74.5        | 465    | 6     | US-10-031-355-12     |
| 22         | 336   | 74.5        | 470    | 5     | US-09-791-537-108421 |
| 23         | 336   | 74.5        | 480    | 6     | US-10-206-008-637    |
| 24         | 335   | 74.3        | 447    | 6     | US-10-206-008-623    |
| 25         | 335   | 74.3        | 476    | 5     | US-09-747-669-3      |
| 26         | 335   | 74.3        | 499    | 6     | US-10-206-008-645    |

|    |     |      |     |   |                     |                   |
|----|-----|------|-----|---|---------------------|-------------------|
| 27 | 334 | 74.1 | 468 | 6 | US-10-058-120-12    | Sequence 12, Appl |
| 28 | 334 | 74.1 | 582 | 6 | US-10-089-500-53    | Sequence 53, Appl |
| 29 | 334 | 74.1 | 582 | 6 | US-10-089-500-57    | Sequence 57, Appl |
| 30 | 333 | 73.8 | 474 | 6 | US-10-206-008-655   | Sequence 655, App |
| 31 | 333 | 73.8 | 476 | 7 | US-60-371-501-15    | Sequence 15, Appl |
| 32 | 330 | 73.2 | 330 | 1 | PCT-US02-09650-1    | Sequence 1, Appl  |
| 33 | 330 | 73.2 | 330 | 1 | PCT-US02-09815-1    | Sequence 15, Appl |
| 34 | 330 | 73.2 | 330 | 5 | US-09-995-898A-15   | Sequence 15, Appl |
| 35 | 330 | 73.2 | 330 | 5 | US-09-791-537-26432 | Sequence 26432, A |
| 36 | 330 | 73.2 | 330 | 6 | US-10-112-582-1     | Sequence 1, Appl  |
| 37 | 330 | 73.2 | 330 | 6 | US-10-047-542-20    | Sequence 20, Appl |
| 38 | 330 | 73.2 | 332 | 5 | US-09-990-586-98    | Sequence 98, Appl |
| 39 | 330 | 73.2 | 470 | 6 | US-10-104-047-3730  | Sequence 3730, Ap |
| 40 | 330 | 73.2 | 473 | 6 | US-10-206-008-578   | Sequence 578, App |
| 41 | 330 | 73.2 | 951 | 5 | US-09-935-868-9     | Sequence 9, Appl  |
| 42 | 329 | 72.9 | 329 | 5 | US-09-791-537-88605 | Sequence 88605, A |
| 43 | 282 | 62.5 | 422 | 6 | US-10-206-008-475   | Sequence 475, App |
| 44 | 251 | 55.7 | 449 | 5 | US-09-304-465A-2    | Sequence 2, Appl  |
| 45 | 251 | 55.7 | 449 | 6 | US-10-253-366-2     | Sequence 2, Appl  |

ALIGNMENTS

RESULT 1

PCT-US02-21323-12

; Sequence 12, Application PC/TUS0221323  
; GENERAL INFORMATION:  
; APPLICANT: Eli Lilly and Company  
; TITLE OF INVENTION: Rapid Improvement of Cognition in Conditions Related to A-beta  
; FILE REFERENCE: X-15240  
; CURRENT APPLICATION NUMBER: PCT/US02/21323  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/313,222  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/383,846  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized antibody  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: humanized 266 antibody preferred heavy chain  
PCT-US02-21323-12

|                       |                 |                                                              |           |             |
|-----------------------|-----------------|--------------------------------------------------------------|-----------|-------------|
| Query Match           | 76.1%           | Score 343;                                                   | DB 1;     | Length 442; |
| Best Local Similarity | 100.0%;         | Pred. No. 1.4e-160;                                          |           |             |
| Matches 343;          | Conservative 0; | Mismatches 0;                                                | Indels 0; | Gaps 0;     |
| Qy                    | 109             | DYWGQGTIVTVSSASTKGPVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT   | 168       |             |
| Db                    | 100             | DIYWGQGTIVTVSSASTKGPVFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT  | 159       |             |
| Qy                    | 169             | SGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQYICNVNHPKSTKVDKVEPKSCDKTH     | 228       |             |
| Db                    | 160             | SGVHTFPAVLQSSGLYSLSSVTPVSSSLGTQYICNVNHPKSTKVDKVEPKSCDKTH     | 219       |             |
| Qy                    | 229             | TCPCPAPPELLGGPSVFLPPPKPKDLMISRTPEVTCVYVVDVSHEDPEVKFNWYDGEV   | 288       |             |
| Db                    | 220             | TCPCPAPPELLGGPSVFLPPPKPKDLMISRTPEVTCVYVVDVSHEDPEVKFNWYDGEV   | 279       |             |
| Qy                    | 289             | HNATKPREQYNSTYRVWVSLTVLHODWLNKKEYCKVSKNKPAPTEKTSKAKGQPR      | 348       |             |
| Db                    | 280             | HNATKPREQYNSTYRVWVSLTVLHODWLNKKEYCKVSKNKPAPTEKTSKAKGQPR      | 339       |             |
| Qy                    | 349             | EPQYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSSGSF | 408       |             |
| Db                    |                 | EPQYITLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSSGSF |           |             |

Db 340 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 399  
Qy 409 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 451  
Db 400 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 442

RESULT 2  
PCT-US02-21323-21  
; Sequence 21, Application PC/TUS0221323  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY  
; TITLE OF INVENTION: Rapid Improvement of Cognition in Conditions Related to A-beta  
; FILE REFERENCE: X-15240  
; CURRENT APPLICATION NUMBER: PCT/US02/21323  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/313,222  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/383,846  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 21  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized antibody  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: heavy chain antibody  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (56)..(56)  
; OTHER INFORMATION: Xaa at position 56 is any amino acid, provided that if Xaa at pos  
; OTHER INFORMATION: ition 56 is Asn and Xaa at position 58 is Ser or Thr, then Xaa at  
; OTHER INFORMATION: position 57 is Asp or Pro  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (57)..(57)  
; OTHER INFORMATION: Xaa at position 57 is any amino acid, provided that if Xaa at pos  
; OTHER INFORMATION: ition 56 is Asn and Xaa at position 58 is Ser or Thr, then Xaa at  
; OTHER INFORMATION: position 57 is Asp or Pro  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (58)..(58)  
; OTHER INFORMATION: Xaa at position 58 is any amino acid, provided that if Xaa at pos  
; OTHER INFORMATION: ition 56 is Asn and Xaa at position 57 is neither Asp nor Pro, th  
; OTHER INFORMATION: en Xaa at position 58 is neither Ser nor Thr  
PCT-US02-21323-21

Query Match 76.1%; Score 343; DB 1; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.4e-160; Indels 0; Gaps 0;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 109 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALT 168  
Db 100 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALT 159  
Qy 169 SGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH 228  
Db 160 SGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH 219  
Qy 229 TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEV 288  
Db 220 TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEV 279  
Qy 289 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPR 348  
Db 280 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPR 339  
Qy 349 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 408  
Db 340 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 399  
Qy 409 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 451  
Db 400 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 442

RESULT 4  
PCT-US02-21324-21  
; Sequence 21, Application PC/TUS0221324  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY  
; TITLE OF INVENTION: USE OF ANTIBODIES HAVING HIGH AFFINITY FOR SOLUBLE A-BETA  
; FILE REFERENCE: X-15047  
; CURRENT APPLICATION NUMBER: PCT/US02/21324  
; CURRENT FILING DATE: 2002-08-14

Db 340 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 399  
Qy 409 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 451  
Db 400 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 442

RESULT 3  
PCT-US02-21324-12  
; Sequence 12, Application PC/TUS0221324  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY  
; TITLE OF INVENTION: USE OF ANTIBODIES HAVING HIGH AFFINITY FOR SOLUBLE A-BETA  
; FILE REFERENCE: X-15047  
; CURRENT APPLICATION NUMBER: PCT/US02/21324  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: 60/313,576  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/383,581  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: humanized antibody  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: Humanized antibody 266 preferred heavy chain variable  
PCT-US02-21324-12

Query Match 76.1%; Score 343; DB 1; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.4e-160; Indels 0; Gaps 0;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 109 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALT 168  
Db 100 DYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALT 159  
Qy 169 SGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH 228  
Db 160 SGVHTFPAVLQSSGLYSLSSVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTH 219  
Qy 229 TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEV 288  
Db 220 TCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEV 279  
Qy 289 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPR 348  
Db 280 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPR 339  
Qy 349 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 408  
Db 340 EPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 399  
Qy 409 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 451  
Db 400 FLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTKQSLSPGK 442

RESULT 4  
PCT-US02-21324-21  
; Sequence 21, Application PC/TUS0221324  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY  
; TITLE OF INVENTION: USE OF ANTIBODIES HAVING HIGH AFFINITY FOR SOLUBLE A-BETA  
; FILE REFERENCE: X-15047  
; CURRENT APPLICATION NUMBER: PCT/US02/21324  
; CURRENT FILING DATE: 2002-08-14





LOCATION: (1)..(442)  
OTHER INFORMATION: Humanized Antibody Heavy Chain  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (36)..(56)  
OTHER INFORMATION: Xaa at position 56 is any amino acid, provided that Xaa at position 57 is Ser or Thr  
OTHER INFORMATION: on 57 is neither Asp nor Pro and Xaa at position 59 is Ser or Thr  
OTHER INFORMATION: then Xaa at position 56 is not Asn  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (57)..(57)  
OTHER INFORMATION: Xaa at position 57 is any amino acid, provided that Xaa at position 58 is Ser or Thr, then Xaa at position 59 is Ser or Thr  
OTHER INFORMATION: position 57 is Asp or Pro  
FEATURE:  
NAME/KEY: MISC\_FEATURE  
LOCATION: (58)..(58)  
OTHER INFORMATION: Xaa at position 58 is any amino acid, provided that Xaa at position 59 is Ser or Thr  
OTHER INFORMATION: position 56 is Asn and Xaa at position 57 is neither Asp nor Pro  
OTHER INFORMATION: then Xaa at position 58 is neither Ser nor Thr  
PCT-US02-26321-16

Query Match 76.1%; Score 343; DB 1; Length 442;  
Best Local Similarity 100.0%; Pred. No. 1.4e-160;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 109 DYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 168  
Db 100 DYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 159  
Qy 169 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 228  
Db 160 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 219  
Qy 229 TCPGPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 288  
Db 220 TCPGPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 279  
Qy 289 HNAKTPREEQYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 348  
Db 280 HNAKTPREEQYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 339  
Qy 349 EPQVYTLPPSRDELTKNOVSLTCLVKGYFSPDIAVWESNGOPENNYKTTTPVLDSDGSF 408  
Db 340 EPQVYTLPPSRDELTKNOVSLTCLVKGYFSPDIAVWESNGOPENNYKTTTPVLDSDGSF 399  
Qy 409 FLYSKLTVDKSRWQOGNVPFSCSVMEALHNHYTQKSLSLSPGK 451  
Db 400 FLYSKLTVDKSRWQOGNVPFSCSVMEALHNHYTQKSLSLSPGK 442

RESULT 7  
PCT-US02-11853-12  
Sequence 12, Application PC/TUS0211853  
GENERAL INFORMATION:  
APPLICANT: Eli Lilly and Company  
TITLE OF INVENTION: Humanized Antibodies  
FILE REFERENCE: X14958  
CURRENT APPLICATION NUMBER: PCT/US02/11853  
CURRENT FILING DATE: 2002-04-26  
PRIOR APPLICATION NUMBER: 60/287539  
PRIOR FILING DATE: 2001-04-30  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 449  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: humanized antibody  
PCT-US02-11853-12  
Query Match 76.1%; Score 343; DB 1; Length 449;

Best Local Similarity 100.0%; Pred. No. 1.5e-160;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 109 DYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 168  
Db 107 DYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 166  
Qy 169 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 228  
Db 167 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 226  
Qy 229 TCPGPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 288  
Db 227 TCPGPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 286  
Qy 289 HNAKTPREEQYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 348  
Db 287 HNAKTPREEQYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 346  
Qy 349 EPQVYTLPPSRDELTKNOVSLTCLVKGYFSPDIAVWESNGOPENNYKTTTPVLDSDGSF 408  
Db 347 EPQVYTLPPSRDELTKNOVSLTCLVKGYFSPDIAVWESNGOPENNYKTTTPVLDSDGSF 406  
Qy 409 FLYSKLTVDKSRWQOGNVPFSCSVMEALHNHYTQKSLSLSPGK 451  
Db 407 FLYSKLTVDKSRWQOGNVPFSCSVMEALHNHYTQKSLSLSPGK 449  
RESULT 8  
PCT-US02-11854A-12  
Sequence 12, Application PC/TUS0211854A  
GENERAL INFORMATION:  
APPLICANT: Eli Lilly and Company  
TITLE OF INVENTION: Humanized Antibodies  
FILE REFERENCE: X-14819  
CURRENT APPLICATION NUMBER: PCT/US02/11854A  
CURRENT FILING DATE: 2002-04-26  
PRIOR APPLICATION NUMBER: US 60/287,653  
PRIOR FILING DATE: 2001-04-30  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 12  
LENGTH: 453  
TYPE: PRT  
ORGANISM: humanized antibody  
PCT-US02-11854A-12

Query Match 76.1%; Score 343; DB 1; Length 453;  
Best Local Similarity 100.0%; Pred. No. 1.5e-160;  
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 109 DYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 168  
Db 111 DYWGQGLTVTVSSASTKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALT 170  
Qy 169 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 228  
Db 171 SGVHTFPAVLQSSGLYSLSVTVVPSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTH 230  
Qy 229 TCPGPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 288  
Db 231 TCPGPCAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEV 290  
Qy 289 HNAKTPREEQYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 348  
Db 291 HNAKTPREEQYNSTYRVVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPR 350  
Qy 349 EPQVYTLPPSRDELTKNOVSLTCLVKGYFSPDIAVWESNGOPENNYKTTTPVLDSDGSF 408  
Db 351 EPQVYTLPPSRDELTKNOVSLTCLVKGYFSPDIAVWESNGOPENNYKTTTPVLDSDGSF 410  
Qy 409 FLYSKLTVDKSRWQOGNVPFSCSVMEALHNHYTQKSLSLSPGK 451  
|||||



; PRIOR APPLICATION NUMBER: 60/234,274  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/234,223  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: 60/228,924  
; PRIOR FILING DATE: 2000-08-30  
; PRIOR APPLICATION NUMBER: 60/224,518  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,369  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/224,519  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,964  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/241,809  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/249,299  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/236,327  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/241,785  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/244,617  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: 60/225,268  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/236,368  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/231,856  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/231,868  
; PRIOR FILING DATE: 2000-12-08  
; PRIOR APPLICATION NUMBER: 60/229,344  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/234,997  
; PRIOR FILING DATE: 2000-09-25  
; PRIOR APPLICATION NUMBER: 60/229,343  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,345  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,287  
; PRIOR FILING DATE: 2000-09-01  
; PRIOR APPLICATION NUMBER: 60/229,513  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/231,413  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/229,509  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: 60/236,367  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/237,039  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,038  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/236,370  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/236,802  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,037  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,040  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/240,960  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/239,935  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/239,937  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/241,787  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,474  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/246,532

; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/249,216  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,210  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/226,681  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,759  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/225,213  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/227,182  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,214  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/235,836  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/230,438  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/215,135  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/225,266  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/249,218  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,208  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,213  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,212  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,207  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,245  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,244  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,217  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,211  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,215  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,264  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,214  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,297  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/232,400  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/231,242  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,081  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,080  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,414  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,244  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,064  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/233,063  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,397  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,399  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,401  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/241,808  
; PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065

Query Match 76.1%; Score 343; DB 6; Length 494;
Best Local Similarity 100.0%; Pred. No. 1.5e-160;
Matches 343; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 109 DWYGGTLLTVSSASTKGPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 168
DB 152 DWYGGTLLTVSSASTKGPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 211
QY 169 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 228
DB 212 SGVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 271
QY 229 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 288
DB 272 TCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 331
QY 289 HNAKTKPREEQYNSTYRVVSVTLVHLDWLNKKEYCKVSNKALPAPIEKTISKAKGQPR 348
DB 332 HNAKTKPREEQYNSTYRVVSVTLVHLDWLNKKEYCKVSNKALPAPIEKTISKAKGQPR 391
QY 349 EQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 408
DB 392 EQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 451
QY 409 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
DB 452 FLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 494

RESULT 12
PCT-US02-21281-18
; Sequence 18, Application PC/TUS0221281
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Interleukin-1 Beta Antibodies
; FILE REFERENCE: X-14900
; CURRENT APPLICATION NUMBER: PCT/US02/21281
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: US 60/307,973
; PRIOR FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: US 60/312,278
; PRIOR FILING DATE: 2001-08-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: patent in version 3.1
; SEQ ID NO 18
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody full-length heavy chain region
PCT-US02-21281-18

Query Match 75.8%; Score 342; DB 1; Length 450;
Best Local Similarity 100.0%; Pred. No. 4.5e-160;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 YWQGGTLTVSSASTKGPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 169
DB 109 YWQGGTLTVSSASTKGPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 168
QY 170 GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 229
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DB 169 GVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 228
QY 230 CPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 289
DB 229 CPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 288
QY 290 NAKTKPREEQYNSTYRVVSVTLVHLDWLNKKEYCKVSNKALPAPIEKTISKAKGQPR 349
DB 289 NAKTKPREEQYNSTYRVVSVTLVHLDWLNKKEYCKVSNKALPAPIEKTISKAKGQPR 348
QY 350 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 409
DB 349 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 408
QY 410 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
DB 409 LYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 450

RESULT 13
PCT-US01-27352-2
; Sequence 2, Application PC/TUS0127352
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; TITLE OF INVENTION: CO-CRYSTAL STRUCTURE OF MONOCLONAL ANTIBODY 5C8 AND
; FILE REFERENCE: A0966PCT
; CURRENT APPLICATION NUMBER: PCT/US01/27352
; CURRENT FILING DATE: 2002-08-31
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: humanized 5c8 heavy chain amino acid
PCT-US01-27352-2

Query Match 75.6%; Score 341; DB 1; Length 448;
Best Local Similarity 100.0%; Pred. No. 1.4e-159;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 111 WQGGTLTVSSASTKGPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 170
DB 108 WQGGTLTVSSASTKGPVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 167
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 230
DB 168 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHT 227
QY 231 CPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 290
DB 228 CPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGV 287
QY 291 AKTKPREEQYNSTYRVVSVTLVHLDWLNKKEYCKVSNKALPAPIEKTISKAKGQPR 350
DB 288 AKTKPREEQYNSTYRVVSVTLVHLDWLNKKEYCKVSNKALPAPIEKTISKAKGQPR 347
QY 351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 410
DB 348 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSF 407
QY 411 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
DB 408 YSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 448

RESULT 14
US-09-791-537-118977
; Sequence 118977, Application US/09791537
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; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 118977
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-118977

Query Match 75.6%; Score 341; DB 5; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.4e-159;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYLKDYFPEPVTVSWNSGALTSG 170
Db 133 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYLKDYFPEPVTVSWNSGALTSG 192

Qy 171 VHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVPEKSCDKTHTC 230
Db 193 VHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVPEKSCDKTHTC 252

Qy 231 PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVYDVDSHEDPEVKFNWYVDGVEVHN 290
Db 253 PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVYDVDSHEDPEVKFNWYVDGVEVHN 312

Qy 291 AKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 350
Db 313 AKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 372

Qy 351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFFL 410
Db 373 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFFL 432

Qy 411 YSKLTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLSPGK 451
Db 433 YSKLTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLSPGK 473

RESULT 15
US-09-791-537-104528
; Sequence 104528, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
; APPLICANT: Danzer, Joseph
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBERS
; FILE REFERENCE: 261/210
; CURRENT APPLICATION NUMBER: US/09/791,537
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 153055
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 104528
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-791-537-104528

Query Match 75.6%; Score 341; DB 5; Length 476;
Best Local Similarity 100.0%; Pred. No. 1.4e-159;
Matches 341; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYLKDYFPEPVTVSWNSGALTSG 170
Db 136 WGQGLTVTVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYLKDYFPEPVTVSWNSGALTSG 195
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Qy 171 VHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVPEKSCDKTHTC 230
Db 196 VHTFPVAVLQSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKKVPEKSCDKTHTC 255
Qy 231 PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVYDVDSHEDPEVKFNWYVDGVEVHN 290
Db 256 PPCPAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVYDVDSHEDPEVKFNWYVDGVEVHN 315
Qy 291 AKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 350
Db 316 AKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIISKAKGQPREP 375
Qy 351 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFFL 410
Db 376 QVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFFL 435
Qy 411 YSKLTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLSPGK 451
Db 436 YSKLTVDKSRWQGNVFCSCVMHEALHNYHTOKSLSLSPGK 476
```

Search completed: October 9, 2002, 19:33:56  
Job time : 60.8265 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:19:35 ; Search time 24.1607 seconds  
(without alignments)  
1793.668 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

Sequence: 1 QVQLVQSGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPGK 451

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 330   | 73.2        | 330    | 1 GHU    | Ig gamma-1 chain C |
| 2          | 230   | 51.0        | 255    | 4 S31866 | Ig gamma-1 chain C |
| 3          | 153   | 33.9        | 234    | 2 PT0207 | Ig gamma chain C r |
| 4          | 140   | 31.0        | 374    | 2 S69339 | Ig heavy chain V r |
| 5          | 109   | 24.2        | 220    | 2 A49444 | Ig gamma-1 heavy C |
| 6          | 90    | 20.0        | 218    | 2 A36040 | Ig heavy chain V-I |
| 7          | 89    | 19.7        | 249    | 2 S69340 | Ig heavy chain VHI |
| 8          | 65    | 14.4        | 377    | 2 A60764 | Ig gamma-3 chain C |
| 9          | 65    | 14.4        | 377    | 2 A23511 | Ig gamma-3 chain C |
| 10         | 63    | 14.0        | 120    | 2 S36278 | Ig heavy chain V r |
| 11         | 62    | 13.7        | 97     | 2 S26652 | Ig gamma-1 chain C |
| 12         | 57    | 12.6        | 327    | 1 G4HU   | Ig gamma-4 chain C |
| 13         | 53    | 11.8        | 241    | 2 S69131 | Ig heavy chain [DO |
| 14         | 53    | 11.8        | 326    | 1 G2HU   | Ig gamma-2 chain C |
| 15         | 51    | 11.3        | 90     | 2 S24248 | Ig heavy chain V r |
| 16         | 48    | 10.6        | 98     | 2 S26889 | Ig heavy chain V r |
| 17         | 48    | 10.6        | 99     | 2 S24259 | Ig heavy chain V r |
| 18         | 48    | 10.6        | 100    | 2 S24258 | Ig heavy chain V r |
| 19         | 48    | 10.6        | 101    | 2 S24257 | Ig heavy chain V r |
| 20         | 48    | 10.6        | 102    | 2 S24260 | Ig heavy chain V r |
| 21         | 48    | 10.6        | 104    | 2 S24255 | Ig heavy chain V r |
| 22         | 48    | 10.6        | 106    | 2 S24256 | Ig heavy chain V r |
| 23         | 48    | 10.6        | 108    | 2 PH1648 | Ig heavy chain V r |
| 24         | 48    | 10.6        | 109    | 2 PH1649 | Ig heavy chain V r |
| 25         | 48    | 10.6        | 112    | 2 PH1647 | Ig heavy chain V r |
| 26         | 48    | 10.6        | 117    | 2 A45953 | Ig heavy chain pre |
| 27         | 48    | 10.6        | 118    | 2 S31121 | Ig heavy chain - h |
| 28         | 48    | 10.6        | 119    | 2 S36005 | Ig heavy chain V r |
| 29         | 48    | 10.6        | 119    | 2 D36005 | Ig heavy chain V r |

#### ALIGNMENTS

##### RESULT 1

##### GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 16-Jul-1999

C:Accession: A93433; S33887; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma gene.

A:Reference number: A93433; NUID:82274238

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: this sequence has the Gm(17) allotypic marker, 97-Iys, and the Gm(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; NUID:83001943

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113;235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; NUID:71064024

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96,'R',98-135 <CUN>

A:Note: this sequence has the Gm(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; NUID:71064025

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',2

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1

Igen Primaerstruktur.  
A:Reference number: A91668; MUID:77070269  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'O', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A>Note: this sequence has the Gln(17) and Gln(1) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL  
A:Reference number: A91723; MUID:83289131  
A:Contents: myeloma protein KOL; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A>Note: this sequence has the Gln(3) and Gln(non-1) markers  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:71064027  
A:Contents: annotation; disulfide bonds  
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enbride cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Intron: 99/1; 114/1; 224/1  
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:27-83,144-204,250-308/bisulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 73.2%; Score 330; DB 1; Length 330;  
Best Local Similarity 100.0%; Pred. No. 4.3e-306;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 181  
DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 60

QY 182 GLYSLSVTVFSSSLGTQTYICNVNHPKSNTPKDKKPEKSCDKTHTCPGPCPAPPELLGG 241  
DB 61 GLYSLSVTVFSSSLGTQTYICNVNHPKSNTPKDKKPEKSCDKTHTCPGPCPAPPELLGG 120

QY 242 PSVFLEPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 301  
DB 121 PSVFLEPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYN 180

QY 302 STYRVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIISKAKGQPREPOVYTLPPSRDE 361  
DB 181 STYRVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIISKAKGQPREPOVYTLPPSRDE 240

QY 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 421  
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300

QY 422 QGQNVFSCSVMHREALNHNHYTQKSLSLSPGK 451  
DB 301 QGQNVFSCSVMHREALNHNHYTQKSLSLSPGK 330

RESULT 2  
S31866  
Ig gamma-1 chain C region - synthetic  
C:Species: synthetic  
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C:Accession: S31866  
R:Filipula, D.  
submitted to the EMBL Data Library, February 1993  
A:Description: Screening method for protein-protein interactions of cloned gene produc  
A:Reference number: S31866  
A:Accession: S31866  
A:Molecule type: mRNA  
A:Residues: 1-255 <FILL>  
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069  
C:Keywords: immunoglobulin  
F:1-22/Region: Escherichia coli outer membrane protein A precursor  
F:23-255/Region: human Ig gamma-1 chain C region

Query Match 51.0%; Score 230; DB 4; Length 255;  
Best Local Similarity 100.0%; Pred. No. 5.8e-211;  
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 KSCDKTHTCPPCPAPPELLGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 281  
DB 26 KSCDKTHTCPPCPAPPELLGSPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 85

QY 282 YVDGVEVHNNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTI 341  
DB 86 YVDGVEVHNNAKTKPREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTI 145

QY 342 KAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 401  
DB 146 KAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPV 205

QY 402 LSDGSEFFLYSKLTVDKSRWQQGNVSCSVMHREALNHNHYTQKSLSLSPGK 451  
DB 206 LSDGSEFFLYSKLTVDKSRWQQGNVSCSVMHREALNHNHYTQKSLSLSPGK 255

RESULT 3  
PT0207  
Ig gamma chain C region - chimpanzee  
C:Species: Pan troglodytes (chimpanzee)  
C:Date: 23-Nov-1991 #sequence\_revision 23-Nov-1991 #text\_change 16-Jul-1999  
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.  
Mol. Immunol. 28, 319-322, 1991  
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.  
A:Reference number: PT0207; MUID:91287716  
A:Accession: PT0207  
A:Molecule type: mRNA  
A:Residues: 1-234 <EHR>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 33.9%; Score 153; DB 2; Length 234;  
Best Local Similarity 100.0%; Pred. No. 1.1e-137;  
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 235 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTK 294  
DB 25 APELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNAKTK 84

QY 295 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIISKAKGQPREPOVYT 354  
DB 85 PREEQYNSTYRVSVLTVLHQDWLNGKEYCKVSKNKAAPAEKTIISKAKGQPREPOVYT 144

QY 355 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 387  
DB 145 LPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 177



## RESULT 4

S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C>Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
C:Accession: S69339; S72664  
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogné, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A>Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687  
A:Accession: S69339  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:CROSS-references: EMBL:X81695  
R:Khamilichi, A.A.  
Submitted to the EMBL Data Library, September 1994  
A:Reference number: S72664  
A:Accession: S72664  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, 'C', 142-374 <KH2>  
A:CROSS-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 31.0%; Score 140; DB 2; Length 374;  
Best Local Similarity 100.0%; Pred. No. 4.1e-125;  
Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 EPKSCDKTCTCPAPPELLGSPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKF 279

Db 143 EPKSCDKTCTCPAPPELLGSPSVFLPPPKDGLMISRTPEVTCVVVDVSHEDPEVKF 202

QY 280 NWTVDGVEVHNKATPREEQYNSTYRVSVLTVLHQDLNGKEYCKVSKNALPAPIETK 339

Db 203 NWTVDGVEVHNKATPREEQYNSTYRVSVLTVLHQDLNGKEYCKVSKNALPAPIETK 262

QY 340 ISKAKGQPREPQVYTLPPSR 359

Db 263 ISKAKGQPREPQVYTLPPSR 282

## RESULT 5

A49444  
Ig gamma-1 heavy chain (New) - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 03-Mar-1994 #sequence\_revision 03-Mar-1994 #text\_change 16-Jul-1999  
R:Saul, F.A.; Poljak, R.J.  
Proteins 14, 363-371, 1992  
A>Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 Å resolution  
A:Reference number: A49444; MUID:93066153  
A:Accession: A49444  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-220 <SAS>  
A>Note: sequence modified after extraction from NCBI backbone  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:137-202/Domain: immunoglobulin homology <IMM>

Query Match 24.2%; Score 109; DB 2; Length 220;  
Best Local Similarity 100.0%; Pred. No. 8.6e-96;  
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 LVTSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVWSNGALTSGVHTFP 175

Db 112 LVTSSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVWSNGALTSGVHTFP 171

QY 176 AVLQSSGLYSLSSVTVTPSSSLGTOTYICNVNHRKPSNTKVDKKEPKSC 224

Db 172 AVLQSSGLYSLSSVTVTPSSSLGTOTYICNVNHRKPSNTKVDKKEPKSC 220

Db 172 AVLQSSGLYSLSSVTVTPSSSLGTOTYICNVNHRKPSNTKVDKKEPKSC 220

## RESULT 6

A36040  
Ig heavy chain V-III region (ART) - human (fragments)  
C:Species: Homo sapiens (man)  
C>Date: 16-Nov-1990 #sequence\_revision 16-Nov-1990 #text\_change 21-Jan-2000  
C:Accession: A36040  
R:Eulitz, M.; Weiss, D.T.; Solomon, A.  
Proc. Natl. Acad. Sci. U.S.A. 87, 6542-6546, 1990  
A>Title: Immunoglobulin heavy-chain-associated amyloidosis.  
A:Reference number: A36040; MUID:90370821  
A:Accession: A36040  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-218 <EUL>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:132-199/Domain: immunoglobulin homology <IMM>

Query Match 20.0%; Score 90; DB 2; Length 218;  
Best Local Similarity 100.0%; Pred. No. 1.1e-77;  
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 345 GQPREQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 404

Db 113 GQPREQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLD 172

QY 405 DGSFFLYSKLTVDKSRWQQGNVFCVMHE 434

Db 173 DGSFFLYSKLTVDKSRWQQGNVFCVMHE 202

## RESULT 7

S69340  
Ig heavy chain VHIII-D-JH-CH3 region - human  
C:Species: Homo sapiens (man)  
C>Date: 28-Oct-1996 #sequence\_revision 27-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: S69340  
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogné, M.  
Eur. J. Biochem. 229, 54-60, 1995  
A>Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687  
A:Accession: S69340  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-249 <KHA>  
A:CROSS-references: EMBL:X81696  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:162-229/Domain: immunoglobulin homology <IMM>

Query Match 19.7%; Score 89; DB 2; Length 249;  
Best Local Similarity 100.0%; Pred. No. 1.1e-76;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 363 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQ 422

Db 161 TKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQ 220

QY 423 QGNVFCVMHEALHNHYTQKSLSLSPGK 451

Db 221 QGNVFCVMHEALHNHYTQKSLSLSPGK 249

## RESULT 8

A60764  
Ig gamma-3 chain C region, form LAT - human  
C:Species: Homo sapiens (man)  
C>Date: 14-May-1993 #sequence\_revision 14-May-1993 #text\_change 16-Jul-1999  
C:Accession: A60764  
R:Huck, S.; Lefranc, G.; Lefranc, M.P.  
Immunogenetics 30, 250-257, 1989

A; Molecule type: protein  
A; Residues: 1-30; 81-326 <PIN>  
C; Genetics:  
C; Gene: PIN1

A:Cross-references: GDB:119340; OMIM:147130  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1; 111/1; 221/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:99-110/Region: hinge  
F:134-203/Domain: immunoglobulin homology <IM2>  
F:240-307/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83/141-201,247-305/Disulfide bonds: #status predicted  
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.6%; Score 57; DB 1; Length 327;  
Best Local Similarity 100.0%; Pred. No. 4e-46;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGT 199  
|||||  
DB 22 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSSSLGT 78  
|||||

RESULT 13  
S69131  
Ig heavy chain (DOT) - human (fragment)  
N:Alternate names: anti-riboflavin IgG Fd fragment  
C:Species: Homo sapiens (man)  
C:Date: 12-Feb-1998 #sequence\_revision 22-May-1998 #text\_change 21-Jan-2000  
C:Accession: S69131  
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.  
Eur. J. Biochem. 228, 886-893, 1995  
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins  
A:Reference number: S69130; MUID:95255298  
A:Accession: S69131  
A:Molecule type: protein  
A:Residues: 1-241 <STO>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid  
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MA>  
F:140-205/Domain: immunoglobulin homology <IMW>  
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 11.8%; Score 53; DB 2; Length 241;  
Best Local Similarity 100.0%; Pred. No. 2e-42;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSS 195  
|||||  
DB 142 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSS 194  
|||||

RESULT 14  
G2HU  
Ig gamma-2 chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Apr-1981 #sequence\_revision 13-Jun-1983 #text\_change 21-Jul-2000  
C:Accession: A93906; A92809; A90752; A93132; A02148  
R:Ellison, J.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A:Title: Linkage and sequence homology of two human immunoglobulin gamma chain components  
A:Reference number: A93906; MUID:82197621  
A:Accession: A93906  
A:Molecule type: DNA  
A:Residues: 1-326 <ELL>  
A:Cross-references: GB:V00554; GB:J00230; NID:932759; PID:CA58438.1; PID:g6066056  
A:Note: Lys-326 is probably removed posttranslationally  
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional analysis  
A:Reference number: A92809; MUID:81007873

A:Contents: myeloma protein TIL  
A:Accession: A92809  
A:Molecule type: protein  
A:Residues: 1-19, Q'21-57, Z', 59, A', 61-193, D', 195-325 <WAN>  
A:Note: Trp-156 is at or near the complement-binding site  
R:Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A:Title: The amino acid sequences of the three heavy chain constant region domains of human immunoglobulin G2  
A:Reference number: A90752; MUID:80001357  
A:Contents: myeloma protein Zie  
A:Accession: A90752  
A:Molecule type: protein  
A:Residues: 1-24, E', 26-57, EV', 60-85, 132-171, Z'22', 175, B', 177-193, D', 195-196, Q', 1  
A:Note: This sequence has since been revised  
R:Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin G2  
A:Reference number: A93132; MUID:80114419  
A:Contents: Zie  
A:Accession: A93132  
A:Molecule type: protein  
A:Residues: 238-275 <HOF>  
R:Hofmann, T.; Parr, D.M.  
Submitted to the Atlas, March 1980  
A:Reference number: A94591  
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A:Note: The revised sequence differs from that shown in having 60-Ala and in the amidated

R:Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A:Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.  
A:Reference number: A90253; MUID:72033500  
A:Contents: annotation; myeloma protein Sa, disulfide bonds  
R:Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A:Title: Structural studies of immunoglobulin G.  
A:Reference number: A93157; MUID:69064124  
A:Contents: annotation; Sa, disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG2  
A:Cross-references: GDB:119338; OMIM:147110  
A:Map position: 14q32.33-14q32.33  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IM1>  
F:133-203/Domain: immunoglobulin homology <IM2>  
F:239-306/Domain: immunoglobulin homology <IM3>  
F:14/Disulfide bonds: interchain (to light chain) #status experimental  
F:27-83/140-200,246-304/Disulfide bonds: #status experimental  
F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.8%; Score 53; DB 1; Length 326;  
Best Local Similarity 100.0%; Pred. No. 2.6e-42;  
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSS 195  
|||||  
DB 22 TAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSSGLYSLSSVVPSS 74  
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RESULT 15  
S24248  
Ig heavy chain V region (VH26) - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Feb-1994 #sequence\_revision 10-Nov-1995 #text\_change 23-Jul-1999  
C:Accession: S24248  
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.  
Submitted to the EMBL Data Library, June 1992  
A:Description: A single VH gene predominates in the rearranged and expressed human B cell repertoire  
A:Reference number: S24247

Search completed: October 9, 2002, 19:25:52  
Job time : 24.1607 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:13:25 ; Search time 13.8061 Seconds  
(without alignments)  
1264.839 Million cell updates/sec

Title: US-09-822-698a-26

Perfect score: 451

Sequence: 1 QVQLVQSGGGLVQPGGSLRL.....MHEALHNYTKSLSLSPGK 451

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID        | Description        |
|------------|-------|-------------|--------|--------------|--------------------|
| 1          | 330   | 73.2        | 330    | 1 GCL_HUMAN  | P01857 homo sapien |
| 2          | 57    | 12.6        | 327    | 1 GC4_HUMAN  | P01861 homo sapien |
| 3          | 53    | 11.8        | 326    | 1 GC2_HUMAN  | P01859 homo sapien |
| 4          | 45    | 10.0        | 290    | 1 GC3_HUMAN  | P01860 homo sapien |
| 5          | 44    | 9.8         | 116    | 1 HV05_CARAU | P19181 carassius a |
| 6          | 37    | 8.2         | 117    | 1 HV3C_HUMAN | P01784 homo sapien |
| 7          | 25    | 5.2         | 323    | 1 GC_RABIT   | P01870 oryctolagus |
| 8          | 23    | 5.1         | 115    | 1 HV3D_HUMAN | P01785 homo sapien |
| 9          | 23    | 5.1         | 116    | 1 HV3R_HUMAN | P01779 homo sapien |
| 10         | 23    | 5.1         | 119    | 1 HV3M_HUMAN | P01774 homo sapien |
| 11         | 23    | 5.1         | 119    | 1 HV3N_HUMAN | P01775 homo sapien |
| 12         | 23    | 5.1         | 119    | 1 HV3P_HUMAN | P01777 homo sapien |
| 13         | 23    | 5.1         | 120    | 1 HV3E_HUMAN | P01766 homo sapien |
| 14         | 21    | 4.7         | 117    | 1 HV3Q_HUMAN | P01776 homo sapien |
| 15         | 20    | 4.4         | 126    | 1 HV01_CANFA | P01772 homo sapien |
| 16         | 19    | 4.2         | 114    | 1 HV3K_HUMAN | P01784 canis famli |
| 17         | 19    | 4.2         | 329    | 1 GC2_CAVPO  | P01862 cavia porce |
| 18         | 17    | 3.8         | 117    | 1 HV17_MOUSE | P01786 mus musculu |
| 19         | 17    | 3.8         | 122    | 1 HV20_MOUSE | P01789 mus musculu |
| 20         | 17    | 3.8         | 122    | 1 HV21_MOUSE | P01780 mus musculu |
| 21         | 17    | 3.8         | 123    | 1 HV18_MOUSE | P01787 mus musculu |
| 22         | 17    | 3.8         | 123    | 1 HV19_MOUSE | P01788 mus musculu |
| 23         | 17    | 3.8         | 123    | 1 HV22_MOUSE | P01791 mus musculu |
| 24         | 17    | 3.8         | 123    | 1 HV23_MOUSE | P01792 mus musculu |
| 25         | 17    | 3.8         | 123    | 1 HV24_MOUSE | P01793 mus musculu |
| 26         | 17    | 3.8         | 123    | 1 HV25_MOUSE | P01794 mus musculu |
| 27         | 17    | 3.8         | 144    | 1 HV26_MOUSE | P01795 mus musculu |
| 28         | 16    | 3.5         | 115    | 1 HV3F_HUMAN | P01767 homo sapien |
| 29         | 16    | 3.5         | 115    | 1 HV3S_HUMAN | P01780 homo sapien |
| 30         | 16    | 3.5         | 122    | 1 HV3A_HUMAN | P01762 homo sapien |
| 31         | 15    | 3.3         | 121    | 1 HV3J_HUMAN | P01771 homo sapien |
| 32         | 14    | 3.1         | 114    | 1 HV3B_HUMAN | P01763 homo sapien |
| 33         | 14    | 3.1         | 116    | 1 HV1A_RABIT | P01826 oryctolagus |

|    |    |     |     |              |                    |
|----|----|-----|-----|--------------|--------------------|
| 34 | 14 | 3.1 | 117 | 1 HV03_CARAU | P19180 carassius a |
| 35 | 13 | 2.9 | 97  | 1 HV56_MOUSE | P18527 mus musculu |
| 36 | 13 | 2.9 | 98  | 1 HV57_MOUSE | P18528 mus musculu |
| 37 | 13 | 2.9 | 116 | 1 HV3Q_HUMAN | P01778 homo sapien |
| 38 | 13 | 2.9 | 116 | 1 HV3T_HUMAN | P01781 homo sapien |
| 39 | 13 | 2.9 | 117 | 1 HV58_MOUSE | P18529 mus musculu |
| 40 | 13 | 2.9 | 117 | 1 HV59_MOUSE | P18530 mus musculu |
| 41 | 13 | 2.9 | 118 | 1 HV3V_HUMAN | P80419 homo sapien |
| 42 | 13 | 2.9 | 119 | 1 HV3I_HUMAN | P01770 homo sapien |
| 43 | 13 | 2.9 | 122 | 1 HV3G_HUMAN | P01768 homo sapien |
| 44 | 13 | 2.9 | 124 | 1 HV01_HUMAN | P01760 homo sapien |
| 45 | 13 | 2.9 | 142 | 1 HV01_RAT   | P01805 rattus norv |

#### ALIGNMENTS

RESULT 1  
GCL\_HUMAN  
ID GCL\_HUMAN STANDARD; PRT; 330 AA.  
AC P01857;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-1 chain C region.  
GN IGHG1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID:9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=82274238; PubMed=6287432;  
RA Ellison J.W., Berson B.J., Hood L.E.;  
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";  
RL Nucleic Acids Res. 10:4071-4079(1982).  
RN [2]  
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).  
RX MEDLINE=71064024; PubMed=5489771;  
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,  
RA Waxdal M.J., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";  
RL Biochemistry 9:3161-3170(1970).  
RN [3]  
RP SEQUENCE OF 136-329 (EU).  
RX MEDLINE=71064025; PubMed=5530842;  
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,  
RA Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";  
RL Biochemistry 9:3171-3181(1970).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN NIE).  
RX MEDLINE=77070269; PubMed=826475;  
RA Ponstingl H., Hilschmann N.;  
RT "The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).  
RN [5]  
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.  
RX MEDLINE=83289131; PubMed=6884994;  
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;  
RT "Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).  
RN [6]  
RP DISULFIDE BONDS.  
RX MEDLINE=71064027; PubMed=4923144;  
RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.

RT Intrachain disulfide bonds.";  
 RL Biochemistry 9:3188-3196(1970).  
 [7]  
 RP DISULFIDE BONDS.  
 RX MEDLINE-77070267; PubMed-1002129;  
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and  
 RT characterization of the protein, the L- and H-chains, the  
 RT cyanogen bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 [8]  
 RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE-81208100; PubMed-7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -!- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE  
 CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)  
 CC MARKER & THE GIM (NON-1) MARKERS.  
 CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF  
 CC 35, 116, 198, 269 & 272.  
 CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES  
 CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES  
 CC 268-272.  
 CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF  
 CC RESIDUES 198, 267 & 272.  
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 CC -----  
 DR EMBL; J00228; AAC84527.1; ALT\_INIT.  
 DR PIR; A02146; GHGU.  
 DR PDB; 1FC1; 15-JUL-92.  
 DR PDB; 1FC2; 15-JUL-92.  
 DR MIM; 147100; -.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003597; Ig\_cl.  
 DR InterPro; IPR003600; Ig\_like.  
 DR Pfam; PF00047; Ig; 3.  
 DR SMART; SM00410; Ig\_Like; 1.  
 DR SMART; SM00407; IG1; 2.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
 3D-structure.  
 FT NON\_TER 1 1  
 FT DOMAIN 1 98  
 FT DOMAIN 99 110  
 FT DOMAIN 111 223  
 FT DOMAIN 224 330  
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 FT DISULFID 103 103  
 FT DISULFID 109 109  
 FT DISULFID 112 112  
 FT DISULFID 144 204  
 FT DISULFID 250 308  
 FT CARBOHYD 180 180  
 FT MOD\_RES 330 330  
 FT VARIANT 97 97  
 FT VARIANT 239 239  
 FT VARIANT 241 241  
 FT STRAND 123 126  
 FT HELIX 130 134

FT TURN 136 137  
 FT STRAND 141 148  
 FT STRAND 158 162  
 FT TURN 163 164  
 FT STRAND 165 166  
 FT STRAND 175 178  
 FT STRAND 183 190  
 FT HELIX 193 197  
 FT TURN 198 199  
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 FT STRAND 274 276  
 FT STRAND 280 281  
 FT TURN 283 284  
 FT STRAND 287 296  
 FT HELIX 297 301  
 FT TURN 302 303  
 FT STRAND 306 312  
 FT TURN 313 314  
 FT TURN 316 317  
 FT STRAND 320 324  
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 QY 122 ASTKGPSVFLPADSKSTSGTAAALCLVQDYEPPEPVVSNMGALTSVHTPEAVLQSS 181  
 DB 1 ASTKGPSVFLPADSKSTSGTAAALCLVQDYEPPEPVVSNMGALTSVHTPEAVLQSS 60  
 QY 182 GLYSLSVVTVFPSSSLGTOTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGG 241  
 DB 61 GLYSLSVVTVFPSSSLGTOTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGG 120  
 QY 242 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYN 301  
 DB 121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYN 180  
 QY 302 STYRVSVLTVLHODMUNGKEYCKKYSNKAALPAPEKTIKAKGQPREPQVYTLPPSRDE 361  
 DB 181 STYRVSVLTVLHODMUNGKEYCKKYSNKAALPAPEKTIKAKGQPREPQVYTLPPSRDE 240  
 QY 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 421  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
 QY 422 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 451  
 DB 301 QQGNVFCSVMHEALHNHYTQKSLSLSPGK 330  
 RESULT 2  
 GC4\_HUMAN  
 ID GC4\_HUMAN STANDARD; PRT; 327 AA.  
 AC P01861;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DE 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Ig gamma-4 chain C region.  
 OS IGHG4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;

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RT RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RN
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RT constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
RN
CC -----
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CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A02150; GAHU.
DR HSSP; P01842; 7FAB.
DR MIM; 147130; .
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; Ig_c1; 2.
DR PROSITE; PS00290; Ig_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98
FT CH1.
FT DOMAIN 99 110
FT HINGE.
FT DOMAIN 111 220
FT CH2.
FT DOMAIN 221 327
FT CH3.
FT DISULFID 14 14
FT INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 106 106
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109
FT INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EBDB811EF208E7A CRC64;

Query Match 12.6%; Score 57; DB 1; Length 327;
Best Local Similarity 100.0%; Pred. No. 2.7e-50;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 143 TAALGCLVKDYFFPEPTVSVNSGALTSVHTFPAVLQSSGLYSLSSVVTVPSSSLGT 199
|||||
DD 22 TAALGCLVKDYFFPEPTVSVNSGALTSVHTFPAVLQSSGLYSLSSVVTVPSSSLGT 78

RESULT 3
ID GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;

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RT "Linkage and sequence homology of two human immunoglobulin gamma
RT heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN
RP SEQUENCE OF 88-115 FROM N.A.
RX TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;
RT "Structure of the hinge-coding segments in human immunoglobulin gamma
RT evolution of a gene family.";
RL Cell 29:671-679(1982).
RN
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RX TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;
RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT genes.";
RL EMBO J. 1:403-407(1982).
RN
RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;
RT "The primary structure of a human IgG2 heavy chain: genetic,
RT evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN
RP SEQUENCE OF 1-85 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=113060;
RA Connell G.E., Parr D.M., Hofmann T.;
RT "The amino acid sequences of the three heavy chain constant region
RT domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN
RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;
RT "A note of the amino acid sequence of residues 381-391 of human
RT immunoglobulins gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN
RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;
RT Submitted (MAR-1980) to the PIR data bank.
RN
RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=9525298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
RT "Characterization of the two unique human anti-flavin monoclonal
RT immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN
RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;
RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN
RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;
RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
RN
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DR EMBL: J00230; AAB59393.1; -.
DR PIR: A02148; G2HU.
DR HSP; P01857; IFC1.
DR MIM; 147110; -.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003597; Ig_cl.
DR InterPro: IPR003600; Ig_like.
DR Pfam: PF00047; Ig; 3.
DR SMART: SM00410; Ig-like; 1.
DR SMART: SM00407; IGcl; 2.
DR PROSITE: PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 219
FT DOMAIN 220 326
FT DOMAIN 327 434
FT DISULFID 14 14
FT DISULFID 27 83
FT DISULFID 102 102
FT DISULFID 103 103
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 140 200
FT DISULFID 246 304
FT SITE 156 156
FT MOD_RES 326 326
FT VARIANT 60 60
FT CONFLICT 109 109
FT SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
Query Match 11.8%; Score 53; DB 1; Length 326;
Best Local Similarity 100.0%; Pred. No. 3.4e-46;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 143 TAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLSGLYSLSVYVPSS 195
Db 22 TAALGCLVKDYFPEPTVSWNSGALTSVHTFPAVLSGLYSLSVYVPSS 74
RESULT 4
GC3_HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RL gamma 3 heavy-chain disease protein Wis.",
RN Biochemistry 19:4304-4308(1980).
RP REVISIONS TO 12-97 OF PROTEIN WIS.
RX MEDLINE=77118561; PubMed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
RL quadruplication of a 15-amino acid residue basic unit.",
RN J. Biol. Chem. 252:883-889(1977).
RP REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN WIS).
RX MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.

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RT Structure of the Fc fragment of immunoglobulin G3.;
RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT gene deletion model.",
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -1- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC NORMALLY PRESENT IN THE HINGE REGION.
CC -1- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC REF. 2.
CC -1- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
CC AND ALL OF THE CH1 REGION.
CC -1- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CC OF THE CH1 REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
CC GAMMA-3 HEAVY CHAINS.
CC -1- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
CC OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -1- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
CC SEGMENT (12-28).
CC -----
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CC -----
CC EMBL: J00231; AAB52805.1; ALT_SEQ.
CC PIR: A02149; G3HUM1.
CC HSP; P01857; IFC1.
CC MIM; 147120; -.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003597; Ig_cl.
CC InterPro: IPR003600; Ig_like.
CC Pfam: PF00047; Ig; 2.
CC SMART: SM00410; Ig-like; 1.
CC SMART: SM00407; IGcl; 1.
CC PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
FT DOMAIN 12 73
FT DOMAIN 74 183
FT DOMAIN 184 289
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6
FT DISULFID 7 7
FT DISULFID 24 24
FT DISULFID 27 27
FT DISULFID 33 33
FT DISULFID 39 39
FT DISULFID 42 42
FT DISULFID 48 48
FT DISULFID 54 54
FT DISULFID 57 57
FT DISULFID 63 63
FT DISULFID 69 69
FT DISULFID 72 72
FT CARBOHYD 140 140
FT MOD_RES 290 290
FT VARIANT 126 127
FT VARIANT 134 134
PYRROLIDONE CARBOXYLIC ACID.
N-LINKED (GLCNAC...),
INTERCHAIN (WITH HEAVY CHAIN DIMER).
INTERCHAIN (WITH HEAVY CHAIN DIMER).
INTERCHAIN (WITH HEAVY CHAIN DIMER).
INTERCHAIN (WITH HEAVY CHAIN DIMER).
INTERCHAIN (WITH HEAVY CHAIN DIMER).
INTERCHAIN (WITH HEAVY CHAIN DIMER).
INTERCHAIN (WITH HEAVY CHAIN DIMER).
INTERCHAIN (WITH HEAVY CHAIN DIMER).
INTERCHAIN (WITH HEAVY CHAIN DIMER).
INTERCHAIN (WITH HEAVY CHAIN DIMER).
N-LINKED (GLCNAC...),
REMOVED POST-TRANSLATIONALLY.
QV -> EB (IN ZUC).
/FTid=VAR_003890.
P -> L (IN OMM).

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FT VARIANT 139 139 /FTid=VAR_003891.
FT F -> Y (IN OMM).
FT /FTid=VAR_003892.
FT VARIANT 182 182 T -> A (IN OMM).
FT /FTid=VAR_003893.
FT VARIANT 227 227 S -> N (IN OMM).
FT /FTid=VAR_003894.
FT VARIANT 227 227 MISSING (IN ZUC).
FT /FTid=VAR_003895.
FT VARIANT 279 279 F -> Y (IN OMM).
FT /FTid=VAR_003896.
SQ SEQUENCE 290 AA; 32331 MW; E69CB95705B2F46 CRC64;

Query Match 10.0%; Score 45; DB 1; Length 290;
Best Local Similarity 100.0%; Pred. No. 4.6e-38; Indels 0; Gaps 0;
Matches 45; Conservative 0; Mismatches 0;

Qy 233 CPAPELLGGPSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEV 277
Db 72 CPAPELLGGPSVFLPPKPKDLMISRTPEVTCVVDVSHEDPEV 116

RESULT 5
ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 5A precursor.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Carassius.
OX NCBI_TaxID=7957;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88144476; PubMed=3125551;
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR; B28966; B28966.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
FT DOMAIN 50 49 FRAMEWORK-1.
FT DOMAIN 54 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 85 116 FRAMEWORK-3.
FT DISULFID 41 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 9.8%; Score 44; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 2.1e-37;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 SGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCA 97
Db 72 SGGSTYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCA 115

RESULT 6
HV3C_HUMAN STANDARD; PRT; 117 AA.
ID HV3C_HUMAN
AC P01764;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region VH26 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81101090; PubMed=6450418;
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region."
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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CC -----
DR EMBL; J00236; AAA53516.1; -
DR EMBL; M35415; AAA58735.1; -
DR PIR; A02047; H3HU26.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E82673F1A3CB0F1 CRC64;

Query Match 8.2%; Score 37; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 3.1e-30;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAK 98
Db 81 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAK 117

RESULT 7
GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-I haplotype."
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype."
RL Biochem. J. 151:337-349(1975).
RN [3]

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RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (in) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -!- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
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CC -----
CC EMBL; M16426; AAA31289.1; -.
CC PIR; A02161; GHRB.
CC HSSP; P01857; 1FC1.
CC InterPro: IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00407; IGCL; 2.
CC PROSITE; PS00290; Ig_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 V -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 Q -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 5.5%; Score 25; DB 1; Length 323;
Best Local Similarity 100.0%; Pred. No. 1.5e-17;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 FPPKPKDTLMISRTPEVTCVVVDVS 271
Db 119 FPPKPKDTLMISRTPEVTCVVVDVS 143

RESULT 8
HV3D_HUMAN STANDARD; PRT; 115 AA.
ID HV3D_HUMAN
AC P01765.
DT 21-JUL-1986 (Rel. 01, Created)
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DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=78005528; PubMed=409716;
RA Wang A.-C., Wang I.Y., Fudenberg H.H.;
RT "Immunoglobulin structure and genetics. Identity between variable
RT regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC -!- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
CC OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC IDENTICAL.
CC PIR; A02048; H3HUTL.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGv; 1.
CC KW Immunoglobulin V region.
CC FT NON_TER 115 115
CC SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 5.1%; Score 23; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 6.4e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGGGLVQPGGSLRLSCAASGFTF 29
Db 7 SGGGLVQPGGSLRLSCAASGFTF 29

RESULT 9
ID HV3R_HUMAN STANDARD; PRT; 116 AA.
AC P01779;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region TUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74142702; PubMed=4522793;
RA Capra J.D., Kehoe J.M.;
RT "Variable region sequences of five human immunoglobulin heavy chains
RT of the VH3 subgroup: definitive identification of four heavy chain
RT hypervariable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGAL MYELOMA
CC PROTEIN.
CC PIR; A02062; ALHUTU.
CC InterPro: IPR003006; Ig_MHC.
CC InterPro: IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGv; 1.
CC KW Immunoglobulin V region.
CC FT NON_TER 116 116
CC SEQUENCE 116 AA; 12431 MW; EB705F53A963F0C CRC64;

Query Match 5.1%; Score 23; DB 1; Length 116;
Best Local Similarity 100.0%; Pred. No. 6.5e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGGGLVQPGGSLRLSCAASGFTF 29
Db 7 SGGGLVQPGGSLRLSCAASGFTF 29
```

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Db 7 SGGGLVQPGGSLRLSCAASGFTF 29
RESULT 10
HV3M_HUMAN
ID HV3M_HUMAN STANDARD; PRT; 119 AA.
AC P01774;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region POM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypic: the complete sequence
RT of the heavy chain variable regions of two immunoglobulin M
RT anti-gamma globulins.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A02057; M3HUPM.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT VARIANT 54 54
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12953 MW; 2E018AF4DCEB2610 CRC64;

Query Match 5.1%; Score 23; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGGGLVQPGGSLRLSCAASGFTF 29
Db 7 SGGGLVQPGGSLRLSCAASGFTF 29
RESULT 11
HV3N_HUMAN
ID HV3N_HUMAN STANDARD; PRT; 119 AA.
AC P01775;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region LAY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=75046755; PubMed=4139708;
RA Capra J.D., Kehoe J.M.;
RT "Structure of antibodies with shared idiotypic: the complete sequence
RT of the heavy chain variable regions of two immunoglobulin M
RT anti-gamma globulins.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:4032-4036(1974).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
DR PIR; A02058; M3HULY.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.

Db 7 SGGGLVQPGGSLRLSCAASGFTF 29
RESULT 12
HV3P_HUMAN
ID HV3P_HUMAN STANDARD; PRT; 119 AA.
AC P01777;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region TEI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=74142702; PubMed=4522793;
RA Capra J.D., Kehoe J.M.;
RT "Variable region sequences of five human immunoglobulin heavy chains
RT of the VH3 subgroup: definitive identification of four heavy chain
RT hypervariable regions.";
RL Proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGS1 MYELOMA
CC PROTEIN.
DR PIR; A02060; G1HUTE.
DR HSSP; P01772; 2IG2.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12802 MW; 7E24DC852C7290A9 CRC64;

Query Match 5.1%; Score 23; DB 1; Length 119;
Best Local Similarity 100.0%; Pred. No. 6.6e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGGGLVQPGGSLRLSCAASGFTF 29
Db 7 SGGGLVQPGGSLRLSCAASGFTF 29
RESULT 13
HV3E_HUMAN
ID HV3E_HUMAN STANDARD; PRT; 120 AA.
AC P01766;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region BRO.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=77117674; PubMed=65324;
RA Capra J.D., Hopper J.E.;
RT "Comparative studies on monotypic IgM lambda and IgG kappa from an

```

```
RT individual patient. III. The complete amino acid sequence of the VH
RL region of the IgM paraprotein.;
CC -) MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE
CC SERUM OF A PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM
CC TYPE.
DR PIR: A02049; M3HUBW.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13227 MW; D3F0428F7C2B5410 CRC64;

Query Match 5.1%; Score 23; DB 1; Length 120;
Best Local Similarity 100.0%; Pred. No. 6.7e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SGGGLVQPGGSLRSLSCAASGFTF 29
Db 7 SGGGLVQPGGSLRSLSCAASGFTF 29

RESULT 14
ID HV30_HUMAN STANDARD; PRT; 117 AA.
AC P01776;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region WAS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74142702; PubMed=4522793;
RA Capra J.D., Kehoe J.M.;
RT "Variable region sequences of five human immunoglobulin heavy chains
RT of the VH3 subgroup: definitive identification of four heavy chain
RT hypervariable regions.";
RL proc. Natl. Acad. Sci. U.S.A. 71:845-848(1974).
CC -) MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
CC PROTEIN.
DR PIR: A02059; GIHW5.
DR HSSP; P01772; 2IG2.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13091 MW; 201DEF0E1E53D9BF CRC64;

Query Match 4.7%; Score 21; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 7.2e-14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SGGGLVQPGGSLRSLSCAASGF 27
Db 7 SGGGLVQPGGSLRSLSCAASGF 27

RESULT 15
ID HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-III region KOL.
```

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primate; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=81072295; PubMed=7441755;
RA Marquart M., Deisenhofer J., Huber R., Palm W.;
RT "Crystallographic refinement and atomic models of the intact
RT immunoglobulin molecule KOL and its antigen-binding fragment at 3.0 A
RT and 1.0-A resolution.";
RL J. Mol. Biol. 141:369-391(1980).
DR PIR: A02055; GIHWK.
DR PDB; 2FB4; 12-JUL-89.
DR PDB; 2IG2; 12-JUL-89.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; 3D-structure.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT DISULFID 105 110
FT STRAND 3 7
FT STRAND 11 12
FT TURN 14 15
FT STRAND 18 25
FT STRAND 29 31
FT HELIX 34 39
FT STRAND 41 42
FT TURN 45 51
FT TURN 53 54
FT STRAND 58 60
FT TURN 62 67
FT STRAND 68 73
FT TURN 74 77
FT STRAND 78 83
FT HELIX 88 90
FT STRAND 92 99
FT STRAND 106 106
FT TURN 107 108
FT STRAND 109 109
FT STRAND 113 113
FT STRAND 120 124
FT NON_TER 126 126
SQ SEQUENCE 126 AA; 13718 MW; E4D71B52B16F8776 CRC64;

Query Match 4.4%; Score 20; DB 1; Length 126;
Best Local Similarity 100.0%; Pred. No. 8.1e-13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 YADSVKGRFTISRDNSKNTL 79
Db 60 YADSVKGRFTISRDNSKNTL 79

Search completed: October 9, 2002, 19:23:37
Job time : 13.8061 secs
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GenCore version 5.1.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:14:10 ; Search time 38.5421 Seconds  
(without alignments)  
2024.299 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 451

Sequence: 1 QVQLVSGGSLVPGGSLRL.....MHEALHNHYTQKSLSLSPGK 451

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 232   | 51.4        | 701    | 4 Q96PQ8 | Q96PQ8 homo sapien |
| 2          | 40    | 8.9         | 113    | 4 Q9UL90 | Q9UL90 homo sapien |
| 3          | 38    | 8.4         | 112    | 4 Q9UGP3 | Q9UGP3 homo sapien |
| 4          | 35    | 7.8         | 147    | 4 Q9Y509 | Q9Y509 homo sapien |
| 5          | 34    | 7.5         | 116    | 4 Q9UL93 | Q9UL93 homo sapien |
| 6          | 34    | 7.5         | 118    | 4 Q9UL72 | Q9UL72 homo sapien |
| 7          | 25    | 5.5         | 597    | 4 Q96BB9 | Q96BB9 homo sapien |
| 8          | 23    | 5.1         | 95     | 4 Q9ULB6 | Q9ULB6 homo sapien |
| 9          | 23    | 5.1         | 118    | 4 Q9UL91 | Q9UL91 homo sapien |
| 10         | 23    | 5.1         | 121    | 4 Q9UL71 | Q9UL71 homo sapien |
| 11         | 19    | 4.2         | 112    | 4 Q9HCC1 | Q9HCC1 homo sapien |
| 12         | 18    | 4.0         | 122    | 4 Q9UL84 | Q9UL84 homo sapien |
| 13         | 17    | 3.8         | 104    | 4 Q9UL87 | Q9UL87 homo sapien |
| 14         | 16    | 3.5         | 131    | 4 Q9UL88 | Q9UL88 homo sapien |
| 15         | 16    | 3.5         | 150    | 4 Q9Y298 | Q9Y298 homo sapien |
| 16         | 16    | 3.5         | 496    | 4 Q96KX8 | Q96KX8 homo sapien |

|    |    |     |     |           |                    |
|----|----|-----|-----|-----------|--------------------|
| 17 | 15 | 3.3 | 384 | 4 Q9UP60  | Q9UP60 homo sapien |
| 18 | 14 | 3.1 | 480 | 11 Q9IXE1 | Q9IXE1 mus musculu |
| 19 | 14 | 3.1 | 494 | 4 Q96K68  | Q96K68 homo sapien |
| 20 | 13 | 2.9 | 119 | 4 Q9UL73  | Q9UL73 homo sapien |
| 21 | 13 | 2.9 | 119 | 11 Q920E7 | Q920E7 mus musculu |
| 22 | 13 | 2.9 | 121 | 4 Q9UL96  | Q9UL96 homo sapien |
| 23 | 13 | 2.9 | 122 | 4 Q9UL75  | Q9UL75 homo sapien |
| 24 | 13 | 2.9 | 124 | 4 Q9UL92  | Q9UL92 homo sapien |
| 25 | 13 | 2.9 | 337 | 6 Q95M34  | Q95M34 equus cabal |
| 26 | 13 | 2.9 | 496 | 4 Q96DK0  | Q96DK0 mus musculu |
| 27 | 12 | 2.7 | 124 | 6 Q9N0W6  | Q9N0W6 oryctolagus |
| 28 | 12 | 2.7 | 124 | 6 Q9N0W4  | Q9N0W4 oryctolagus |
| 29 | 12 | 2.7 | 157 | 4 Q95378  | Q95378 homo sapien |
| 30 | 12 | 2.7 | 298 | 11 Q9QVF0 | Q9QVF0 mus musculu |
| 31 | 12 | 2.7 | 437 | 11 Q9RIA4 | Q9RIA4 mus musculu |
| 32 | 12 | 2.7 | 463 | 11 Q9LIC4 | Q9LIC4 mus musculu |
| 33 | 12 | 2.7 | 468 | 11 Q9L31  | Q9L31 mus musculu  |
| 34 | 12 | 2.7 | 473 | 11 Q9L25  | Q9L25 mus musculu  |
| 35 | 12 | 2.7 | 488 | 11 Q9LW1  | Q9LW1 mus musculu  |
| 36 | 12 | 2.7 | 613 | 4 Q96EY0  | Q96EY0 mus musculu |
| 37 | 11 | 2.4 | 64  | 11 Q61750 | Q61750 mus musculu |
| 38 | 11 | 2.4 | 102 | 11 Q9JL79 | Q9JL79 mus musculu |
| 39 | 11 | 2.4 | 110 | 11 Q9JL83 | Q9JL83 mus musculu |
| 40 | 11 | 2.4 | 117 | 11 Q921C6 | Q921C6 mus musculu |
| 41 | 11 | 2.4 | 119 | 4 Q9UL94  | Q9UL94 homo sapien |
| 42 | 11 | 2.4 | 120 | 11 Q920E8 | Q920E8 mus musculu |
| 43 | 11 | 2.4 | 134 | 6 P83049  | P83049 sus scrofa  |
| 44 | 11 | 2.4 | 139 | 11 Q924R5 | Q924R5 mus musculu |
| 45 | 11 | 2.4 | 473 | 11 Q9D8L4 | Q9D8L4 mus musculu |

#### ALIGNMENTS

##### RESULT 1

Q96PQ8 PRELIMINARY: PRT: 701 AA.  
 AC Q96PQ8;  
 DT 01-DEC-2001 (TRENBLrel. 19, Created)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21477448; PubMed=11593034;  
 RA Hu Z., Garen A.;  
 RT "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).  
 DR EMBL; AF272774; AAK58686.1; .  
 SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 51.4%; Score 232; DB 4; Length 701;  
 Best Local Similarity 100.0%; Pred. No. 3.8e-232;  
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 EPKSCDKTHCTCPPELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 279  
 |||||  
 Db 470 EPKSCDKTHCTCPPELGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 529  
 |||||  
 QY 280 NMYVDGVEVHNKATPREQNTSYRYVVSULTVLHQLNGKEYCKVSKNALPAIEKT 339  
 |||||  
 Db 530 NMYVDGVEVHNKATPREQNTSYRYVVSULTVLHQLNGKEYCKVSKNALPAIEKT 569  
 |||||  
 QY 340 ISKAKQPREPQVYITLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 399  
 |||||  
 Db 590 ISKAKQPREPQVYITLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTP 649  
 |||||  
 QY 400 PVLDSGSPFLSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 451

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|||||
Db 650 PVLDSGSEFLYKTYDKSRWQGNFSCSVMHLEALHNYTKLSLSPGK 701
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RESULT 2
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57FDD19086D07F CRC64;

Query Match 8.9%; Score 40; DB 4; Length 113;
Best Local Similarity 100.0%; Pred. No. 3.2e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YVADSVKGRFTISRDNKNTLYLQNMNSLRADTAIVYCAK 98
|||||
Db 59 YVADSVKGRFTISRDNKNTLYLQNMNSLRADTAIVYCAK 98
|||||

RESULT 3
Q9UGP3 PRELIMINARY; PRT; 112 AA.
AC Q9UGP3;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
GN IGH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Zafiroopoulos A., Kandilogianaki M., Dahlenborg C., Borrebaeck C.A.K.,
RA Krambovitis E.;
RA "Induction of somatic mutations in human B cells by in vitro
 immunization.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ122560; CAB65078.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 112
SQ SEQUENCE 112 AA; 12226 MW; 0A1F17082C7A8CE3 CRC64;
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Query Match 8.4%; Score 38; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 3.8e-31;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 YADSVKGRFTISRDNKNTLYLQNMNSLRADTAIVYCA 97
|||||
Db 43 YADSVKGRFTISRDNKNTLYLQNMNSLRADTAIVYCA 80
|||||

RESULT 4
Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RA "A CD10-positive subset of malignant cells is identified in multiple
 myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAAA7BC925C CRC64;

Query Match 7.8%; Score 35; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 6.3e-28;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 108 IDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGG 142
|||||
Db 113 IDYWGQGLTVTVSSASTKGPSVFPLAPSSKSTSGG 147
|||||

RESULT 5
Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
 (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RA "Myosin-reactive autoantibodies in rheumatic carditis and normal
 fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
```

```
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 4; Length 116;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRADTA 92
DQ 58 YYADSVKGRFTISRDNKNTLYLQMSLRADTA 91

RESULT 6
Q9UL72 PRELIMINARY; PRT; 118 AA.
AC Q9UL72
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035042; AAD56278.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 118
SQ SEQUENCE 118 AA; 12872 MW; B4D1A5944B2D5CCA CRC64;

Query Match
Best Local Similarity 100.0%; Score 34; DB 4; Length 118;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 YYADSVKGRFTISRDNKNTLYLQMSLRADTA 92
DQ 58 YYADSVKGRFTISRDNKNTLYLQMSLRADTA 91

RESULT 7
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOPHYSAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RA Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
DR
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DR EMBL; BC015760; AAH15760.1; -.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match
Best Local Similarity 100.0%; Score 25; DB 4; Length 597;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 ISGGSGSTYYADSVKGRFTISRDN 75
DQ 70 ISGGSGSTYYADSVKGRFTISRDN 94

RESULT 8
Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE IMMUNOGLOBULIN HEAVY CHAIN (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RT "Human VH gene sequence.";
RL Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 95
SQ SEQUENCE 95 AA; 10527 MW; 90A8C6D16D22574A CRC64;

Query Match
Best Local Similarity 100.0%; Score 23; DB 4; Length 95;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SGGGLVQPGGSLRLSCAASGFTF 29
DQ 6 SGGGLVQPGGSLRLSCAASGFTF 28

RESULT 9
Q9UL91 PRELIMINARY; PRT; 118 AA.
AC Q9UL91
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035023; AAD56259.1; -.
DR HSSP; P01772; 2FB4.
DR
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DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 118
FT NON_TER 118
SQ SEQUENCE 118 AA; 12843 MW; D0633949F2AC149D CRC64;

Query Match 5.1%; Score 23; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.6e-15; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 7 SGGGLVPGGSLRLSCAASGFTF 29
Db 7 SGGGLVPGGSLRLSCAASGFTF 29
|||||
RESULT 10
Q9UL71 PRELIMINARY; PRT; 121 AA.
AC Q9UL71
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT)..
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035043; AAD56279.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 121
FT NON_TER 121
SQ SEQUENCE 121 AA; 13154 MW; 2F045CCFA5D50736 CRC64;

Query Match 5.1%; Score 23; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 1.6e-15; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 55 GGSYYVADSVKGRFTISRDNK 77
Db 55 GGSYYVADSVKGRFTISRDNK 77
|||||
RESULT 11
Q9HCC1 PRELIMINARY; PRT; 112 AA.
AC Q9HCC1
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SINGLE CHAIN FV (FRAGMENT)..
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX Kikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;
RA "An antibody fragment2A3 specific for native lysozyme :isolation from a
RT
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RT human synthetic phage display library and characterization.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBDJ databases.
DR EMBL: AS049915; BAB16829.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00409; Ig; 1.
DR SMART: SM00406; Igv; 1.
DR SMART: SM00410; Ig_Like; 1.
FT NON_TER 112
FT NON_TER 112
SQ SEQUENCE 112 AA; 12243 MW; 24FLA45EC3B84788 CRC64;

Query Match 4.2%; Score 19; DB 4; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.1e-11; Indels 0; Gaps 0;
Matches 19; Conservative 0; Mismatches 0;

QY 79 LYLQMNLSRAEDTAVYYCA 97
Db 79 LYLQMNLSRAEDTAVYYCA 97
|||||
RESULT 12
Q9UL84 PRELIMINARY; PRT; 122 AA.
AC Q9UL84
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT)..
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL: AF035030; AAD56266.1; -.
DR HSSP: P01772; 2FB4.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00406; Igv; 1.
FT NON_TER 122
FT NON_TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 4.0%; Score 18; DB 4; Length 122;
Best Local Similarity 100.0%; Pred. No. 2.5e-10; Indels 0; Gaps 0;
Matches 18; Conservative 0; Mismatches 0;

QY 81 LQMNLSRAEDTAVYYCAK 98
Db 81 LQMNLSRAEDTAVYYCAK 98
|||||
RESULT 13
Q9UL87 PRELIMINARY; PRT; 104 AA.
AC Q9UL87
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
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DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035027; AAD56263.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 104
SQ SEQUENCE 104 AA; 11598 MW; 611D1A3F40E96E7B CRC64;

Query Match 3.8%; Score 17; DB 4; Length 104;
Best Local Similarity 100.0%; Pred. No. 2.4e-09;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 WVRQAPGKGLEWVSGIS 52
DB 15 WVRQAPGKGLEWVSGIS 31

RESULT 14
Q9UL88 PRELIMINARY; PRT; 131 AA.
AC Q9UL88;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN HEAVY CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035026; AAD56262.1; -.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 1
FT NON_TER 131
SQ SEQUENCE 131 AA; 14142 MW; 96E7D668E375DEA0 CRC64;

Query Match 3.5%; Score 16; DB 4; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.2e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 PGGSLRLSCAASGFTF 29
DB 14 PGGSLRLSCAASGFTF 29

RESULT 15

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Q9Y298 PRELIMINARY; PRT; 150 AA.
ID Q9Y298;
AC 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE IGG VH PROTEIN PRECURSOR (FRAGMENT).
GN IGG VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98322155; PubMed=9657749;
RA Jacquemin M.G., Vander Elst L.P.L.;
RT "Mechanism and kinetics of factor VIII inactivation: study with an
RT IgG4 monoclonal antibody derived from a hemophilia A patient with
RT inhibitor.";
RL Blood 92:496-506(1998).
DR EMBL; AJ224083; CAAL1829.1; -.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT NON_TER 150
SQ SEQUENCE 150 AA; 16031 MW; 563D164AB22802D5 CRC64;

Query Match 3.5%; Score 16; DB 4; Length 150;
Best Local Similarity 100.0%; Pred. No. 3.7e-08;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 117 VTVSSASTKGPSVFPL 132
DB 132 VTVSSASTKGPSVFPL 147

Search completed: October 9, 2002, 19:24:58
Job time : 39.5421 secs

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XX Claim 12; Page 106-108; 126pp; English.

XX The invention relates to an isolated tumour-associated antigen mucin-1

CC (MUC-1)-specific binding member comprising an antigen binding domain

CC region having an antibody variable light (VL) or heavy (VH) region,

CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific

CC binding member is useful for diagnosing cancer, preferably adenocarcinoma

CC The binding of MUC1-specific binding member to MUC1 is detected by a

CC detection method selected from enzyme-linked immunosorbent assay,

CC magnetic resonance imaging, scintillation counting, and X-ray film.

CC MUC1-specific binding member is useful for treating cancer, preferably

CC adenocarcinoma, in an individual, where the cancer is present in tissue

CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific

CC binding member is useful for diagnosing and imaging MUC1-expressing

CC cancer cells and tissues, for purifying or isolating non-glycosylated,

CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-

CC containing molecules, and for therapeutically or prophylactically

CC treating cancer. The present sequence is human recombinant immunoglobulin

CC (Ig) heavy chain region (variable VH and CH constant heavy chain).

XX SQ Sequence 451 AA;

Query Match 100.0%; Score 2411; DB 22; Length 451;

Best Local Similarity 100.0%; Pred. No. 5.2e-136;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLVWVSGISGGSTYY 60

DB 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLVWVSGISGGSTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120

DB 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGLTVTS 120

QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 180

DB 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 180

QY 181 SGLYSLSSVTVTPSSSLGTQYICNVNHPKSNNTKVDKVEPKSCDKTHCPCPAPELLG 240

DB 181 SGLYSLSSVTVTPSSSLGTQYICNVNHPKSNNTKVDKVEPKSCDKTHCPCPAPELLG 240

QY 241 GPSVFLPPPKPDKTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQY 300

DB 241 GPSVFLPPPKPDKTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQY 300

QY 301 NSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360

DB 301 NSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360

QY 361 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSR 420

DB 361 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVDKSR 420

QY 421 WQGGNVFSCSVMHREALNHHYTKQSLSPGK 451

DB 421 WQGGNVFSCSVMHREALNHHYTKQSLSPGK 451

RESULT 2

AAV68810

ID AAV68810 standard; Protein; 449 AA.

XX AC AAV68810;

XX DT 16-MAY-2000 (first entry)

XX DE A rat heavy chain region and a human hinge region.

XX KW CD3 antigen complex; chimeric antibody; immunosuppression; heavy chain;

XX CD3 antigen-T-cell receptor complex; graft rejection; cancer.

OS Synthetic.

OS Rattus sp.

OS Homo sapiens.

PN WO200005268-A1.

XX 03-FEB-2000.

XX 21-JUL-1999; 99WO-GB02380.

XX 21-JUL-1998; 98GB-0015909.

XX (BTGI-) BTG INT LTD.

PA Waldmann H, Frewin M;

PI WPI; 2000-182655/16.

DR N-PSDB; AAZ60599.

XX New humanized anti-CD3 antibodies, used for treating cancer or for

PT immunosuppression and preventing graft rejection -

XX Disclosure; Page 45-47; 56pp; English.

XX The present sequence represents the heavy chain variable region of a rat

CC immunoglobulin G (IgG) antibody which is specific for the CD3 antigen

CC complex, and the human CH1-hinge-aglycosylCH2CH3. The specification

CC describes chimeric human/rodent anti-CD3 antibodies, which have a

CC rodent CD3 light chain variable region and a human heavy chain variable

CC region. The anti-CD3 antibodies can render T-cells non-functional by

CC antibody blockade of the CD3 antigen-T-cell receptor (TCR) complex.

CC They can be used for immunosuppression, particularly for the control

CC of graft rejection. The antibodies can also enhance or re-direct T-cell

CC responses to antigens. They can be used in the treatment of cancer.

XX SQ Sequence 449 AA;

Query Match 94.2%; Score 2270; DB 21; Length 449;

Best Local Similarity 94.9%; Pred. No. 1.3e-127;

Matches 431; Conservative 5; Mismatches 10; Indels 8; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLVWVSGISGGSTYY 60

DB 1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSFPMWVROAPGKGLVWVSTISTSGRTYY 60

QY 61 ADSVKGRFTISRDNKNTLYLQNSLRAEDTAVYYCAK--HTGGGVWDPIDYWGQGLTV 117

DB 61 RDSVKGRETIISRDNSKNTLYLQNSLRAEDTAVYYCAKFRQYSGG-----FDYWGQGLTV 115

QY 118 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 177

DB 116 TVSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 175

QY 178 LOSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNNTKVDKVEPKSCDKTHCPCPAPE 237

DB 176 LOSGLYSLSSVTVTPSSSLGTQYICNVNHPKSNNTKVDKVEPKSCDKTHCPCPAPE 235

QY 238 LLGGPSVFLFPPKPKDKTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 297

DB 236 LLGGPSVFLFPPKPKDKTLMISRPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295

QY 298 EYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 357

DB 296 EYASTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 355

QY 358 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVD 417

DB 356 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFELYSKLTVD 415

QY 418 KSRWQGGNVFSCSVMHREALNHHYTKQSLSPGK 451

DB 416 KSRWQGGNVFSCSVMHREALNHHYTKQSLSPGK 449



CC treatment of a mammal and prevention of disorders caused by the aberrant  
CC protein expression or activity. The polypeptides can be used as  
CC molecular weight markers, food supplements, and in antibody production.  
CC The polypeptides are used to identify compounds which bind to the  
CC polypeptides. Polynucleotides of the invention are used as probes and  
CC primers, for sequencing, for chromosome or gene mapping, in the  
CC production of recombinant proteins, and in generating anti-sense DNA or  
CC RNA and in gene therapy. Polypeptides of the invention can be used to  
CC target drugs to a tumour, in assays to determine biological activity, to  
CC raise antibodies/elicite an immune response, to determine quantitative  
CC protein levels, as tissue markers, and to isolate receptors or ligands.  
CC Polypeptides of the invention may also be useful in treating platelet  
CC disorders, stem cell disorders, regenerating bone, cartilage, tendon,  
CC ligament and/or nerve tissue, wound healing, treating burns, promoting  
CC the proliferation, differentiation and survival of stem cells, as a  
CC contraceptive, treating osteoporosis and osteoarthritis, anaemia,  
CC Alzheimer's, Parkinson's and Huntington's diseases, amyotrophic lateral  
CC sclerosis, stroke, immune deficiencies resulting from bacterial, viral or  
CC fungal infection or from autoimmunity, cancer, allergy, asthma,  
CC graft-versus-host diseases, eczema, haemophilia, thrombosis,  
CC anti-inflammatory diseases, nervous system disorders, and infection.  
CC The present sequence represents a protein of the invention.

XX SQ Sequence 477 AA;

Query Match 92.5%; Score 2229.5; DB 22; Length 477;  
Best Local Similarity 91.5%; Pred. No. 3.6e-125; Indels 13; Gaps 2;  
Matches 422; Conservative 10; Mismatches 16;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSGISGGSTYY 60  
DB 20 QVQLVESGGGVQVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSGISGGSTYY 79  
QY 61 ADSVKGGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHTGGVWDP-----IDY 110  
DB 80 ADSVKGGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHTGGVWDP-----IDY 136  
QY 111 WGOGTLTVVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNMNSGALTSG 170  
DB 137 WGOGTLTVVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNMNSGALTSG 196  
QY 171 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTNTKVDKVKPKSCDKTHTC 230  
DB 197 VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTNTKVDKVKPKSCDKTHTC 256  
QY 231 PPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVIN 290  
DB 257 PPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVIN 316  
QY 291 AKTKPREEQYNSTYRVYSVLTVQLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 350  
DB 317 AKTKPREEQYNSTYRVYSVLTVQLHQLDNLNGKEYKCKVSNKALPAPIEKTISKAKGQPREP 376  
QY 351 QVTLPPSRDELTKNQVSLTCLVKGFYPSDITAVESWGNGPENNYKTTTPVLDSGSPFL 410  
DB 377 QVTLPPSRDELTKNQVSLTCLVKGFYPSDITAVESWGNGPENNYKTTTPVLDSGSPFL 436  
QY 411 YSKLTVDKSRWQOGNVPFCVSMHEALHNHYTQKSLSLSPGK 451  
DB 437 YSKLTVDKSRWQOGNVPFCVSMHEALHNHYTQKSLSLSPGK 477

RESULT 5

AAR20057 standard; Protein; 475 AA.

XX AC AAR20057;

XX DT 25-MAR-1992 (first entry)

XX DE Heavy chain of 3D6 anti-HIV antibody.

XX KW Plasmid pUC3D6HC; human immunodeficiency virus; AIDS;

complementarity determining region.  
KW XX Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT Region 20..49  
FT /label= signal  
FT /label= Framework\_1  
FT Region 50..54  
FT /label= CDR-1  
FT Region 55..68  
FT /label= Framework\_2  
FT Region 69..85  
FT /label= CDR\_2  
FT Region 86..117  
FT /label= Framework\_3  
FT Region 118..134  
FT /label= CDR\_3  
FT Region 135..145  
FT /label= Framework\_4  
FT Region 146..475  
FT /label= Constant\_region  
XX XX WO9118983-A.  
XX PD 12-DEC-1991.  
XX PF 28-MAY-1991; 91WO-1000067.  
XX PR 29-MAY-1990; 90AT-0001178.  
XX PA (JUNG/) JUNGBAUER A.  
XX PI Reigenhauer M, Himmeler G, Kohl J, Steindl F;  
XX DR WPI; 1992-007468/01.  
XX DR N-PSDB; AAQ20066.  
XX PT Recombinant protein which binds to complex viral antigen and  
XX cell line, used for detecting HIV-1 antigen  
XX PS Claim 2; Page 24; 52pp; German.  
XX CC The variable region of the heavy chain is used in a recombinant  
XX protein which the variable region from the kappa light chain of 3D6,  
XX the two V regions being joined by a linker. The recombinant protein  
XX binds to HIV gp160.  
XX CC See also AAQ20067 and AAQ20068.  
XX SQ Sequence 475 AA;

Query Match 92.4%; Score 2228.5; DB 13; Length 475;  
Best Local Similarity 92.8%; Pred. No. 4.1e-125; Indels 5; Gaps 1;  
Matches 423; Conservative 7; Mismatches 21;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSGISGGSTYY 60  
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPGKLEWVSGISGGSTYY 79  
QY 61 ADSVKGGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGT 115  
DB 80 ADSVKGGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHTGGVWDPIDYWGQGT 139  
QY 116 LVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFP 175  
DB 140 MVTVSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSNMNSGALTSGVHTFP 199  
QY 176 AVQLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTNTKVDKVKPKSCDKTHTCPCPA 235  
DB 200 AVQLQSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTNTKVDKVKPKSCDKTHTCPCPA 259

QY 236 PELLGSPVFLPPPKDLMISRTPEVTCVVDVSHEDPEVFNWYVDGVEVHNATKP 295  
 DB 260 PELLGSPVFLPPPKDLMISRTPEVTCVVDVSHEDPEVFNWYVDGVEVHNATKP 319  
 QY 296 REEQNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREQVYTL 355  
 DB 320 REEQNSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREQVYTL 379  
 QY 356 PPSDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLT 415  
 DB 380 PPSDELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLT 439  
 QY 416 VDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 451  
 DB 440 VDKSRWQGNVFCSCVMHEALHNHYTKLSLSLSPGK 475

RESULT 6  
 AAB81987  
 ID AAB81987 standard; Protein: 582 AA.  
 AC AAB81987;  
 DT 03-JUL-2001 (first entry)  
 DE Ganglioside GD3 specific antibody related protein SEQ ID NO: 53.  
 XX Ganglioside; GD3; complementarity determining region; CDR; antibody;  
 KW cancer.  
 OS Synthetic.  
 PN WC200123432-A1.  
 PD 05-APR-2001.  
 PF 29-SEP-2000; 2000WO-JP06774.  
 PR 30-SEP-1999; 99JP-0278291.  
 PR 06-APR-2000; 2000JP-0105088.  
 PA (KYOW ) KYOWA HAKKO KOGYO KK.  
 XX Hanai N, Shitara K, Nakamura K, Niwa R;  
 PI WPI; 2001-266143/27.  
 DR New human type complementation-determining region-transplanted antibody  
 XX and derivatives against ganglioside GD3, useful in diagnosis and  
 PT therapy of e.g. tumours, with low antigenicity, little side effects but  
 PT potent activity in cancer -  
 XX Claim 41; Page 166-172; 183pp; Japanese.  
 PS The present invention describes a monoclonal antibody which can react  
 XX specifically with ganglioside GD3. The antibody and its derivatives are  
 CC useful in the diagnosis and therapy of tumours, particularly cancer  
 CC diagnosis. The present sequence is a protein used in the exemplification  
 CC of the invention.  
 XX  
 XX Sequence 582 AA;  
 SQ Query Match 91.9%; Score 2216; DB 22; Length 582;  
 Best Local Similarity 92.7%; Pred. No. 2.8e-124;  
 Matches 418; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 1 QVQLVQSGGLVQPQGLSLKCAAGFTFRSNAMGWTRQAPKGLKSWISGSGSTYY 60  
 DB 1 EVQLVESGGDFVQPGSLRVSCAASGFAFSYAMSWRQAPKGLKSWIISGSGSTYY 60  
 QY 61 ADSVKGRFTISRDNKNTLYLQMSIRAEEDTAVYCAKHTGGGVWDPIDYWGQGLTVTS 120  
 DB 61 SDSVKGRFTISRDNKNTLYLQMSIRAEEDTAVYCAKHTGGGVWDPIDYWGQGLTVTS 118

QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 180  
 DB 119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 178  
 QY 181 SGLYSLSVTVVSPSSSLGTQTYICNVNHNKPSNTKVKPEKSCDKHTHCPCPAPELLG 240  
 DB 179 SGLYSLSVTVVSPSSSLGTQTYICNVNHNKPSNTKVKPEKSCDKHTHCPCPAPELLG 238  
 QY 241 GPSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVFNWYVDGVEVHNATKPRESQY 300  
 DB 239 GPSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVFNWYVDGVEVHNATKPRESQY 298  
 QY 301 NSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRD 360  
 DB 299 NSTYRVVSVLTVLHODWLNKKEYCKVSNKALPAPIEKTISKAKGQPREQVYTLPPSRD 358  
 QY 361 ELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSR 420  
 DB 359 ELTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSR 418  
 QY 421 WQGNVFCSCVMHEALHNHYTKLSLSLSPGK 451  
 DB 419 WQGNVFCSCVMHEALHNHYTKLSLSLSPGK 449

RESULT 7  
 AAY29458  
 ID AAY29458 standard; Protein: 452 AA.  
 AC AAY29458;  
 DT 05-OCT-1999 (first entry)  
 DE Recombinant immunoglobulin SEQ ID NO:71.  
 XX Antibody; humanised; anti-IL-8 monoclonal antibody; interleukin 8;  
 KW diagnosis; inflammatory disorder; conjugate; immunoglobulin;  
 KW fusion protein.  
 OS Synthetic.  
 XX WO9937779-A1.  
 PN 29-JUL-1999.  
 PD 19-JAN-1999; 99WO-US01081.  
 PF 24-JUL-1998; 98US-0122513.  
 PR 22-JAN-1998; 98US-0012116.  
 PR 20-FEB-1998; 98WO-US03337.  
 PR 24-JUL-1998; 98US-0121952.  
 XX (GETH ) GENENTECH INC.  
 XX Hsei V, Koumenis I, Leong SJ, Presta LG, Shahrokh Z;  
 PI Zapata GA;  
 XX WPI; 1999-469134/39.  
 DR New conjugates of nonproteinaceous polymers with antibody fragments,  
 PT used for treating inflammatory disorders  
 PT Disclosure; Page 354-355; 360pp; English.  
 PS The present invention describes a novel conjugate having one or more  
 XX antibody fragments covalently attached to one or more nonproteinaceous  
 CC polymer molecules, where the apparent size of the conjugate is at least  
 CC about 500 kDa. Conjugates of antibody fragments which bind the human  
 CC interleukin (IL) 8 with a nonproteinaceous polymer can be used for  
 CC treating inflammatory disorders e.g. acute lung injury, ischemic  
 CC reperfusion disorder, and autoimmune diseases. They can also be used  
 CC for treating e.g. inflammatory skin diseases including psoriasis and

CC atopic dermatitis, systemic scleroderma and sclerosis, and asthmatic  
CC diseases. The conjugates can also be used as reagents in an animal  
CC model system for in vivo study of the biological functions of the  
CC antigen recognised by the conjugate. The present sequence represents  
CC a recombinant immunoglobulin protein from the present invention.  
XX  
SQ Sequence 452 AA;

Query Match 91.7%; Score 2211.5; DB 20; Length 452;  
Best Local Similarity 92.5%; Pred. No. 4e-124;  
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

Qy 1 QVQLVSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 EVQLVSGGGLVPGGSLRLSCAASGYSFSSHYMHVWRQAPGKLEWVGYIDPSNGETTY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAK--HTGGGVWDPIDYWGQGLT 118  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 NQFKGRFTISRDNKNTAYLQMSLRADTAIVYCARGDYRYNGDWF-FDVWGQGLT 119  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 179 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHCCPPCPAPEL 238  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 180 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHCCPPCPAPEL 239  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 239 LGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 240 LGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 299 QYNSTYRVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISRKAKGQPREPQVYTLPPS 358  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 300 QYNSTYRVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISRKAKGQPREPQVYTLPPS 359  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 359 RDELTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSLKLTVDK 418  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 360 REEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSLKLTVDK 419  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 8  
AAB30322  
ID AAB30322 standard; Protein; 452 AA.  
AC AAB30322;  
XX  
XX 12-FEB-2001 (first entry)  
XX  
DE Humanised anti-IL-8 antibody related protein seq ID NO: 71.  
XX  
XX Humanised antibody; anti-IL-8; interleukin-8; inflammation; septic shock;  
KW adult respiratory distress syndrome; multiple organ failure;  
KW bacterial pneumonia; inflammatory bowel disease.  
XX  
OS Unidentified.  
XX  
XX US6133426-A.  
XX  
XX 17-OCT-2000.  
XX  
XX 20-FEB-1998; 98US-0026985.  
XX  
XX 21-FEB-1997; 97US-0039664.  
PR 22-JAN-1998; 98US-0074330.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Presta LG, Leong SR, Gonzalez TN;

XX WPI; 2000-686027/67.  
XX Humanized anti-interleukin 8 monoclonal antibody variant useful for  
PT treating inflammatory disorders, such as adult respiratory distress  
PT syndrome, hypovolemic shock and ulcerative colitis -  
XX  
XX Disclosure; Column 199-202; 24Opp; English.  
XX  
XX The present invention provides a number of humanised monoclonal anti-IL-8  
CC antibodies which can be used in the diagnosis and treatment of  
CC inflammatory disorders, including adult respiratory distress syndrome,  
CC septic shock, multiple organ failure, bacterial pneumonia and  
CC inflammatory bowel disease. The present sequence comprises one of the  
CC antibodies of the invention.  
XX  
SQ Sequence 452 AA;

Query Match 91.7%; Score 2211.5; DB 21; Length 452;  
Best Local Similarity 92.5%; Pred. No. 4e-124;  
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

Qy 1 QVQLVSGGGLVPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 1 EVQLVSGGGLVPGGSLRLSCAASGYSFSSHYMHVWRQAPGKLEWVGYIDPSNGETTY 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAIVYCAK--HTGGGVWDPIDYWGQGLT 118  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 61 NQFKGRFTISRDNKNTAYLQMSLRADTAIVYCARGDYRYNGDWF-FDVWGQGLT 119  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 179 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHCCPPCPAPEL 238  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 180 QSSGLYSLSVWTVPPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHCCPPCPAPEL 239  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 239 LGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 240 LGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 299 QYNSTYRVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISRKAKGQPREPQVYTLPPS 358  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 300 QYNSTYRVSVLTVHLQDWLNGKEYCKVSNKALPAPIEKTISRKAKGQPREPQVYTLPPS 359  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 359 RDELTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSLKLTVDK 418  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 360 REEMTKNQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSLKLTVDK 419  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 9  
AAV77766  
ID AAV77766 standard; Protein; 452 AA.  
XX  
XX AAV77766;  
XX  
XX 06-JUN-2000 (first entry)  
XX  
XX Humanised anti-IL-8 antibody related protein seq ID No:71.  
XX  
KW Interleukin-8; IL-8; monoclonal antibody; MAb; anti-IL-8; 6G4V11N3A;  
KW inflammatory disorder; adult respiratory distress syndrome;  
KW affinity purification.  
XX  
OS Homo sapiens.  
XX  
XX US6025158-A.  
PN  
XX



PD 15-FEB-2000.  
XX 20-FEB-1998; 98US-0027449.  
XX 21-FEB-1997; 97US-0038664.  
PR 22-JAN-1998; 98US-0074330.  
XX (GETH ) GENENTECH INC.  
XX Presta LG, Leong SR, Gonzalez TN;  
XX WPI; 2000-181809/16.  
XX  
XX New nucleic acid molecule encodes a polypeptide which is an  
PT anti-interleukin-8 monoclonal antibody or antibody fragment useful for  
PT the production of anti-interleukin-8 monoclonal antibodies or fragments  
PT  
XX  
XX Examples; Columns 199-202; 188pp; English.  
XX  
XX The invention relates to an anti-interleukin-8 (IL-8) monoclonal antibody  
CC (MAB). The anti-IL-8 MAB comprises a sequence containing the CDRs  
CC (complementarity determining regions) of the humanized anti-IL-8  
CC 6G4.2.5V11N35A light chain; and amino acids 24-253 of the humanized  
CC anti-IL-8 6G4.2.5V11N35A heavy chain. The anti-IL-8 Mabs and fragments  
CC can be used in diagnosis, for affinity purification of IL-8 from  
CC recombinant cell culture or natural sources and for the treatment of  
CC inflammatory disorders e.g. adult respiratory distress syndrome. Nucleic  
CC acids encoding the anti-IL-8 MAB can be associated in a vector with  
CC another gene encoding another protein or protein fragment to produce a  
CC fusion protein which can make isolation and/or purification of the  
CC protein an easier process.  
XX  
XX Sequence 452 AA;

Query Match 91.7%; Score 2211.5; DB 21; Length 452;  
Best Local Similarity 92.5%; Pred. No. 4e-124;  
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 OVQLVQSGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTY 60  
DB 1 EVQLVQSGGLVQPGSLRLSCAASGYSFSSHYMHVRQAPGKGLVWVSDPSNGETTY 60  
QY 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADDAEDTAVYICARGDYRYNGDWDF-FDVWGQGTLYT 118  
DB 61 NQFKGRFTLSRDNSKNTLYIQMNSLRADDAEDTAVYICARGDYRYNGDWDF-FDVWGQGTLYT 119  
QY 119 VSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178  
DB 120 VSSASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 179  
QY 179 QSSGLYSLSVVTPVSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPEL 238  
DB 180 QSSGLYSLSVVTPVSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPEL 239  
QY 239 LGGPSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNMYDGVGVHNAKTPREE 298  
DB 240 LGGPSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNMYDGVGVHNAKTPREE 299  
QY 299 QYNSTYRVVSVLTVTHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358  
DB 300 QYNSTYRVVSVLTVTHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359  
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEFESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 418  
DB 360 RDELTKNQVSLTCLVKGFYPSDIAVEFESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 419  
QY 419 SRQQGNVSCSVMHEALHNHYTQKSLSLSPGK 451  
DB 420 SRQQGNVSCSVMHEALHNHYTQKSLSLSPGK 452

RESULT 10

AA42066  
ID AAR42066 standard; Protein; 459 AA.  
XX  
XX AAR42066;  
XX 29-APR-1994 (first entry)  
DT  
XX Human anti-HBs heavy chain.  
DE  
XX Antibody; Ab; light; heavy; chain; hepatitis B;  
KW HB; surface antigen.  
XX  
XX Homo sapiens.  
OS  
XX Key Location/Qualifiers  
FH Peptide 1..9  
FT /label= sig\_peptide  
FT Protein 10..459  
FT /label= mat\_protein  
XX  
XX W09320205-A.  
XX 14-OCT-1993.  
XX 30-MAR-1993; 93WO-JP00396.  
XX 30-MAR-1992; 93JP-0074678.  
XX (SUNR ) SUNTORY LTD.  
XX Arima K, Kurihara T, Matsukura S, Nishihara T, Tsuruoka N;  
PI WPI; 1993-336913/42.  
DR N-PSDB; AA049944.  
XX  
XX Human anti-hepatitis B surface antigen antibody gene - can be  
PT used to produce L and H chains of the antibody in large quantity  
PT  
XX Disclosure; Fig 6-8; 46pp; Japanese.  
XX  
XX Polynucleotides encoding the L and H chains of human anti-HBs  
CC Ab are given in AA049943-049944. The Ab can be easily produced in  
CC large quantities for therapeutic use.  
XX  
XX Sequence 459 AA;

Query Match 91.6%; Score 2207.5; DB 14; Length 459;  
Best Local Similarity 92.7%; Pred. No. 7e-124;  
Matches 418; Conservative 9; Mismatches 23; Indels 1; Gaps 1;

QY 1 OVQLVQSGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGGSTY 60  
DB 10 QVQLVESGGGVQPGSLRLSCAASGFTFSSNMHWVRQAPGKGLVAVILYDGNHKEY 69  
QY 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADDAEDTAVYICAKHTGGGVMDPIDYWGQGTLYT 120  
DB 70 ADSVKGRFTISRDNSKNTLYIQMNSLRADDAEDTAVYICAKHTGGGVMDPIDYWGQGTLYT 128  
QY 121 SASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 180  
DB 129 SASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 188  
QY 181 SGYSLSVVTPVSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPEL 240  
DB 189 SGYSLSVVTPVSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPEL 248  
QY 241 GPSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNMYDGVGVHNAKTPREE 300  
DB 249 GPSVFLPPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNMYDGVGVHNAKTPREE 308  
QY 301 NSTYRVVSVLTVTHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSD 360  
DB 309 NSTYRVVSVLTVTHQDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSD 368

QY 361 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPPVLDSGGSEFFLYSKLTVDKSR 420  
 DQ 369 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPPVLDSGGSEFFLYSKLTVDKSR 428  
 QY 421 WQQGNVFSCSVMHEALHNHYTOKLSLSLSPGK 451  
 DQ 429 WQQGNVFSCSVMHEALHNHYTOKLSLSLSPGK 459

## RESULT 11

AAW69316  
 ID AAW69316 standard; Protein; 452 AA.

XX AAW69316;

DT 15-FEB-1999 (first entry)

DE Anti-IL-8 humanised antibody 6G4V11N35A.choSD.9.

XX Humanised antibody; chimeric antibody; monoclonal antibody; mouse;  
 KW human; Fab; interleukin-8; inflammation; immunotherapy; psoriasis;  
 KW inflammatory bowel disease; Crohn's disease; ulcerative colitis;  
 KW ischaemic reperfusion; adult respiratory distress syndrome;  
 KW dermatitis; meningitis; encephalitis; uveitis; autoimmune disease;  
 KW rheumatoid arthritis; Sjorgen's syndrome; vasculitis;  
 KW leukocyte diapedesis; multiple organ injury syndrome; septicemia;  
 KW trauma; alcoholic hepatitis; pneumonia; pleurisy; alveolitis;  
 KW vasculitis; bronchitis; bronchiectasis; cystic fibrosis; diagnosis;  
 KW therapy; 6G4V11N35A.choSD.9.

XX Chimeric - Mus sp.

OS Chimeric - Homo sapiens.

XX WO9837200-A2.

XX 27-AUG-1998.

XX 20-FEB-1998; 98WO-US03337.

XX 22-JAN-1998; 98US-0012116.

PR 21-FEB-1997; 97US-0804444.

XX (GETH ) GENENTECH INC.

XX Hsai V, Koumenis I, Leong SR, Presta LR, Shahrokh Z;

PI Zapata GA;

DR WPI; 1998-467563/40.

XX N-PSDB; AAV44956.

XX New conjugates of antibody fragments - having covalently attached  
 PT non-proteinaceous polymer molecules, particularly polyethylene  
 PT glycol, for improving the residence time in the circulation.

XX Example P; Fig 48A-Z; 328pp; English.

XX This polypeptide is encoded by vector plasmid p6G4V11N35A.choSD.9  
 CC (see AAV44956). It comprises a humanised 6G4V11N35A IgG containing  
 CC complementarity determining regions of murine anti-interleukin-8  
 CC (IL-8) monoclonal antibody (MAB) 6G5.2.5 (see AAV69309-10) in a human  
 CC template. Humanised anti-IL-8 MABs (see AAV69301-04) are described  
 CC for use in diagnostic applications and in the treatment of  
 CC inflammatory disorders. The invention provides conjugates of an  
 CC antibody fragment and a polymer, such as PEG, that have improved  
 CC half-life, mean residence time, and/or clearance rate. The  
 CC conjugates can be used for immune therapy of e.g. psoriasis,  
 CC responses associated with inflammatory bowel disease (such as  
 CC Crohn's disease and ulcerative colitis), ischemic reperfusion,  
 CC adult respiratory distress syndrome, dermatitis, meningitis,  
 CC encephalitis, uveitis, autoimmune diseases such as rheumatoid  
 CC arthritis, Sjorgen's syndrome, vasculitis, diseases involving  
 CC leukocyte diapedesis, central nervous system inflammatory disorder,

CC multiple organ injury syndrome secondary to septicemia or trauma,  
 CC alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex  
 CC mediated diseases, inflammations of the lung, including pleurisy,  
 CC alveolitis, vasculitis, pneumonia, chronic bronchitis,  
 CC bronchiectasis, and cystic fibrosis.

XX Sequence 452 AA;

Query Match 91.4%; Score 2202.5; DB 19; Length 452;

Best Local Similarity 92.1%; Pred. No. 1.4e-123;

Matches 417; Conservative 10; Mismatches 23; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPQGSRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGSGSTYY 60

DB 1 EVQLVQSGGGLVQPQGSRLSCAASGYSFSSHYHWHVRQAPGKGLEWGYIDPSNGETTY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAK--HTGGGVWDPIDYNGQGTTLTV 118

DB 61 NQKFKGRFTLSRDNSKNTAYLQMSLRAEDTAVYYCARGDYRYNGDNF-FDVMGQGTTLTV 119

QY 119 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVL 178

DB 120 VSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSAHLTFPAVL 179

QY 179 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPEL 238

DB 180 QSSGLYSLSSVTVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPEL 239

QY 239 LGGPSVFLFPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 298

DB 240 LGGPSVFLFPKPKDRLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 299

QY 299 QYNSTYRWVSVLTVLHODWLNGKEYCKVSKNKPAPLEKTIISKAKGQPREPQVYTLPPS 358

DB 300 QYNSTYRWVSVLTVLHODWLNGKEYCKVSKNKPAPLEKTIISKAKGQPREPQVYTLPPS 359

QY 359 RDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPPVLDSGGSEFFLYSKLTVDK 418

DB 360 REEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPPVLDSGGSEFFLYSKLTVDK 419

QY 419 SRWQGNVFSCSYMHEALHNHYTOKLSLSLSPGK 451

DB 420 SRWQGNVFSCSYMHEALHNHYTOKLSLSLSPGK 452

## RESULT 12

AAW47453

ID AAW47453 standard; Protein; 477 AA.

XX AAW47453;

XX 24-JUN-1994 (first entry)

XX chiT84.12 H3 heavy chain.

DE Chimeric; carcinoembryonic antigen; CCA; murine; mouse; constant;

XX region; transform; myeloma cell; light chain; tumour.

XX Synthetic.

XX WO9325237-A.

XX 23-DEC-1993.

XX 15-JUN-1993; 93WO-US05709.

XX 15-JUN-1992; 92US-0904074.

XX (CITY ) CITY OF HOPE.

XX (YANG ) YANG Y.

XX Fischer R, Paxton R, Shively JE, Wu A, Yang YHJ;

PI Yang YH;

```
XX DR WPI; 1994-007204/01.
XX DR N-PSDB; AAQ54655.
XX PT New chimaeric T84.12 antibody active against carcinoembryonic
XX PT antigen - has murine variable and human constant regions, also
XX PT DNA encoding it and transformed myeloma cells
XX PS Claim 1; Page 22-23; 27pp; English.
XX CC The sequences (AAQ54651-52) show the light and heavy chain cDNAs
XX CC of murine T84.12. The T84.12 antibody is directed against the
XX CC tumour marker carcinoma embryonic antigen, and is useful for
XX CC tumour imaging and immunotherapy.
XX CC The amino acid sequence given in the specification has been
XX CC incorrectly identified as a nucleic acid sequence, therefore
XX CC unacceptable characters have been represented as an 'N'.
XX CC The amino acid sequence given below has been derived from the
XX CC cDNA, by the indexer.
XX SQ Sequence 477 AA;
Query Match 90.8%; Score 2190; DB 15; Length 477;
Best Local Similarity 91.08; Pred. No. 8e-123;
Matches 413; Conservative 16; Mismatches 17; Indels 8; Gaps 3;
QY 1 QVOLVSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
Db 29 EVKLVEGGGFKPGGSLKLSAASGFTFSYAMSWVRQTPPEKRLWEVASIS-SDGITFY 87
QY 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADETAVYCAK---HTGGGVDPIDYWGOGTLV 117
Db 88 VDSVKGRTFISRDNARNILYLQMSLRSEDTAMTCARIDYICGGG---FGYWGOGTLA 143
QY 118 TVSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 177
Db 144 TVSAASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAV 203
QY 178 LQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSTNTKVDKKVPPKSCDKTHTCPCPAPE 237
Db 204 LQSSGLYSLSSVTVVPSSSLGTQYICNVNHPKSTNTKVDKKVPPKSCDKTHTCPCPAPE 263
QY 238 LLGGPSVFLPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATPKRE 297
Db 264 LLGGPSVFLPPKKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKATPKRE 323
QY 298 EQNSTYRVVSVLTVLDHQLWNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 357
Db 324 EQNSTYRVVSVLTVLDHQLWNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 383
QY 358 SRDELTKNOVSLTCLVKGYFSDTAIVESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 417
Db 384 SRDELTKNOVSLTCLVKGYFSDTAIVESNGQPENNYKTPPVLDSDGSFFLYSKLTVD 443
QY 418 KSRWQGNVFSCSVHREALHNYHTQKLSLSPGK 451
Db 444 KSRWQGNVFSCSVHREALHNYHTQKLSLSPGK 477
RESULT 13
AAR24812
ID AAR24812 standard; Protein; 466 AA.
XX AC AAR24812;
XX DT 28-DEC-1992 (first entry)
XX DE Sequence encoded by the chimeric H chain cDNA contained in pTB1373.
XX KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;
XX KW antithrombotic agent; myocardial infarction therapy.
XX OS Synthetic.
```

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XX FH Key Location/Qualifiers
XX FT 13..19 /label= Leader
XX FT 20..134 /label= VH
XX FT 135..232 /label= CH1
XX FT 233..247 /label= hinge
XX FT 248..357 /label= CH2
XX FT 358..464 /label= CH3
XX FT Misc-difference 465 /note= "translated stop codon"
XX PN EP491351-A.
XX PD 24-JUN-1992.
XX XX 17-DEC-1991; 91EP-0121591.
XX PF 18-DEC-1990; 90JP-0413829.
XX PR 11-NOV-1991; 91JP-0294464.
XX XX (TAKE) TAKEDA CHEM IND LTD.
XX PI Iwasa S, Taka H, Watanabe T, Tada H;
XX DR WPI; 1992-209528/26.
XX DR N-PSDB; AAQ25692.
XX PT Chimeric monoclonal antibodies - contain anti-human fibrin
XX PT antibody light and heavy chain variable and constant for treating
XX PT thrombotic conditions e.g. myocardial infarction
XX PS Example; Figure 11; 87pp; English.
XX CC Plasmid pTB1373 contains the whole length of a mouse-human
XX CC chimeric anti-human fibrin heavy chain cDNA open reading
XX CC frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin
XX CC chimeric Aa-producing transformant FIB1-H01/X63 as a template
XX CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
XX CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH
XX CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
XX CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
XX CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
XX CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CLH
XX CC respectively as a primer for first strand cDNA synthesis and the
XX CC primer combination of 5'CLH and 3'C2H, of 5'EH and 3'CLH and of
XX CC 5'SH and 3'EH respectively as primers for PCR. The amplified gene
XX CC products were isolated and used to produce plasmids. After
XX CC confirmation of the cDNA sequence of each plasmid, the cDNA
XX CC encoding LH, VH, CH1 and CH2CH3 were joined together to give
XX CC plasmid pTB1373 contg. the whole length chimeric H chain
XX CC (LH, VH, CH1, CH2CH3), also abbreviated as IgH-FIB.
XX SQ Sequence 466 AA;
Query Match 90.7%; Score 2186; DB 13; Length 466;
Best Local Similarity 90.9%; Pred. No. 1.4e-122;
Matches 410; Conservative 19; Mismatches 16; Indels 6; Gaps 2;
QY 1 QVOLVSGGGLVQPGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
Db 20 EVLVESGGGLVQPGSLKLSAASGFTFSYAMSWVRQTPPEKRLWEVASIS-VGGTTY 78
QY 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADETAVYCAKHTGGGVDPIDYWGOGTLVTVS 120
Db 79 PDSMKGRFTISRDNARNILYLQMSLRSEDTAMTCARIDYICGGG---GNFADAMDWGOGTLVTVS 133
QY 121 SASSTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 180
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Db 134 SASFKGSEVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLOS 193
Qy 181 SGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCTPCPAPPELLG 240
Db 194 SGLYSLSVTVTPSSSLGTQTYICTVNHKPSNTKVDKKVEPKSCDKTHTCTPCPAPPELLG 253
Qy 241 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQY 300
Db 254 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQY 313
Qy 301 NSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPREPOVYITLPSRD 360
Db 314 NSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPREPOVYITLPSRE 373
Qy 361 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSR 420
Db 374 EMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLTVDKSR 433
Qy 421 WQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
Db 434 WQGNVFSCSVMHEALHNHYTQKSLSLSPGK 464

RESULT 14
AAR33311
ID AAR33311 standard; Protein; 453 AA.
XX
AC AAR33311;
XX
DT 05-JUL-1993 (first entry)
XX
DE Humanised MaE11 Version 1 (intact IgG) heavy chain.
XX
KW Antibody; high affinity; FcEH; low affinity; FCEL;
KW IgE receptor; histamine; mast cell; basophil; Kabat;
KW CDR; murine; MAE11; Fab; humael1v1.
XX
OS Synthetic.
XX
PN W09304173-A.
XX
PD 04-MAR-1993.
XX
PF 14-AUG-1992; 92WO-0506860.
XX
PR 14-AUG-1991; 91US-0744768.
PR 07-MAY-1992; 92US-0879495.
XX
PA (GETH) GENENTECH INC.
XX
PI Jardieu PM, Presta IG;
XX
PD WPI; 1993-094004/11.
XX
PT Polypeptide(s) binding to specific Fc epsilon receptors - act as
PT IgE antagonists; useful for treating and preventing IgE-mediated
PT disorders e.g. allergies
XX
PS Example 4; Fig 3; 113pp; English.
XX
CC Residues were selected from MaE11 and inserted or substituted into
CC a human Fab antibody background (Vh region Kabat subgroup III and Vh
CC region kappa subgroup I). A first version, humael1v1 or version 1 is
CC given below. The affinity of version 1 was assayed and found to be
CC ca. 100 times lower than that of the donor antibody MaE11.
CC Therefore, further modifications in the sequence of version 1
CC were made.
XX
SQ Sequence 453 AA;
XX
Query Match 90.3%; Score 2177; DB 14; Length 453;
,Best Local Similarity 91.6%; Pred. No. 4.5e-122;

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Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;
Qy 1 QYQLVQSGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPKGLGWVSGISGGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSYGISYGSYWNIRQAPKGLGWASIT-YDGSIN 59
Qy 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWDPIDYWGQGLT 118
Db 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVWQGLT 118
Qy 119 VSSAST--KGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPA 176
Db 119 VSSASTKKGSGSEVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPA 178
Qy 177 VLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCTPCPAP 236
Db 179 VLQSSGLYSLSVTVTPSSSLGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHTCTPCPAP 238
Qy 237 ELGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPR 296
Db 239 ELGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPR 298
Qy 297 EEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPREPOVYITLP 356
Db 299 EEQYNSTYRVVSVLTVLHODWLNKGEYKCKVSNKALPAPIETKISKAKGQPREPOVYITLP 358
Qy 357 PSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLT 416
Db 359 PSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFPLYSKLT 418
Qy 417 DKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
Db 419 DKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453

RESULT 15
AAY85199
ID AAY85199 standard; protein; 453 AA.
XX
AC AAY85199;
XX
DT 29-JUN-2000 (first entry)
XX
DE Heavy chain amino acid sequence of the humanised MaE11 antibody.
XX
KW Immunoglobulin E; IgE; anti-human IgE; bispecific antibody; FCEL; FCBH;
KW low affinity binding receptor; high affinity binding receptor; allergy;
KW diagnosis; treatment; histamine release; heavy chain; prevent; chimeric.
XX
OS Mus sp.
OS Homo sapiens.
XX
PN US6037453-A.
XX
PD 14-MAR-2000.
XX
PF 06-JUN-1995; 95US-0466151.
XX
PR 15-MAR-1995; 95US-0405617.
PR 14-AUG-1992; 92WO-US06860.
PR 26-JAN-1994; 94US-0185899.
XX
PA (GETH) GENENTECH INC.
XX
PI Presta IG, Jardieu PM;
XX
PD WPI; 2000-269913/23.
XX
PT New bispecific antibodies, useful for treating immunoglobulin
PT E-mediated disease, binds to IgE, but only when on the low affinity
PT receptor, and to an antigen other than IgE
XX
PS Claim 14; Fig 3; 48pp; English.

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XX This sequence represents the heavy chain amino acid sequence of a  
CC humanised mouse anti-human immunoglobulin E (IgE) antibody. The invention  
CC relates to a bispecific antibody that binds specifically to IgE when IgE  
CC is bound to its low affinity receptor (FcεR1), but does not bind to IgE,  
CC when IgE is bound to its high affinity receptor (FcεR2). The bispecific  
CC antibody comprises an IgE-binding arm with human framework residues of a  
CC recipient human antibody and donor murine CDR (complementarity  
CC determining region) residues, but with at least one human CDR residue  
CC replacing the analogous murine residue. The antibody also comprises an Fv  
CC that is specific for a predetermined antigen other than IgE. The  
CC antibodies work by displacing bound IgE from its receptor, or via  
CC competitive inhibition of its binding. The bispecific antibodies are used  
CC for diagnosis, treatment and prevention of allergy and other IgE-mediated  
CC diseases, also, when immobilised, for the isolation of FcεR1 from cells  
CC (for research or therapy). The bispecific antibodies of the invention do  
CC not cause granulation or release of histamine from mast cells.

XX SQ Sequence 453 AA;  
Query Match 90.3%; Score 2177; DB 21; Length 453;  
Best Local Similarity 91.6%; Pred. No. 4.5e-122;  
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;  
QY 1 QYQLVQSGGLVQPGGSLRLSCAASGFTFRSN-AMGHWROAPCKGLEWYSGISGGSGSTY 59  
DB 1 EVOLVESGGGLVQPGGSLRLSCAVSGYSITSGYSWMNIRQAPCKGLEWVASIT-YDGSSTN 59  
QY 60 YADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCAKHTG-GGYWDPIDYWGQGLT 118  
DB 60 YADSVKGRFTISRDNKNTLYLQNSLRRAEDTAVYYCARGSHVFGHWH-FAVMGQGLT 118  
QY 119 VSSAST--KGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTP 176  
DB 119 VSSASTKGKPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTP 178  
QY 177 VLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPPCP 236  
DB 179 VLQSSGLYSLSSVWTVPSSSLGTQTYICNVNHPKSNPKVDKVEPKSCDKTHTCPPCP 238  
QY 237 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 296  
DB 239 ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTP 298  
QY 297 EEQYNSTYRVSVLTVQLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 356  
DB 299 EEQYNSTYRVSVLTVQLHQLDMLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358  
QY 357 PSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPVLDSDGSFFLYSKLT 416  
DB 359 PSREMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPTPVLDSDGSFFLYSKLT 418  
QY 417 DKSRWQOGNWFSCVWHEALNHNHYTKSLSPGK 451  
DB 419 DKSRWQOGNWFSCVWHEALNHNHYTKSLSPGK 453

Search completed: October 9, 2002, 19:10:30  
Job time : 50.3214 secs



Db 61 NQKGRFTLSRDNKNTAYLQMSLRAEDTAVYYCARGDYRYNGDWF-FDVMGQGTILVT 119  
QY 119 VSSASTKGPSVFPLAPSSKTSKGTALCLVKDYKPEPVTVSWNSGALTSGVHTFPAVL 178  
Db 120 VSSASTKGPSVFPLAPSSKTSKGTALCLVKDYKPEPVTVSWNSGALTSGVHTFPAVL 179  
QY 179 QSSGLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKTHTCPCPAPEL 238  
Db 180 QSSGLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKTHTCPCPAPEL 239  
QY 239 LGGSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 298  
Db 240 LGGSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPREE 299  
QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358  
Db 300 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359  
QY 359 RDELTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDK 418  
Db 360 REETKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDK 419  
QY 419 SRWQGNVFSCVSMHEALHNHYTQKSLSLSPGK 451  
Db 420 SRWQGNVFSCVSMHEALHNHYTQKSLSLSPGK 452

## RESULT 4

US-08-157-101A-7  
; Sequence 7, Application US/08157101A  
; Patent No. 5808032  
; GENERAL INFORMATION:  
; APPLICANT: KURIHARA, TATSUYA  
; APPLICANT: MATSUKURA, SHIGEKAZU  
; APPLICANT: TSURUOKA, NOBUO  
; APPLICANT: ARIMA, KENJI  
; APPLICANT: NISHIHARA, TATSURO  
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: PILLSBURY, MADISON & SUTRO  
; STREET: 1100 NEW YORK AVENUE, N.W.  
; CITY: WASHINGTON  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/157,101A  
; FILING DATE: 05-APR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: TITUS, MARIANA K  
; REGISTRATION NUMBER: 35843  
; REFERENCE/DOCKET NUMBER: 9437/204199  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3711  
; TELEFAX: 202-822-0944  
; TELEX: 6714627 CUCH  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 459 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide

US-08-157-101A-7

Query Match 91.6%; Score 2207.5; DB 1; Length 459;  
Best Local Similarity 92.7%; Pred. No. 1.5e-166;  
Matches 418; Conservative 9; Mismatches 23; Indels 1; Gaps 1;  
QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSRNAMGWVROAPGKGLWVSGISGGSGSTYY 60  
Db 10 QVQLVSGGGVQPGGSLRLSCAASGFTFSNMMHWVROAPGKGLWVAVILYDGNHKEY 69  
QY 61 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIDYWGQGTILTVTS 120  
Db 70 ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYYCAKHTGGVWDPIDYWGQGTILTVTS 128  
QY 121 SASTKGPSVFPLAPSSKTSKGTALCLVKDYKPEPVTVSWNSGALTSGVHTFPAVLQ 180  
Db 129 SASTKGPSVFPLAPSSKTSKGTALCLVKDYKPEPVTVSWNSGALTSGVHTFPAVLQ 188  
QY 181 SGLYSLSVSVTVVPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKTHTCPCPAPEL 240  
Db 189 SGLYSLSVSVTVVPSSSLGTQYICNVNHPKNTKVDKKVEPKSCDKTHTCPCPAPEL 248  
QY 241 GPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQ 300  
Db 249 GPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQ 308  
QY 301 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360  
Db 309 NSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 368  
QY 361 ELTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSR 420  
Db 369 ELTKNOVSLTCLVKGFPYSDIAVEWESNGQPENNYKTTTPPVLDSDGSFFLYSLKLTVDKSR 428  
QY 421 WOQGNVFSCVSMHEALHNHYTQKSLSLSPGK 451  
Db 429 WOQGNVFSCVSMHEALHNHYTQKSLSLSPGK 459

## RESULT 5

US-08-466-151-8  
; Sequence 8, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/466,151  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/466163  
; FILING DATE: 06-Jun-1995  
; APPLICATION NUMBER: 08/405617  
; FILING DATE: 15-MAR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/185899  
; FILING DATE: 26-JAN-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/879495  
; FILING DATE: 07-MAY-1992

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-8

Query Match 90.3%; Score 2177; DB 3; Length 453;
Best Local Similarity 91.6%; Pred. No. 3.8e-164;
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPGKLEWVSGISGGSGSTY 59
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKLEWVASIT-YDGSN 59
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 60 YADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCAKHTG-GGVWDPTIDYWGQGLT 118
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 YADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARGSHYFGHH-FAVWGQGLT 118
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QY 119 VSSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 176
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 119 VSSASTKGGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 178
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 177 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPPCPAP 236
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPPCPAP 238
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 237 ELLGSPSVFLPPPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
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QY 297 EEOYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 356
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Db 299 EEOYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358
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QY 357 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLT 416
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 359 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLT 418
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QY 417 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
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Db 419 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
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RESULT 6
US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-163B-8

Query Match 90.3%; Score 2177; DB 3; Length 453;
Best Local Similarity 91.6%; Pred. No. 3.8e-164;
Matches 417; Conservative 13; Mismatches 19; Indels 6; Gaps 5;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPGKLEWVSGISGGSGSTY 59
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Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNWIRQAPGKLEWVASIT-YDGSN 59
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QY 60 YADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCAKHTG-GGVWDPTIDYWGQGLT 118
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Db 60 YADSVKGRFTISRDNKNTLYQMNSLRAEDTAVYYCARGSHYFGHH-FAVWGQGLT 118
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QY 119 VSSAST--KGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 176
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 119 VSSASTKGGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPA 178
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QY 177 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPPCPAP 236
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 VLQSSGLYSLSSVTVPSSSLGTQTYICNVNHPKSNKVDKVPKSCDKTHTCPPCPAP 238
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 237 ELLGSPSVFLPPPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 296
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 ELLGSPSVFLPPPKDFTLMSRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPR 298
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 297 EEOYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 356
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Db 299 EEOYNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTL 358
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QY 357 PSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLT 416
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 359 PSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLT 418
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 417 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 419 DKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 453
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RESULT 7
US-08-887-352B-14
; Sequence 14, Application US/08887352B
; Patent No. 5994511
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of
; TITLE OF INVENTION: Improving Polypeptides
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Winpatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,352B
; FILING DATE: 03-Jul-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
```



; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-887-352B-14

Query Match 90.0%; Score 2169; DB 2; Length 451;  
Best Local Similarity 91.4%; Pred. No. 1.6e-163;  
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVSGGGLVOPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKLEWVSGTSGGGSTY 59  
Db 1 EVQLVESGGGLVOPGGSLRLSCAVSGYSITGYSWNWIRQAPGKLEWVASIT-YDGSIN 59  
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVMDPIDYWGQGLT 118  
Db 60 YNPVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGSHYFGHWH-FAVWGQGLT 118  
QY 119 VSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVHTFPAVL 178  
Db 119 VSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVHTFPAVL 178  
QY 179 QSSGLXSLSSVTVPPSSSLGTQTYICNVNHPKPSNTKVDKVKPEKSCDKTHTCPCPAPEL 238  
Db 179 QSSGLXSLSSVTVPPSSSLGTQTYICNVNHPKPSNTKVDKVKPEKSCDKTHTCPCPAPEL 238  
QY 239 LGGPSVFLFPKPKDILMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298  
Db 239 LGGPSVFLFPKPKDILMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298  
QY 299 QYNSTYRVSVLVTLVHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPS 358  
Db 299 QYNSTYRVSVLVTLVHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPS 358  
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418  
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418  
QY 419 SRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451  
Db 419 SRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

## RESULT 8

US-08-887-352B-16  
; Sequence 16, Application US/08887352B  
; Patent No. 5994511  
; GENERAL INFORMATION:  
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe  
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of  
; TITLE OF INVENTION: Improving Polypeptides  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/887,352B  
; FILING DATE: 03-Jul-1997

; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Svoboda, Craig C.  
; REGISTRATION NUMBER: 39,044  
; REFERENCE/DOCKET NUMBER: P1123  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650/225-1489  
; TELEFAX: 650/952-9881  
; INFORMATION FOR SEQ ID NO: 16:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 451 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
; US-08-887-352B-16

Query Match 90.0%; Score 2169; DB 2; Length 451;

Best Local Similarity 91.4%; Pred. No. 1.6e-163;  
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVSGGGLVOPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKLEWVSGTSGGGSTY 59  
Db 1 EVQLVESGGGLVOPGGSLRLSCAVSGYSITGYSWNWIRQAPGKLEWVASIT-YDGSIN 59  
QY 60 YADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKHTG-GGVMDPIDYWGQGLT 118  
Db 60 YNPVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCARGSHYFGHWH-FAVWGQGLT 118  
QY 119 VSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVHTFPAVL 178  
Db 119 VSSASTKGPSVFLPAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSVHTFPAVL 178  
QY 179 QSSGLXSLSSVTVPPSSSLGTQTYICNVNHPKPSNTKVDKVKPEKSCDKTHTCPCPAPEL 238  
Db 179 QSSGLXSLSSVTVPPSSSLGTQTYICNVNHPKPSNTKVDKVKPEKSCDKTHTCPCPAPEL 238  
QY 239 LGGPSVFLFPKPKDILMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298  
Db 239 LGGPSVFLFPKPKDILMSRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREE 298  
QY 299 QYNSTYRVSVLVTLVHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPS 358  
Db 299 QYNSTYRVSVLVTLVHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPVYTLPPS 358  
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418  
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418  
QY 419 SRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451  
Db 419 SRWQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451

## RESULT 9

US-08-466-151-65  
; Sequence 65, Application US/08466151  
; Patent No. 6037453  
; GENERAL INFORMATION:  
; APPLICANT: Jardieu, Paula M.  
; APPLICANT: Presta, Leonard G.  
; TITLE OF INVENTION: Immunoglobulin Variants  
; NUMBER OF SEQUENCES: 65  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 1 DNA Way  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET INFORMATION: P0718P2CID1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 451 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-08-466-151-65

Query Match 90.0%; Score 2169; DB 3; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKGLWVSGISGGSTY 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKGLWVASIT-YDGSN 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 60 YADSVKGRFTISRDNKNTLYQMNSLRADETAVYICAKHTG-GGVWDPIDYWGQGLT 118
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Db 60 YNPSVKGRITISRDDSKNTFYQMNSLRADETAVYICARGSHYFGHHW-FAVWGQGLT 118
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Qy 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFP 178
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Db 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFP 178
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Qy 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 238
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Db 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 238
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Qy 239 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 298
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Db 239 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 298
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Qy 299 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYTLPP 358
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Db 299 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYTLPP 358
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Qy 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
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Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
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Qy 419 SRWQOGNVSFSCVMHEALHNHYTQKSLSLSPGK 451
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 419 SRWQOGNVSFSCVMHEALHNHYTQKSLSLSPGK 451
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RESULT 10
US-09-109-207C-14
; Sequence 14, Application US/09109207C
; Patent No. 617213
;

; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAE11
;
US-09-109-207C-14

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVRQAPGKGLWVSGISGGSTY 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGYSITSGYSNNIRQAPGKGLWVASIT-YDGSN 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 60 YADSVKGRFTISRDNKNTLYQMNSLRADETAVYICAKHTG-GGVWDPIDYWGQGLT 118
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 YNPSVKGRITISRDDSKNTFYQMNSLRADETAVYICARGSHYFGHHW-FAVWGQGLT 118
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFP 178
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 119 VSSASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNVNSGALTSGVHTFP 178
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 238
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 179 QSSGLYSLSVVTPSSSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPCPAPEL 238
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 239 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 298
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 239 LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 298
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 299 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYTLPP 358
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 299 QYNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTIISKAKGPREPQVYTLPP 358
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 359 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDK 418
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 419 SRWQOGNVSFSCVMHEALHNHYTQKSLSLSPGK 451
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 419 SRWQOGNVSFSCVMHEALHNHYTQKSLSLSPGK 451
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 11
US-09-109-207C-16
; Sequence 16, Application US/09109207C
; Patent No. 6172213
;
GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypept
; FILE REFERENCE: P1123R1
; CURRENT APPLICATION NUMBER: US/09/109,207C
; CURRENT FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/051,554
; PRIOR FILING DATE: 1997-07-03
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
;

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;
; FEATURE:
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
US-09-109-207C-16

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGVSIITSGYSNWIRQAPGKGLWVASIT-YDGSN 59

QY 60 YADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTFLVT 118
Db 60 YNPVKGRITISRDDSKNTFFLQMNLSRAEDTAVYYCARGSHYFGHHW-FAVWGQGTFLVT 118

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVL 178

QY 179 QSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238
Db 179 QSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238

QY 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298

QY 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
Db 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
Db 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 12
US-09-296-005-14
; Sequence 14, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypeptides
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; EARLIER FILING DATE: 1999-04-21
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 14
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
US-09-296-005-14

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGVSIITSGYSNWIRQAPGKGLWVASIT-YDGSN 59

QY 60 YADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTFLVT 118
Db 60 YNPVKGRITISRDDSKNTFFLQMNLSRAEDTAVYYCARGSHYFGHHW-FAVWGQGTFLVT 118

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVL 178

QY 179 QSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238
Db 179 QSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238

QY 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298

QY 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
Db 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
Db 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 13
US-09-296-005-16
; Sequence 16, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypepti
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; EARLIER FILING DATE: 1999-04-21
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
US-09-296-005-16

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGVSIITSGYSNWIRQAPGKGLWVASIT-YDGSN 59

QY 60 YADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTFLVT 118
Db 60 YNPVKGRITISRDDSKNTFFLQMNLSRAEDTAVYYCARGSHYFGHHW-FAVWGQGTFLVT 118

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVL 178

QY 179 QSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238
Db 179 QSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238

QY 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298

QY 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
Db 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
Db 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
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QY 60 YADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTFLVT 118
Db 60 YNPVKGRITISRDDSKNTFFLQMNLSRAEDTAVYYCARGSHYFGHHW-FAVWGQGTFLVT 118

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVL 178

QY 179 QSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238
Db 179 QSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238

QY 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298

QY 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
Db 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
Db 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

RESULT 13
US-09-296-005-16
; Sequence 16, Application US/09296005
; Patent No. 6290957
; GENERAL INFORMATION:
; APPLICANT: Henry B. Lowman, Leonard G. Presta, Paula M. Jardieu, John Lowe
; TITLE OF INVENTION: Improved Anti-IgE Antibodies and Method of Improving Polypepti
; FILE REFERENCE: P1123C1r
; CURRENT APPLICATION NUMBER: US/09/296,005
; EARLIER FILING DATE: 1999-04-21
; EARLIER FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 16
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Artificial
; NAME/KEY: Artificial
; LOCATION: 1-451
; OTHER INFORMATION: Heavy chain sequence derived from MAEL1
US-09-296-005-16

Query Match 90.0%; Score 2169; DB 4; Length 451;
Best Local Similarity 91.4%; Pred. No. 1.6e-163;
Matches 414; Conservative 13; Mismatches 22; Indels 4; Gaps 4;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSN-AMGWVROAPGKGLWVSGISGSGSTY 59
Db 1 EVQLVESGGGLVQPGGSLRLSCAVSGVSIITSGYSNWIRQAPGKGLWVASIT-YDGSN 59

QY 60 YADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTG-GGVWDPIDYWGQGTFLVT 118
Db 60 YNPVKGRITISRDDSKNTFFLQMNLSRAEDTAVYYCARGSHYFGHHW-FAVWGQGTFLVT 118

QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVL 178
Db 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVL 178

QY 179 QSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238
Db 179 QSSGLYSLSVVTVPPSSSLGQTQYICNVNHNKPSNTKYDKKVEPKSCDKTHTCCPCPAPEL 238

QY 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298
Db 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNKATKPREE 298

QY 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358
Db 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 358

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
Db 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418

QY 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
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Db 359 REEMTKNOVSLICLYKGFYPSDIAVEWESNGQPENNNYKTTTPPVLDSDGSEFFLYSKLTVDK 418

Qy 419 SRWQGNVFSQSVMHQALHNHYTQKSLSLSPGK 451

Db 419 SRWQGNVFSQSVMHQALHNHYTQKSLSLSPGK 451

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:10:35 ; Search time 177.754 seconds  
(without alignments)  
893.051 Million cell updates/sec

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Perfect score: 2411  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 3502263

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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26: /cgn2\_6/ptodata/2/paa/US60\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 3          | 2228.5 | 92.4        | 663    | 1  | PCT-US01-32140-32 |
| 4          | 2228.5 | 92.4        | 4852   | 1  | PCT-US01-32140-33 |
| 5          | 2224.5 | 92.3        | 499    | 21 | US-09-760-479-645 |
| 6          | 2223.5 | 92.2        | 494    | 21 | US-09-760-479-636 |
| 7          | 2214.5 | 91.8        | 449    | 20 | US-09-680-148-2   |

|    |        |      |     |    |                   |
|----|--------|------|-----|----|-------------------|
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| 9  | 2211.5 | 91.7 | 452 | 14 | US-09-012-116-71  |
| 10 | 2211.5 | 91.7 | 452 | 15 | US-09-121-952A-71 |
| 11 | 2211.5 | 91.7 | 452 | 15 | US-09-122-513A-71 |
| 12 | 2211.5 | 91.7 | 452 | 16 | US-09-234-182A-71 |
| 13 | 2211.5 | 91.7 | 452 | 16 | US-09-234-340A-71 |
| 14 | 2211.5 | 91.7 | 452 | 18 | US-09-489-394-71  |
| 15 | 2211.5 | 91.7 | 452 | 21 | US-09-726-258-71  |
| 16 | 2207.5 | 91.6 | 459 | 5  | US-08-157-101-7   |
| 17 | 2196   | 91.1 | 476 | 21 | US-09-760-479-599 |
| 18 | 2177   | 90.3 | 453 | 7  | US-08-328-597-8   |
| 19 | 2177   | 90.3 | 453 | 8  | US-08-405-617-8   |
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| 21 | 2177   | 90.3 | 453 | 22 | US-09-802-096-8   |
| 22 | 2177   | 90.3 | 453 | 23 | US-09-925-179-8   |
| 23 | 2169   | 90.0 | 451 | 12 | US-08-887-352-14  |
| 24 | 2169   | 90.0 | 451 | 12 | US-08-887-352-16  |
| 25 | 2169   | 90.0 | 451 | 12 | US-08-887-352A-14 |
| 26 | 2169   | 90.0 | 451 | 12 | US-08-887-352A-16 |
| 27 | 2169   | 90.0 | 451 | 15 | US-09-109-207-14  |
| 28 | 2169   | 90.0 | 451 | 15 | US-09-109-207-16  |
| 29 | 2169   | 90.0 | 451 | 15 | US-09-109-207-14  |
| 30 | 2169   | 90.0 | 451 | 15 | US-09-109-207-16  |
| 31 | 2169   | 90.0 | 451 | 21 | US-09-716-028-14  |
| 32 | 2169   | 90.0 | 451 | 21 | US-09-716-028-16  |
| 33 | 2169   | 90.0 | 451 | 23 | US-09-920-171-14  |
| 34 | 2169   | 90.0 | 451 | 23 | US-09-920-171-16  |
| 35 | 2169   | 90.0 | 451 | 23 | US-09-925-179-65  |
| 36 | 2168   | 89.9 | 451 | 12 | US-08-887-352-18  |
| 37 | 2168   | 89.9 | 451 | 12 | US-08-887-352A-18 |
| 38 | 2168   | 89.9 | 451 | 15 | US-09-109-207-18  |
| 39 | 2168   | 89.9 | 451 | 15 | US-09-109-207-18  |
| 40 | 2168   | 89.9 | 451 | 16 | US-09-282-846-2   |
| 41 | 2168   | 89.9 | 451 | 18 | US-09-483-588-2   |
| 42 | 2168   | 89.9 | 451 | 20 | US-09-680-145-2   |
| 43 | 2168   | 89.9 | 451 | 21 | US-09-713-425-2   |
| 44 | 2168   | 89.9 | 451 | 21 | US-09-716-028-18  |
| 45 | 2168   | 89.9 | 451 | 21 | US-09-792-938-2   |

ALIGNMENTS

RESULT 1  
US-09-822-698A-26  
; Sequence 26, Application US/09822698A  
; GENERAL INFORMATION:  
; APPLICANT: Hoogenboom, Hendricus R.J.M.  
; APPLICANT: Henderikx, Maria P.G.  
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
; FILE REFERENCE: DXX-015.1 US  
; CURRENT APPLICATION NUMBER: US/09/822,698A  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/538,913  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 26  
; TYPE: PRT  
; LENGTH: 451  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: immunoglobulin heavy chain of MUC1-specific PH1-IgG1  
US-09-822-698A-26

Query Match 100.0%; Score 2411; DB 22; Length 451;  
Best Local Similarity 100.0%; Pred. No. 1.3e-186;  
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 QVQLVQSGGGLVQPGGSLRLCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60  
DB 1 QVQLVQSGGGLVQPGGSLRLCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60





|                                                                 |                                                                 |
|-----------------------------------------------------------------|-----------------------------------------------------------------|
| ; ORGANISM: Homo Sapien                                         |                                                                 |
| PCT-US01-32140-32                                               |                                                                 |
| Query Match 92.4%; Score 2228.5; DB 1; Length 663;              |                                                                 |
| Best Local Similarity 93.3%; Pred. No. 1.5e-171;                |                                                                 |
| Matches 420; Conservative 9; Mismatches 20; Indels 1; Gaps 1;   |                                                                 |
| QY 1                                                            | QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSYTY 60   |
| DB 215                                                          | EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSYTY 274  |
| ; QY 61                                                         |                                                                 |
| ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTGGGWDPIDYWGQGLTVTVS 120    |                                                                 |
| DB 275                                                          |                                                                 |
| PDSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTGGGWDPIDYWGQGLTVTVS 333    |                                                                 |
| ; QY 121                                                        |                                                                 |
| SASTKGPSVFPPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180 |                                                                 |
| DB 334                                                          |                                                                 |
| SASTKGPSVFPPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 393 |                                                                 |
| ; QY 181                                                        |                                                                 |
| SGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPELIG 240 |                                                                 |
| DB 394                                                          |                                                                 |
| SGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPELIG 453 |                                                                 |
| ; QY 241                                                        |                                                                 |
| GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 300  |                                                                 |
| DB 454                                                          |                                                                 |
| GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 513  |                                                                 |
| ; QY 301                                                        |                                                                 |
| NSTYRVVSVLTVLHDWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360  |                                                                 |
| DB 514                                                          |                                                                 |
| NSTYRVVSVLTVLHDWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 573  |                                                                 |
| ; QY 361                                                        |                                                                 |
| ELTKNOVSLTCLVKGYFSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 420  |                                                                 |
| DB 574                                                          |                                                                 |
| ELTKNOVSLTCLVKGYFSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 633  |                                                                 |
| ; QY 421                                                        |                                                                 |
| WQGNVFCSCVMHEALHNYTKQSLSPG 450                                  |                                                                 |
| DB 634                                                          |                                                                 |
| WQGNVFCSCVMHEALHNYTKQSLSPG 663                                  |                                                                 |
| RESULT 4                                                        |                                                                 |
| PCT-US01-32140-33                                               |                                                                 |
| ; Sequence 33, Application PC/TUS0132140                        |                                                                 |
| ; GENERAL INFORMATION:                                          |                                                                 |
| ; APPLICANT: BIOGEN, INC.                                       |                                                                 |
| ; APPLICANT: GABER, Ellen                                       |                                                                 |
| ; APPLICANT: LYNE, Paul                                         |                                                                 |
| ; APPLICANT: SALDHANA, Jose W.                                  |                                                                 |
| ; TITLE OF INVENTION: HUMANIZED ANTI-LT-BETA-R ANTIBODIES       |                                                                 |
| ; FILE REFERENCE: A100 PCT                                      |                                                                 |
| ; CURRENT APPLICATION NUMBER: PCT/US01/32140                    |                                                                 |
| ; CURRENT FILING DATE: 2001-10-12                               |                                                                 |
| ; PRIOR APPLICATION NUMBER: 60/240,285                          |                                                                 |
| ; PRIOR FILING DATE: 2000-10-13                                 |                                                                 |
| ; PRIOR APPLICATION NUMBER: 60/275,289                          |                                                                 |
| ; PRIOR FILING DATE: 2001-03-13                                 |                                                                 |
| ; PRIOR APPLICATION NUMBER: 60/299,987                          |                                                                 |
| ; PRIOR FILING DATE: 2001-06-21                                 |                                                                 |
| ; NUMBER OF SEQ ID NOS: 33                                      |                                                                 |
| ; SOFTWARE: FastSeq for Windows Version 4.0                     |                                                                 |
| ; SEQ ID NO 33                                                  |                                                                 |
| ; LENGTH: 4852                                                  |                                                                 |
| ; TYPE: PRT                                                     |                                                                 |
| ; ORGANISM: Homo Sapien                                         |                                                                 |
| PCT-US01-32140-33                                               |                                                                 |
| Query Match 92.4%; Score 2228.5; DB 1; Length 4852;             |                                                                 |
| Best Local Similarity 93.3%; Pred. No. 2.4e-170;                |                                                                 |
| Matches 420; Conservative 9; Mismatches 20; Indels 1; Gaps 1;   |                                                                 |
| QY 1                                                            | QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSYTY 60   |
| DB 4404                                                         | EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSYTY 4463 |

|                                                                  |                                                                |
|------------------------------------------------------------------|----------------------------------------------------------------|
| ; ORGANISM: Homo Sapien                                          |                                                                |
| PCT-US01-32140-32                                                |                                                                |
| Query Match 92.4%; Score 2228.5; DB 1; Length 663;               |                                                                |
| Best Local Similarity 93.3%; Pred. No. 1.5e-171;                 |                                                                |
| Matches 420; Conservative 9; Mismatches 20; Indels 1; Gaps 1;    |                                                                |
| QY 1                                                             | QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSYTY 60  |
| DB 215                                                           | EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSYTY 274 |
| ; QY 61                                                          |                                                                |
| ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTGGGWDPIDYWGQGLTVTVS 120     |                                                                |
| DB 275                                                           |                                                                |
| PDSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTGGGWDPIDYWGQGLTVTVS 333     |                                                                |
| ; QY 121                                                         |                                                                |
| SASTKGPSVFPPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 180  |                                                                |
| DB 334                                                           |                                                                |
| SASTKGPSVFPPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 393  |                                                                |
| ; QY 181                                                         |                                                                |
| SGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPELIG 240  |                                                                |
| DB 394                                                           |                                                                |
| SGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPCPAPELIG 453  |                                                                |
| ; QY 241                                                         |                                                                |
| GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 300   |                                                                |
| DB 454                                                           |                                                                |
| GPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 513   |                                                                |
| ; QY 301                                                         |                                                                |
| NSTYRVVSVLTVLHDWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360   |                                                                |
| DB 514                                                           |                                                                |
| NSTYRVVSVLTVLHDWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 573   |                                                                |
| ; QY 361                                                         |                                                                |
| ELTKNOVSLTCLVKGYFSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 420   |                                                                |
| DB 574                                                           |                                                                |
| ELTKNOVSLTCLVKGYFSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 633   |                                                                |
| ; QY 421                                                         |                                                                |
| WQGNVFCSCVMHEALHNYTKQSLSPG 450                                   |                                                                |
| DB 634                                                           |                                                                |
| WQGNVFCSCVMHEALHNYTKQSLSPG 663                                   |                                                                |
| RESULT 5                                                         |                                                                |
| US-09-760-479-645                                                |                                                                |
| ; Sequence 645, Application US/09760479                          |                                                                |
| ; GENERAL INFORMATION:                                           |                                                                |
| ; APPLICANT: ROSEN ET AL.                                        |                                                                |
| ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies    |                                                                |
| ; FILE REFERENCE: PTZ53                                          |                                                                |
| ; CURRENT APPLICATION NUMBER: US/09/760,479                      |                                                                |
| ; CURRENT FILING DATE: 2001-01-16                                |                                                                |
| ; Prior application data removed - refer to PALM or file wrapper |                                                                |
| ; NUMBER OF SEQ ID NOS: 945                                      |                                                                |
| ; SOFTWARE: PatentIn Ver. 2.0                                    |                                                                |
| ; SEQ ID NO 645                                                  |                                                                |
| ; LENGTH: 499                                                    |                                                                |
| ; TYPE: PRT                                                      |                                                                |
| ; ORGANISM: Homo sapiens                                         |                                                                |
| US-09-760-479-645                                                |                                                                |
| Query Match 92.3%; Score 2224.5; DB 21; Length 499;              |                                                                |
| Best Local Similarity 91.9%; Pred. No. 2.1e-171;                 |                                                                |
| Matches 421; Conservative 13; Mismatches 17; Indels 7; Gaps 2;   |                                                                |
| QY 1                                                             | QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSGSYTY 60  |
| DB 42                                                            | QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGSETIY 101  |
| ; QY 61                                                          |                                                                |
| ADSVKGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTGGGWDPIDYWGQGLTVTVS 113     |                                                                |
| DB 102                                                           |                                                                |
| GDSVGRFTISRDNKNTLYLQMSLRAEDTAVYCAKHTGGGWDPIDYWGQGLTVTVS 161      |                                                                |
| ; QY 114                                                         |                                                                |
| GTLTVSSASTKGPSVFPPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHT 173   |                                                                |
| DB 162                                                           |                                                                |
| GTLTVSSASTKGPSVFPPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHT 221   |                                                                |
| ; QY 174                                                         |                                                                |
| FPAVLQSSGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPC 233  |                                                                |
| DB 222                                                           |                                                                |
| FPAVLQSSGLYSLSVVTVTPSSSLGTQTYICNVNHPKSNKVDKKVEPKSCDKTHTCPPC 281  |                                                                |
| ; QY 234                                                         |                                                                |
| PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 293 |                                                                |
| DB 282                                                           |                                                                |
| PAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 341 |                                                                |
| ; QY 294                                                         |                                                                |
| KPREQYNSTYRVVSVLTVLHDWLNKGEYCKVSNKALPAPIEKTISKAKGQPREPQVY 353    |                                                                |



Matches 418; Conservative 13; Mismatches 13; Indels 6; Gaps 2;

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Qy 2 VOLVQGGGLVOPGGSLRLSCAASGFTFRSNAMGWVQAPCKGLEWVSGISGSGSTYYA 61
Db 21 IQLVSGGGVVRPGGSLRLSCAASGFTDDYCMGWVQAPCKGLEWVSGINWGGSTGYA 80
Qy 62 DSVKGRFTISRDNKNTLYLQMSLRADTAAYCYCAKHTGGVWDPIIDYWGQGTTLVTSS 121
Db 81 DSVKGRFTISRDNKNTLYLQMSLRADTAAYCYCAKHTGGVWDPIIDYWGQGTTLVTSS 134
Qy 122 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVLQSS 181
Db 135 ASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVLQSS 194
Qy 182 GLYSLSVTVVPSLSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPAPPELLGG 241
Db 195 GLYSLSVTVVPSLSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPAPPELLGG 254
Qy 242 PSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYN 301
Db 255 PSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNATKPREQYN 314
Qy 302 STYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 361
Db 315 STYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 374
Qy 362 LTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 421
Db 375 MTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 434
Qy 422 QCNQNFVSCSVMEALHNHYTQKSLSLSPGK 451
Db 435 QCNQNFVSCSVMEALHNHYTQKSLSLSPGK 464

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RESULT 9

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US-09-012-116-71
; Sequence 71, Application US/09012116
; GENERAL INFORMATION:
; APPLICANT: Hsei, Vanessa
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/012,116
; FILING DATE: 22-Jan-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:

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; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-012-116-71
Query Match 91.7%; Score 2211.5; DB 14; Length 452;
Best Local Similarity 92.5%; Pred. No. 2.1e-170;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;
Qy 1 QVOLVQGGGLVOPGGSLRLSCAASGFTFRSNAMGWVQAPCKGLEWVSGISGSGSTYYA 60
Db 1 EVOLVQGGGLVOPGGSLRLSCAASGYSFSSHYHWHVQAPCKGLEWVGYIDPSNCEITY 60
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRADTAAYCYCAKHTGGVWDPIIDYWGQGTTLVT 118
Db 61 NOKFKGRFTISRDNKNTLYLQMSLRADTAAYCYCAKHTGGVWDPIIDYWGQGTTLVT 119
Qy 119 VSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVL 178
Db 120 VSSASTKGPSVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSVGHVTFPAVL 179
Qy 179 QSGGLYSLSVTVVPSLSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPAPEL 238
Db 180 QSGGLYSLSVTVVPSLSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPPAPEL 239
Qy 239 LGGPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNATKPREE 298
Db 240 LGGPSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNATKPREE 299
Qy 299 QYNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 358
Db 300 QYNSTYRVVSVLTVLHQLDNLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPS 359
Qy 359 RELTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDK 418
Db 360 REEMTKNQVSLTCLVKGFPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDK 419
Qy 419 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451
Db 420 SRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 452

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RESULT 10

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US-09-121-952A-71
; Sequence 71, Application US/09121952A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/121,952A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330

```

```

; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-121-952A-71

Query Match 91.7%; Score 2211.5; DB 15; Length 452;
Best Local Similarity 92.5%; Pred. No. 2.1e-170;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAWGVRQAPGKGLWVGISGSGSTVY 60
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGYFSFSSHYMHVVRQAPGKGLWVGIDPSNGEITY 60
QY 61 ADSVKGRTTISRDNSKNTLYIQMNSLRAEDTAVYYCAK--HTGGGVWDPIDYWGQGLTVT 118
Db 61 NQKFKGRTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDMF-FDWMGQGLTVT 119
QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
Db 120 VSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179
QY 179 QSSGLYSLSVVTVPSVSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL 238
Db 180 QSSGLYSLSVVTVPSVSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL 239
QY 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNKYVDGVEVHNKTKPREE 298
Db 240 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNKYVDGVEVHNKTKPREE 299
QY 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 300 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDK 418
Db 360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDK 419
QY 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSLSPGK 451
Db 420 SRWQGNVFCSCVMHEALHNHYTOKLSLSLSPGK 452

RESULT 11
US-09-122-513A-71
; Sequence 71, Application US/09122513A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; APPLICANT: Shahrakh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES
; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California

```

```

; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/122,513A
; FILING DATE: 24-Jul-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074330
; FILING DATE: 22-JAN-1998
; PRIOR APPLICATION NUMBER: 60/075467
; FILING DATE: 20-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R4-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 71:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-122-513A-71

Query Match 91.7%; Score 2211.5; DB 15; Length 452;
Best Local Similarity 92.5%; Pred. No. 2.1e-170;
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAWGVRQAPGKGLWVGISGSGSTVY 60
Db 1 EVQLVQSGGGLVQPGGSLRLSCAASGYFSFSSHYMHVVRQAPGKGLWVGIDPSNGEITY 60
QY 61 ADSVKGRTTISRDNSKNTLYIQMNSLRAEDTAVYYCAK--HTGGGVWDPIDYWGQGLTVT 118
Db 61 NQKFKGRTLSRDNSKNTAYLQMNSLRAEDTAVYYCARGDYRYNGDMF-FDWMGQGLTVT 119
QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
Db 120 VSSASTKGPSVFPLAPSSKSTSGGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179
QY 179 QSSGLYSLSVVTVPSVSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL 238
Db 180 QSSGLYSLSVVTVPSVSLGTQTYICNVNHPKPSNTKVDKKVEPKSCDKTHCTCPCPAPEL 239
QY 239 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNKYVDGVEVHNKTKPREE 298
Db 240 LGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNKYVDGVEVHNKTKPREE 299
QY 299 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db 300 QYNSTYRVVSVLTVLDHQLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDK 418
Db 360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSEFFLYSKLTVDK 419
QY 419 SRWQGNVFCSCVMHEALHNHYTOKLSLSLSPGK 451
Db 420 SRWQGNVFCSCVMHEALHNHYTOKLSLSLSPGK 452

RESULT 12
US-09-234-182A-71
; Sequence 71, Application US/09234182A
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsei, Vanessa

```

APPLICANT: Koumenis, Iphigenia  
 APPLICANT: Leong, Steven R.  
 APPLICANT: Presta, Leonard G.  
 APPLICANT: Shahrokh, Zahra  
 APPLICANT: Zapata, Gerardo A.  
 TITLE OF INVENTION: ANTI-BODY FRAGMENT-POLYMER CONJUGATES AND  
 TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES  
 NUMBER OF SEQUENCES: 72  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 1 DNA Way  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: WinPatIn (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/234,182A  
 FILING DATE: 20-Jan-1999  
 CLASSIFICATION: 424  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/074330  
 FILING DATE: 22-JAN-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/094003  
 FILING DATE: 24-JUL-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/094013  
 FILING DATE: 24-JUL-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/075467  
 FILING DATE: 20-FEB-1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Love, Richard B.  
 REGISTRATION NUMBER: 34,659  
 REFERENCE/DOCKET NUMBER: P1085R4-1A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650/225-5530  
 TELEFAX: 650/952-9881  
 INFORMATION FOR SEQ ID NO: 71:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 452 amino acids  
 TYPE: Amino Acid  
 TOPOLOGY: Linear  
 US-09-234-182A-71

Query Match 91.7%; Score 2211.5; DB 16; Length 452;  
 Best Local Similarity 92.5%; Pred. No. 2.le-170;  
 Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;  
 QY 1 QVOLVQSGGLVOPGGSURLSCAASGFTFRSNAMGWVROAPKGLWVSGISGSGSTVY 60  
 DB 1 EVOLVQSGGLVOPGGSURLSCAASGYSFSSHYHWHVROAPKGLWVGYIDPSNGETTY 60  
 QY 61 ADSVKGRFTISRDNSKNTLYIQMSLRAEDTAVYICAK--HTGGGVWDPIDYWGOGTLVT 118  
 DB 61 NQKFKGRFTLSRDNSKNTAYIQMSLRAEDTAVYICARGDYRYNGDMF-FDYWGOGTLVT 119  
 QY 119 VSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178  
 DB 120 VSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179  
 QY 179 QSSGLVSLSVTVVPSVSSLGCTQYICNVNHPKSNVTKVDKVEPKSCDKTHTCPPCPAPEL 238  
 DB 180 QSSGLVSLSVTVVPSVSSLGCTQYICNVNHPKSNVTKVDKVEPKSCDKTHTCPPCPAPEL 239  
 QY 239 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNRYVDGVVHNAKTKPREE 298  
 DB 240 LGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNRYVDGVVHNAKTKPREE 299

QY 299 QYNSTYRVSVLTIVLHODWLNKKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPS 358  
 DB 300 QYNSTYRVSVLTIVLHODWLNKKEYCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPS 359  
 QY 359 RDELTKNOVSLTCLVKGFPYSDIAVESNGOPENNYKTPPVLDSDGSEFFLYSKLTVDK 418  
 DB 360 REEMTKNOVSLTCLVKGFPYSDIAVESNGOPENNYKTPPVLDSDGSEFFLYSKLTVDK 419  
 QY 419 SRWQOGNVFSCVMHEALHNHYTKLSLSLSPGK 451  
 DB 420 SRWQOGNVFSCVMHEALHNHYTKLSLSLSPGK 452

RESULT 13  
 US-09-234-340A-71  
 ; Sequence 71, Application US/09234340A  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genentech, Inc., Haei, Vanessa  
 ; APPLICANT: Koumenis, Iphigenia  
 ; APPLICANT: Leong, Steven R.  
 ; APPLICANT: Presta, Leonard G.  
 ; APPLICANT: Shahrokh, Zahra  
 ; APPLICANT: Zapata, Gerardo A.  
 ; TITLE OF INVENTION: METHODS OF TREATING INFLAMMATORY DISEASES  
 ; TITLE OF INVENTION: WITH ANTI-IL-8 ANTIBODY FRAGMENT-POLYMER CONJUGATES  
 ; NUMBER OF SEQUENCES: 72  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 1 DNA Way  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WinPatIn (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/234,340A  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/121,952  
 ; FILING DATE: 24-Jul-1998  
 ; APPLICATION NUMBER: 60/074330  
 ; FILING DATE: 22-JAN-1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 60/075467  
 ; FILING DATE: 20-FEB-1998  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Love, Richard B.  
 ; REGISTRATION NUMBER: 34,659  
 ; REFERENCE/DOCKET NUMBER: P1085R4  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650/225-5530  
 ; TELEFAX: 650/952-9881  
 ; INFORMATION FOR SEQ ID NO: 71:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 452 amino acids  
 ; TYPE: Amino Acid  
 ; TOPOLOGY: Linear  
 ; US-09-234-340A-71

Query Match 91.7%; Score 2211.5; DB 16; Length 452;  
 Best Local Similarity 92.5%; Pred. No. 2.le-170;  
 Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;  
 QY 1 QVOLVQSGGLVOPGGSURLSCAASGFTFRSNAMGWVROAPKGLWVSGISGSGSTVY 60  
 DB 1 EVOLVQSGGLVOPGGSURLSCAASGYSFSSHYHWHVROAPKGLWVGYIDPSNGETTY 60

|  |    |     |                                                              |     |
|--|----|-----|--------------------------------------------------------------|-----|
|  | Qy | 61  | ADSVGRGTISRDNKSNFLYLQNNLSRAEDTAVYCAK--HTGGVWDPDIDYQGQGLTVT   | 118 |
|  |    |     | :                                                            |     |
|  | Db | 61  | NQKFGRFTLSDRNKNNTAYLQNNLSRAEDTAVYCARGYRNGDMF-FDWGQGLTVT      | 119 |
|  |    |     | :                                                            |     |
|  | Qy | 119 | VSSASTKGPSVFPLAPSSKSTSGTAALGCLVKDYFPPEPVTVSNNSGALTSGVHTEPAVL | 178 |
|  |    |     | :                                                            |     |
|  | Db | 120 | VSSASTKGPSVFPLAPSSKSTSGTAALGCLVKDYFPPEPVTVSNNSGALTSGVHTEPAVL | 179 |
|  |    |     | :                                                            |     |
|  | Qy | 179 | QSGLSYSLSSVVTVPPSSSLGTQTYICNVNHNKPSNTKVOKVEPKSCDKTHTCPCPAPEL | 238 |
|  |    |     | :                                                            |     |
|  | Db | 180 | QSGLSYSLSSVVTVPPSSSLGTQTYICNVNHNKPSNTKVOKVEPKSCDKTHTCPCPAPEL | 239 |
|  |    |     | :                                                            |     |
|  | Qy | 239 | LGPSPVFELPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGEVHNAKTRPEE | 298 |
|  |    |     | :                                                            |     |
|  | Db | 240 | LGPSPVFELPPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGEVHNAKTRPEE | 299 |
|  |    |     | :                                                            |     |
|  | Qy | 299 | QYNSTRYRVVSVLTVLDHDLWGKEYCKYSNKKALPAPIEKTSIRAKGOPREPOVYTLPDS | 358 |
|  |    |     | :                                                            |     |
|  | Db | 300 | QYNSTRYRVVSVLTVLDHDLWGKEYCKYSNKKALPAPIEKTSIRAKGOPREPOVYTLPDS | 359 |
|  |    |     | :                                                            |     |
|  | Qy | 359 | RDELTKNQVSLTCLVKGFYPSDIAVWESNGOPPENNYKTTTPVLDSDGSFFLYSKITVDK | 418 |
|  |    |     | :                                                            |     |
|  | Db | 360 | REMTEKNQVSLTCLVKGFYPSDIAVWESNGOPPENNYKTTTPVLDSDGSFFLYSKITVDK | 419 |
|  |    |     | :                                                            |     |
|  | Qy | 419 | SRWQQGNFVCFSVMHEALHHNHYYTKSLSLSPGK 451                       |     |
|  |    |     | :                                                            |     |
|  | Db | 420 | SRWQQGNFVCFSVMHEALHHNHYYTKSLSLSPGK 452                       |     |
|  |    |     | :                                                            |     |

```

RESULT 14
US-09-489-394-71
; Sequence 71, Application US/09489394
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc., Hsai, Vanessa
; APPLICANT: Koumenis, Iphigenia
; APPLICANT: Leong, Steven R.
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND USES OF SAME
; FILE REFERENCE: P108586
; CURRENT APPLICATION NUMBER: US/09/489, 394
; CURRENT FILING DATE: 2000-01-21
; EARLIER APPLICATION NUMBER: US 60/116,787
; EARLIER FILING DATE: 1999-01-21
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 71
; LENGTH: 452
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-452
; OTHER INFORMATION: recombinant immunoglobulin
US-09-489-394-71

```

Query Match 91.7%; Score 2211.5; DB 18; Length 452;  
Best Local Similarity 92.5%; Pred. No. 2.1e-170;  
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

|    |     |                                                                           |     |
|----|-----|---------------------------------------------------------------------------|-----|
| Qy | 1   | QVQLVQSGGGLVQPGGSLRLISCAASGFTFRSNAMGWVWVQAQPKGLEWVSGISGGSGTYY             | 60  |
|    |     | :     :     :     :     :     :     :     :     :     :     :     :     : |     |
| Db | 1   | EVQLVQSGGGLVQPGGSLRLISCAASGTSFSSHYMHVWVQAQPKGLEWVGIIDPSNGETTY             | 60  |
|    |     | :     :     :     :     :     :     :     :     :     :     :     :       |     |
| Qy | 61  | ADSVAGRTISRDNSKNTLYIQMNSLRAREDVATVYCAK--HTGGVWDPIIDYQGQGLTVT              | 118 |
|    |     | :     :     :     :     :     :     :     :     :     :     :     :       |     |
| Db | 61  | NQKFGRGRTLSRDNSKNTAYLQMNSLRAREDVATVYCAARGDYRYNGDWF-EDVWGQGTGLTVT          | 119 |
|    |     | :     :     :     :     :     :     :     :     :     :     :     :       |     |
| Qy | 119 | VSSASTKGPSVFPPLAPSSKSTSGGTAAALGCLVKYDPEPPVTVSNNSGALTSGVHPTPAVL            | 178 |
|    |     | :     :     :     :     :     :     :     :     :     :     :     :       |     |
| Db | 120 | VSSASTKGPSVFPPLAPSSKSTSGGTAAALGCLVKDIFPEPVTVSNNSGALTSGVHPTPAVL            | 179 |
|    |     | :     :     :     :     :     :     :     :     :     :     :     :       |     |
| Qy | 179 | QSSGLYLSVVVYVPSSSLGTQTYICNVNHRKPSNTKVKDKVPEKPSCDKTHCTPCCPAPEL             | 238 |

|    |     |                                                                 |     |
|----|-----|-----------------------------------------------------------------|-----|
| Db | 180 | QSSGLYLSUSSVVYVPSSSLGTHQYICNVNHIKVSNTKVDKKVDPKSCDKTHTCPCPAPEL   | 239 |
| Qy | 239 | LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGEVHNAKTRPREE     | 298 |
| Db | 240 | LGGPSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVGEVHNAKTRPREE     | 299 |
| Qy | 299 | QYNSTYRVVSVLTVHLHDLWNLNGREYKCKVSNKALPAPIEKTISAKAGQPREPQVYITLPPS | 358 |
| Db | 300 | QYNSTYRVVSVLTVHLHDLWNLNGREYKCKVSNKALPAPIEKTISAKAGQPREPQVYITLPPS | 359 |
| Qy | 359 | RDELTKNQVSLTCLVKGFYPSDIAVENESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK    | 418 |
| Db | 360 | REEMTKNQVSLTCLVKGFYPSDIAVENESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK    | 419 |
| Qy | 419 | SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK                               | 451 |
| Db | 420 | SRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK                               | 452 |

RESULT 15  
US-09-726-258-71  
Sequence 71, Application US/09726258  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc., Hsei, Vanessa  
APPLICANT: Koumenis, Iphigenia  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
APPLICANT: Shahrokhi, Zahra  
APPLICANT: Zapata, Gerardo A.  
TITLE OF INVENTION: ANTIBODY FRAGMENT-POLYMER CONJUGATES AND  
TITLE OF INVENTION: HUMANIZED ANTI-IL-8 MONOCLONAL ANTIBODIES  
NUMBER OF SEQUENCES: 72  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/726,258  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/234,182  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/094003  
FILING DATE: 24-JUL-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: PI08584-1A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 71:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 452 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-09-726-258-71

Query Match 91.7%; Score 2211.5; DB 21; Length 452;  
Best Local Similarity 92.5%; Pred. No. 2.le-170;  
Matches 419; Conservative 9; Mismatches 22; Indels 3; Gaps 2;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLEWVSGISGGSTYY 60

```
Db :|||||
1 EYQLVQSGGLVQPGGLRLSCAAGSYFSSHYMHWRQAPCKGLEWVGYLDPSNGETTY 60
QY 61 ADSVKGRTTISRDNKNTLYLQNSLRAREDYVYCAK--HTGGGVWDPIDYWGOGTLVT 118
Db :|||||
61 NQKFKGRTTISRDNKNTLYLQNSLRAREDYVYCARGDYRYNGDNF-FDVWQOGTLVT 119
QY 119 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 178
Db :|||||
120 VSSASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVL 179
QY 179 QSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPEL 238
Db :|||||
180 QSSGLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPEL 239
QY 239 LGGPSVFPLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298
Db :|||||
240 LGGPSVFPLPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 299
QY 299 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358
Db :|||||
300 QYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 359
QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 418
Db :|||||
360 REEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDK 419
QY 419 SRWQOGNVFCSVMHEALHNHYTQKSLSLSPGK 451
Db :|||||
420 SRWQOGNVFCSVMHEALHNHYTQKSLSLSPGK 452
```

Search completed: October 9, 2002, 19:19:31  
Job time : 181.754 secs





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:11:10 ; Search time 59,8265 Seconds  
(without alignments)  
2085.589 Million cell updates/sec

Title: US-09-822-698A-26  
Perfect score: 2411  
Sequence: 1 QVQIVQSGGLVQPGGSLRL.....MHEALHNYTKSLSPGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1006125 seqs, 276659714 residues

Total number of hits satisfying chosen parameters: 1006125

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query No. | Score | Match | Length | DB ID                | Description       |
|------------|-----------|-------|-------|--------|----------------------|-------------------|
| 1          | 2270      | 94.2  | 449   | 5      | US-09-736-371-21     | Sequence 21, Appl |
| 2          | 2270      | 94.2  | 449   | 5      | US-09-736-371B-21    | Sequence 21, Appl |
| 3          | 2245      | 93.1  | 449   | 1      | PCT-US02-11853-12    | Sequence 12, Appl |
| 4          | 2245      | 93.1  | 468   | 1      | PCT-US02-11853-20    | Sequence 20, Appl |
| 5          | 2236.5    | 92.8  | 442   | 1      | PCT-US02-21323-12    | Sequence 12, Appl |
| 6          | 2236.5    | 92.8  | 442   | 1      | PCT-US02-21324-12    | Sequence 12, Appl |
| 7          | 2236.5    | 92.8  | 442   | 1      | PCT-US02-26321-12    | Sequence 12, Appl |
| 8          | 2229.5    | 92.5  | 477   | 5      | US-09-791-537-118979 | Sequence 118979,  |
| 9          | 2226.5    | 92.3  | 442   | 1      | PCT-US02-21323-21    | Sequence 21, Appl |
| 10         | 2226.5    | 92.3  | 442   | 1      | PCT-US02-21324-21    | Sequence 21, Appl |
| 11         | 2226.5    | 92.3  | 442   | 1      | PCT-US02-26321-16    | Sequence 16, Appl |
| 12         | 2224.5    | 92.3  | 499   | 6      | US-10-206-008-645    | Sequence 645, App |
| 13         | 2223.5    | 92.2  | 494   | 6      | US-10-206-008-636    | Sequence 636, App |
| 14         | 2216      | 91.9  | 582   | 6      | US-10-089-500-53     | Sequence 53, Appl |
| 15         | 2214.5    | 91.8  | 449   | 5      | US-09-304-465A-2     | Sequence 2, Appl  |
| 16         | 2214.5    | 91.8  | 449   | 5      | US-10-253-366-2      | Sequence 2, Appl  |
| 17         | 2209.5    | 91.6  | 473   | 5      | US-09-791-537-118977 | Sequence 118977,  |
| 18         | 2196      | 91.1  | 476   | 6      | US-10-206-008-599    | Sequence 599, App |
| 19         | 2189      | 90.8  | 470   | 6      | US-10-040-047-3730   | Sequence 3730, Ap |
| 20         | 2181      | 90.5  | 470   | 6      | US-10-020-786-9      | Sequence 9, Appl  |
| 21         | 2172.5    | 90.1  | 444   | 5      | US-09-674-716B-53    | Sequence 53, Appl |
| 22         | 2171      | 90.0  | 582   | 6      | US-10-089-500-57     | Sequence 57, Appl |
| 23         | 2170      | 90.0  | 476   | 6      | US-10-020-786-11     | Sequence 11, Appl |
| 24         | 2169      | 90.0  | 451   | 6      | US-10-113-996-14     | Sequence 14, Appl |
| 25         | 2169      | 90.0  | 451   | 6      | US-10-113-996-16     | Sequence 16, Appl |
| 26         | 2169      | 90.0  | 451   | 6      | US-10-019-586-2      | Sequence 2, Appl  |

|    |        |      |     |   |                      |                   |
|----|--------|------|-----|---|----------------------|-------------------|
| 27 | 2168   | 89.9 | 451 | 6 | US-10-113-996-18     | Sequence 18, Appl |
| 28 | 2162.5 | 89.7 | 467 | 5 | US-09-791-537-132460 | Sequence 132460,  |
| 29 | 2160   | 89.6 | 478 | 5 | US-09-758-173-8      | Sequence 8, Appl  |
| 30 | 2160   | 89.6 | 478 | 5 | US-09-526-098-8      | Sequence 8, Appl  |
| 31 | 2160   | 89.6 | 478 | 5 | US-09-948-429B-8     | Sequence 8, Appl  |
| 32 | 2160   | 89.6 | 478 | 5 | US-09-971-631-8      | Sequence 8, Appl  |
| 33 | 2160   | 89.6 | 478 | 6 | US-10-124-807-8      | Sequence 8, Appl  |
| 34 | 2160   | 89.6 | 478 | 6 | US-10-124-905-8      | Sequence 8, Appl  |
| 35 | 2160   | 89.6 | 478 | 6 | US-10-030-390-8      | Sequence 8, Appl  |
| 36 | 2158.5 | 89.5 | 455 | 5 | US-09-791-537-95084  | Sequence 95084, A |
| 37 | 2135.5 | 88.6 | 467 | 1 | PCT-US02-20181-2     | Sequence 2, Appl  |
| 38 | 2131   | 88.4 | 478 | 6 | US-10-104-047-3812   | Sequence 3812, Ap |
| 39 | 2115   | 87.7 | 430 | 6 | US-10-206-008-715    | Sequence 715, App |
| 40 | 2115   | 87.7 | 430 | 6 | US-10-211-364-1052   | Sequence 1052, Ap |
| 41 | 2113.5 | 87.7 | 469 | 5 | US-09-791-537-32261  | Sequence 32261, A |
| 42 | 2109.5 | 87.5 | 465 | 6 | US-10-031-355-5      | Sequence 5, Appl  |
| 43 | 2109.5 | 87.5 | 465 | 6 | US-10-031-355-12     | Sequence 12, Appl |
| 44 | 2106.5 | 87.4 | 448 | 1 | PCT-US01-27352-2     | Sequence 2, Appl  |
| 45 | 2102.5 | 87.2 | 489 | 6 | US-10-104-047-3329   | Sequence 3329, Ap |

ALIGNMENTS

RESULT 1

US-09-736-371-21  
; Sequence 21, Application US/09736371

; GENERAL INFORMATION:

; APPLICANT: Waldmann, Herman

; APPLICANT: Frewin, Mark

; TITLE OF INVENTION: AGLYCOSYLATED ANTIBODIES

; FILE REFERENCE: Waldmann

; CURRENT APPLICATION NUMBER: US/09/736,371

; CURRENT FILING DATE: 2002-04-25

; PRIOR APPLICATION NUMBER: 9815909.8

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: PCT/GB99/02380

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: Patentln Ver. 2.1

; SEQ ID NO 21

; LENGTH: 449

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-736-371-21

Query Match 94.2%; Score 2270; DB 5; Length 449;  
Best Local Similarity 94.9%; Pred. No. 2.2e-111;  
Matches 431; Conservative 5; Mismatches 10; Indels 8; Gaps 2;

QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVQAPKGLVWVSGISGGSTYY 60

Db 1 EVOLLESGGLVQPGGSLRLSCAASGFTFSFPMAVWVQAPKGLVWVSTISGGRTYY 60

QY 61 ADSVKGRFTISRDNSKNTLYIQMNSLRADETAVYYCAK---HTGGGVWDPIDYWGQGLV 117

Db 61 RDSVKGRFTISRDNSKNTLYIQMNSLRADETAVYYCAKFRQISGG-----FDWGGQGLV 115

QY 118 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVVDYFPEPVTVSNWSGALTSGVHTFPVAV 177

Db 116 TVSSASTKGPSVFPPLAPSKSTSGGTAALGCLVVDYFPEPVTVSNWSGALTSGVHTFPVAV 175

QY 178 LQSSGLYLSVVTVTPSSSLGQTIVICNVNHPKSNVTKVDKVEPKSCDKHTHTCPCPAPE 237

Db 176 LQSSGLYLSVVTVTPSSSLGQTIVICNVNHPKSNVTKVDKVEPKSCDKHTHTCPCPAPE 235

QY 238 LLGGPSVFLPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 297

Db 236 LLGGPSVFLPPKPKDMLISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPRE 295

QY 298 EQNSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVVTLPP 357

Db 296 EQYSTYRVVSVLTVLDHQLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPVVTLPP 355



PCT-US02-11853-20

Query Match 93.1%; Score 2245; DB 1; Length 468;  
Best Local Similarity 93.2%; Pred. No. 4.7e-110;  
Matches 422; Conservative 10; Mismatches 15; Indels 6; Gaps 2;

QY 1 QYQLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKLEWYSGISGSGSY 60  
DB 20 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKLEWYSGISGSGSY 79  
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAK--HTGGGVWDPIDYWGQGLTV 118  
DB 80 SDNVKGRFTISKNAKSLYLQMNLSRAEDTAVYYCVRYDHYSGS----SDYWGQGLTV 135  
QY 119 VSSASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 178  
DB 136 VSSASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 195  
QY 179 QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPEL 238  
DB 196 QSSGLYSLSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPEL 255  
QY 239 LGSPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 298  
DB 256 LGSPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 315  
QY 299 QYNTRYRVSVSLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 358  
DB 316 QYNTRYRVSVSLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPS 375  
QY 359 RDELTKNOVSLTCLVKGYFSPDIAVESNGQPNENYKTPPVLDSDGSFELYSLKLTVDK 418  
DB 376 RDELTKNOVSLTCLVKGYFSPDIAVESNGQPNENYKTPPVLDSDGSFELYSLKLTVDK 435  
QY 419 SRWQGNVFCSCVMHEALHNHYTKQSLSPGK 451  
DB 436 SRWQGNVFCSCVMHEALHNHYTKQSLSPGK 468

RESULT 5  
PCT-US02-21323-12  
; Sequence 12, Application PC/TUS0221323  
; GENERAL INFORMATION:  
; APPLICANT: Eli Lilly and Company  
; TITLE OF INVENTION: Rapid Improvement of Cognition in Conditions Related to A-beta  
; FILE REFERENCE: X-15240  
; CURRENT APPLICATION NUMBER: PCT/US02/21323  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: US 60/313,222  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: humanized antibody  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: humanized 266 antibody preferred heavy chain  
PCT-US02-21323-12

Query Match 92.8%; Score 2236.5; DB 1; Length 442;  
Best Local Similarity 93.8%; Pred. No. 1.2e-109;  
Matches 423; Conservative 7; Mismatches 12; Indels 9; Gaps 1;  
QY 1 QYQLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKLEWYSGISGSGSY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKLEWYSGISGSGSY 60

QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120  
DB 61 PDTVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCASG-----DYWGQGLTVTVS 111  
QY 121 SASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 180  
DB 112 SASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 171  
QY 181 SGLYSLSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPEL 240  
DB 172 SGLYSLSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPEL 231  
QY 241 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 300  
DB 232 GPSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 291  
QY 301 NSTRYRVSVSLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 360  
DB 292 NSTRYRVSVSLTVLHODWLNKGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRD 351  
QY 361 ELTKNOVSLTCLVKGYFSPDIAVESNGQPNENYKTPPVLDSDGSFELYSLKLTVDKSR 420  
DB 352 ELTKNOVSLTCLVKGYFSPDIAVESNGQPNENYKTPPVLDSDGSFELYSLKLTVDKSR 411  
QY 421 WQGNVFCSCVMHEALHNHYTKQSLSPGK 451  
DB 412 WQGNVFCSCVMHEALHNHYTKQSLSPGK 442

RESULT 6  
PCT-US02-21324-12  
; Sequence 12, Application PC/TUS0221324  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY  
; TITLE OF INVENTION: USE OF ANTIBODIES HAVING HIGH AFFINITY FOR SOLUBLE A-BETA  
; FILE REFERENCE: X-15047  
; CURRENT APPLICATION NUMBER: PCT/US02/21324  
; CURRENT FILING DATE: 2002-08-14  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/313,576  
; PRIOR FILING DATE: 2002-05-28  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: humanized antibody  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: Humanized antibody 266 preferred heavy chain variable  
PCT-US02-21324-12

Query Match 92.8%; Score 2236.5; DB 1; Length 442;  
Best Local Similarity 93.8%; Pred. No. 1.2e-109;  
Matches 423; Conservative 7; Mismatches 12; Indels 9; Gaps 1;  
QY 1 QYQLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKLEWYSGISGSGSY 60  
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKLEWYSGISGSGSY 60  
QY 61 ADSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCAKHTGGGVWDPIDYWGQGLTVTVS 120  
DB 61 PDTVKGRFTISRDNKNTLYLQMNLSRAEDTAVYYCASG-----DYWGQGLTVTVS 111  
QY 121 SASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 180  
DB 112 SASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVYSWNSGALTSGVHFFPAVL 171  
QY 181 SGLYSLSVVTVPSSSLGTQTYICNVNHPKNTKVDKKVEPKSCDKTHTCPPCPAPEL 240

Db 172 SGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPELLG 231  
Qy 241 GPSVFLFPKPKDKTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNKTKPREEQY 300  
Db 232 GPSVFLFPKPKDKTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNKTKPREEQY 291  
Qy 301 NSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPOVYITLPPSRD 360  
Db 292 NSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPOVYITLPPSRD 351  
Qy 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 420  
Db 352 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 411  
Qy 421 WOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451  
Db 412 WOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 442

RESULT 7  
PCT-US02-26321-12  
; Sequence 12, Application PC/TUS0226321  
; GENERAL INFORMATION:  
; APPLICANT: ELI LILLY AND COMPANY and WASHINGTON UNIVERSITY  
; TITLE OF INVENTION: ASSAY METHOD FOR ALZHEIMER'S DISEASE  
; FILE REFERENCE: 8792/292  
; CURRENT APPLICATION NUMBER: PCT/US02/26321  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: 60/334, 987  
; PRIOR FILING DATE: 2001-10-23  
; PRIOR APPLICATION NUMBER: 60/313, 221  
; PRIOR FILING DATE: 2001-08-17  
; PRIOR APPLICATION NUMBER: 60/313, 224  
; PRIOR FILING DATE: 2001-08-17  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 12  
; LENGTH: 442  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Humanized antibody  
; FEATURE:  
; NAME/KEY: MISC\_FEATURE  
; LOCATION: (1)..(442)  
; OTHER INFORMATION: HUMANIZED ANTIBODY HEAVY CHAIN  
PCT-US02-26321-12

Query Match 92.8%; Score 2236.5; DB 1; Length 442;  
Best Local Similarity 93.8%; Pred No. 1.2e-109;  
Matches 423; Conservative 7; Mismatches 12; Indels 9; Gaps 1;  
Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLEWVSGISGGSTYY 60  
Db 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSRYSMGWVROAPGKGLELVAQINSVGNSTYY 60  
Qy 61 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCAKHTGGVWDPDTPYWGQGLTVTVS 120  
Db 61 PDTVKGRTISRDNKNTLYLQNSLRADTAIVYCAASG-----DYWGQGLTVTVS 111  
Qy 121 SASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 180  
Db 112 SASTKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 171  
Qy 181 SGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPELLG 240  
Db 172 SGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKKVEPKSCDKTHTCPPCPAPELLG 231  
Qy 241 GPSVFLFPKPKDKTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNKTKPREEQY 300  
Db 232 GPSVFLFPKPKDKTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHNKTKPREEQY 291

Qy 301 NSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPOVYITLPPSRD 360  
Db 292 NSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPOVYITLPPSRD 351  
Qy 361 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 420  
Db 352 ELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSR 411  
Qy 421 WOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451  
Db 412 WOQGNVFSCSVMHEALHNHYTQKSLSLSPGK 442

RESULT 8  
US-09-791-537-118979  
; Sequence 118979, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 118979  
; LENGTH: 477  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-791-537-118979

Query Match 92.5%; Score 2229.5; DB 5; Length 477;  
Best Local Similarity 91.5%; Pred No. 3.1e-109;  
Matches 422; Conservative 10; Mismatches 16; Indels 13; Gaps 2;  
Qy 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVROAPGKGLEWVSGISGGSTYY 60  
Db 20 QVQLVESGGGVQVQGRSLRLSCAASGFTFSNYGMHWVROAPGKLEWVAALWYDGSNKYY 79  
Qy 61 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCAKHTGGVWDP-----IDY 110  
Db 80 ADSVKGRTISRDNKNTLYLQNSLRADTAIVYCARE---GRWVRYTITTTIGYIFDY 136  
Qy 111 WGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 170  
Db 137 WGQGLTVTVSSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSG 196  
Qy 171 VHTFPVQLQSGGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKKVEPKSCDKTHTC 230  
Db 197 VHTFPVQLQSGGLYSLSSVVTVPSSSLGTQTYICNVNHPKSNKTKVDKRVKPKSCDKTHTC 256  
Qy 231 PPCPAPELLGGPSVFLPDKPKDTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHN 290  
Db 257 PPCPAPELLGGPSVFLPDKPKDTLMISRTPEVTCVVVDVSHEDPEVFNNYVDGVEVHN 316  
Qy 291 AKTPREQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREP 350  
Db 317 AKTPREQYNSTYRVVSVLTVLHQDWLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREP 376  
Qy 351 QVYTLTPSRDELTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFL 410  
Db 377 QVYTLTPSRDEMTKNQVSLTCLVKGYFPPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFL 436  
Qy 411 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 451  
Db 437 YSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 477

RESULT 9  
PCT-US02-21323-21  
; Sequence 21, Application PC/TUS0221323

```

: GENERAL INFORMATION:
: APPLICANT: Eli Lilly and Company
: TITLE OF INVENTION: Rapid Improvement of Cognition in Conditions Related to A-beta
: FILE REFERENCE: X-15240
: CURRENT APPLICATION NUMBER: PCT/US02/21323
: PRIORITY FILING DATE: 2002-08-14
: PRIOR APPLICATION NUMBER: US 60/313,222
: PRIOR FILING DATE: 2001-08-17
: PRIOR APPLICATION NUMBER: US 60/383,846
: PRIOR FILING DATE: 2002-05-28
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 21
: LENGTH: 442
: TYPE: PRT
: ORGANISM: artificial sequence
: FEATURE:
: OTHER INFORMATION: humanized antibody
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (1)..(442)
: OTHER INFORMATION: heavy chain antibody
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (57)..(57)
: OTHER INFORMATION: Xaa at position 57 is any amino acid, provided that if Xaa at position 57 is Ser or Thr, then Xaa at position 58 is Ser or Thr, then Xaa at position 59 is Ser or Thr, then Xaa at position 56 is not Asn
: OTHER INFORMATION: position 57 is Asp or Pro
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (56)..(56)
: OTHER INFORMATION: Xaa at position 56 is any amino acid, provided that if Xaa at position 56 is Ser or Thr, then Xaa at position 57 is Ser or Thr, then Xaa at position 58 is Ser or Thr, then Xaa at position 59 is Ser or Thr, then Xaa at position 56 is not Asn
: OTHER INFORMATION: Thr, then Xaa at position 56 is not Asn
: FEATURE:
: NAME/KEY: MISC_FEATURE
: LOCATION: (58)..(58)
: OTHER INFORMATION: Xaa at position 58 is any amino acid, provided that if Xaa at position 58 is Ser or Thr, then Xaa at position 59 is Ser or Thr, then Xaa at position 56 is not Asn
: OTHER INFORMATION: Thr, then Xaa at position 56 is not Asn
: OTHER INFORMATION: en Xaa at position 58 is neither Ser nor Thr
: PCT-US02-21323-21

```

QY 421 WOQGNFSCSVMEALHNHYTKLSLSPGK 451  
 Db 412 WOQGNFSCSVMEALHNHYTKLSLSPGK 442

RESULT 10  
 PCT-US02-21324-21  
 : Sequence 21, Application PC/TUS02211324  
 : GENERAL INFORMATION:  
 : APPLICANT: ELI LILLY AND COMPANY  
 : TITLE OF INVENTION: USE OF ANTIBODIES HAVING HIGH AFFINITY FOR SOLUBLE A-BETA TO T  
 : TITLE OF INVENTION: CONDITIONS AND DISEASES RELATED TO A-BETA  
 : FILE REFERENCE: X-15047  
 : CURRENT APPLICATION NUMBER: PCT/US02/21324  
 : CURRENT FILING DATE: 2002-08-14  
 : PRIOR APPLICATION NUMBER: 60/313,576  
 : PRIOR FILING DATE: 2001-08-17  
 : PRIOR APPLICATION NUMBER: 60/383,581  
 : PRIOR FILING DATE: 2002-05-28  
 : NUMBER OF SEQ ID NOS: 21  
 : SOFTWARE: PatentIn version 3.1  
 : SEQ ID NO 21  
 : LENGTH: 442  
 : TYPE: PRT  
 : ORGANISM: humanized antibody  
 : FEATURE:  
 : NAME/KEY: MISC\_FEATURE  
 : LOCATION: (36)..(56)  
 : OTHER INFORMATION: Xaa at position 56 is any amino acid provided that if Xaa at p  
 : OTHER INFORMATION: tion 57 is neither Asp nor Pro and Xaa at position 59 is Ser o  
 : OTHER INFORMATION: hr, then Xaa at position 56 is not Asn  
 : FEATURE:  
 : NAME/KEY: MISC\_FEATURE  
 : LOCATION: (1)..(442)  
 : OTHER INFORMATION: heavy chain antibody  
 : FEATURE:  
 : NAME/KEY: MISC\_FEATURE  
 : LOCATION: (57)..(57)  
 : OTHER INFORMATION: Xaa at position 57 is any amino acid, provided that if Xaa at  
 : OTHER INFORMATION: tion 56 is Asn and Xaa at position 58 is Ser or Thr, then Xaa  
 : OTHER INFORMATION: position 57 is Asp or Pro  
 : FEATURE:  
 : NAME/KEY: MISC\_FEATURE  
 : LOCATION: (58)..(58)  
 : OTHER INFORMATION: Xaa at position 58 is any amino acid, provided that if Xaa at  
 : OTHER INFORMATION: tion 56 is Asn and Xaa at position 57 is neither Asp nor Pro,  
 : OTHER INFORMATION: en Xaa at position 58 is neither Ser nor Thr  
 : PCT-US02-21324-21

```

QY 301 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRD 360
DB 292 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRD 351
QY 361 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 420
DB 352 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 411
QY 421 WQGNVFCSCVMHEALHNNHYTKQSLSPGK 451
DB 412 WQGNVFCSCVMHEALHNNHYTKQSLSPGK 442

RESULT 11
PCT-US02-26321-16
; Sequence 16, Application PC/TUS0226321
; GENERAL INFORMATION:
; APPLICANT: ELI LILLY AND COMPANY AND WASHINGTON UNIVERSITY
; TITLE OF INVENTION: ASSAY METHOD FOR ALZHEIMER'S DISEASE
; FILE REFERENCE: 8792/292
; CURRENT APPLICATION NUMBER: PCT/US02/26321
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: 60/334,987
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/313,221
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/313,224
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized Antibody
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(442)
; OTHER INFORMATION: Humanized Antibody Heavy Chain
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (56)..(56)
; OTHER INFORMATION: Xaa at position 56 is any amino acid, provided that Xaa at position 57 is Ser or Thr
; OTHER INFORMATION: on 57 is neither Asp nor Pro and Xaa at position 59 is Ser or Thr
; OTHER INFORMATION: , then Xaa at position 56 is not Asn
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (57)..(57)
; OTHER INFORMATION: Xaa at position 57 is any amino acid, provided that Xaa at position 58 is Ser or Thr, then Xaa at position 59 is Ser or Thr
; OTHER INFORMATION: position 57 is Asp or Pro
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (58)..(58)
; OTHER INFORMATION: Xaa at position 58 is any amino acid, provided that Xaa at position 59 is Ser or Thr
; OTHER INFORMATION: then Xaa at position 58 is neither Ser nor Thr
PCT-US02-26321-16

Query Match 92.3%; Score 2226.5; DB 1; Length 442;
Best Local Similarity 93.3%; Pred. No. 4.2e-109;
Matches 421; Conservative 7; Mismatches 14; Indels 9; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGSGSVY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLVWVSGISGSGSVY 60
QY 61 ADSVKGRTISDKNLTLLQMNLSRAEDTAVYCAKHTGGVWDPIYWGQGLTVTS 120
DB 61 PDTVKGRTISDKNLTLLQMNLSRAEDTAVYCAKHTGGVWDPIYWGQGLTVTS 111

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QY 121 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLAS 180
DB 112 SASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLAS 171
QY 181 SGLYSLSVVVPSSSLGTQYICNVNHNKPSNTKYDKKVEPKSCDKTHHTCCPCPAPPELLG 240
DB 172 SGLYSLSVVVPSSSLGTQYICNVNHNKPSNTKYDKKVEPKSCDKTHHTCCPCPAPPELLG 231
QY 241 GPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENYVDGVEVHNAKTKPREEQY 300
DB 232 GPSVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKENYVDGVEVHNAKTKPREEQY 291
QY 301 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRD 360
DB 292 NSTYRVSVLTVLHODWLNKGYKCKVSNKALPAPIEKTISKAKGPREPQVYTLPPSRD 351
QY 361 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 420
DB 352 ELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSR 411
QY 421 WQGNVFCSCVMHEALHNNHYTKQSLSPGK 451
DB 412 WQGNVFCSCVMHEALHNNHYTKQSLSPGK 442

RESULT 12
US-10-206-008-645
; Sequence 645, Application US/10206008
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PTZ53C1N
; CURRENT APPLICATION NUMBER: US/10/206,008
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 09/760,479
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/225,757
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/226,868
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/216,647
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,267
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/216,880
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/225,270
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/251,869
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/235,834
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/234,274
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: 60/234,223

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| 2  | PRIOR APPLICATION NUMBER: 60/249,210 |
| 3  | PRIOR FILING DATE: 2000-11-17        |
| 4  | PRIOR APPLICATION NUMBER: 60/226,681 |
| 5  | PRIOR FILING DATE: 2000-08-22        |
| 6  | PRIOR APPLICATION NUMBER: 60/225,759 |
| 7  | PRIOR FILING DATE: 2000-08-14        |
| 8  | PRIOR APPLICATION NUMBER: 60/225,213 |
| 9  | PRIOR FILING DATE: 2000-08-14        |
| 10 | PRIOR APPLICATION NUMBER: 60/227,182 |
| 11 | PRIOR FILING DATE: 2000-08-22        |
| 12 | PRIOR APPLICATION NUMBER: 60/225,214 |
| 13 | PRIOR FILING DATE: 2000-08-14        |
| 14 | PRIOR APPLICATION NUMBER: 60/225,836 |
| 15 | PRIOR FILING DATE: 2000-09-27        |
| 16 | PRIOR APPLICATION NUMBER: 60/230,438 |
| 17 | PRIOR FILING DATE: 2000-09-06        |
| 18 | PRIOR APPLICATION NUMBER: 60/215,135 |
| 19 | PRIOR FILING DATE: 2000-06-30        |
| 20 | PRIOR APPLICATION NUMBER: 60/225,266 |
| 21 | PRIOR FILING DATE: 2000-08-14        |
| 22 | PRIOR APPLICATION NUMBER: 60/249,218 |
| 23 | PRIOR FILING DATE: 2000-11-17        |
| 24 | PRIOR APPLICATION NUMBER: 60/249,208 |
| 25 | PRIOR FILING DATE: 2000-11-17        |
| 26 | PRIOR APPLICATION NUMBER: 60/249,213 |
| 27 | PRIOR FILING DATE: 2000-11-17        |
| 28 | PRIOR APPLICATION NUMBER: 60/249,212 |
| 29 | PRIOR FILING DATE: 2000-11-17        |
| 30 | PRIOR APPLICATION NUMBER: 60/249,207 |
| 31 | PRIOR FILING DATE: 2000-11-17        |
| 32 | PRIOR APPLICATION NUMBER: 60/249,245 |
| 33 | PRIOR FILING DATE: 2000-11-17        |
| 34 | PRIOR APPLICATION NUMBER: 60/249,244 |
| 35 | PRIOR FILING DATE: 2000-11-17        |
| 36 | PRIOR APPLICATION NUMBER: 60/249,217 |
| 37 | PRIOR FILING DATE: 2000-11-17        |
| 38 | PRIOR APPLICATION NUMBER: 60/249,211 |
| 39 | PRIOR FILING DATE: 2000-11-17        |
| 40 | PRIOR APPLICATION NUMBER: 60/249,215 |
| 41 | PRIOR FILING DATE: 2000-11-17        |
| 42 | PRIOR APPLICATION NUMBER: 60/249,264 |
| 43 | PRIOR FILING DATE: 2000-11-17        |
| 44 | PRIOR APPLICATION NUMBER: 60/249,214 |
| 45 | PRIOR FILING DATE: 2000-11-17        |
| 46 | PRIOR APPLICATION NUMBER: 60/249,297 |
| 47 | PRIOR FILING DATE: 2000-11-17        |
| 48 | PRIOR APPLICATION NUMBER: 60/232,400 |
| 49 | PRIOR FILING DATE: 2000-09-14        |
| 50 | PRIOR APPLICATION NUMBER: 60/231,242 |
| 51 | PRIOR FILING DATE: 2000-09-08        |
| 52 | PRIOR APPLICATION NUMBER: 60/232,081 |
| 53 | PRIOR FILING DATE: 2000-09-08        |
| 54 | PRIOR APPLICATION NUMBER: 60/232,080 |
| 55 | PRIOR FILING DATE: 2000-09-08        |
| 56 | PRIOR APPLICATION NUMBER: 60/231,414 |
| 57 | PRIOR FILING DATE: 2000-09-08        |
| 58 | PRIOR APPLICATION NUMBER: 60/231,244 |
| 59 | PRIOR FILING DATE: 2000-09-08        |
| 60 | PRIOR APPLICATION NUMBER: 60/233,064 |
| 61 | PRIOR FILING DATE: 2000-09-14        |
| 62 | PRIOR APPLICATION NUMBER: 60/233,063 |
| 63 | PRIOR FILING DATE: 2000-09-14        |
| 64 | PRIOR APPLICATION NUMBER: 60/232,397 |
| 65 | PRIOR FILING DATE: 2000-09-14        |
| 66 | PRIOR APPLICATION NUMBER: 60/232,399 |
| 67 | PRIOR FILING DATE: 2000-09-14        |
| 68 | PRIOR APPLICATION NUMBER: 60/232,401 |
| 69 | PRIOR FILING DATE: 2000-09-14        |
| 70 | PRIOR APPLICATION NUMBER: 60/241,808 |
| 71 | PRIOR FILING DATE: 2000-10-20        |
| 72 | PRIOR APPLICATION NUMBER: 60/241,826 |
| 73 | PRIOR FILING DATE: 2000-10-20        |
| 74 | PRIOR APPLICATION NUMBER: 60/241,786 |





; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/236,802  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,037  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/237,040  
; PRIOR FILING DATE: 2000-10-02  
; PRIOR APPLICATION NUMBER: 60/240,960  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/239,935  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/239,937  
; PRIOR FILING DATE: 2000-10-13  
; PRIOR APPLICATION NUMBER: 60/241,787  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,474  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/246,532  
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; PRIOR APPLICATION NUMBER: 60/249,216  
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; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/226,681  
; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,759  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/225,213  
; PRIOR FILING DATE: 2000-08-14  
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; PRIOR FILING DATE: 2000-08-22  
; PRIOR APPLICATION NUMBER: 60/225,214  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/235,836  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: 60/230,438  
; PRIOR FILING DATE: 2000-09-06  
; PRIOR APPLICATION NUMBER: 60/215,135  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: 60/225,266  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/249,218  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,208  
; PRIOR FILING DATE: 2000-11-17  
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; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,212  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,207  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,245  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,244  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,217  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,211  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,215  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,264  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,214  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/249,297  
; PRIOR FILING DATE: 2000-11-17  
; PRIOR APPLICATION NUMBER: 60/232,400  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/231,242  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/232,081  
; PRIOR FILING DATE: 2000-09-08

; PRIOR APPLICATION NUMBER: 60/232,080  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,414  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/231,244  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,064  
; PRIOR FILING DATE: 2000-09-14  
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; PRIOR FILING DATE: 2000-09-14  
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; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,399  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/232,401  
; PRIOR FILING DATE: 2000-09-14  
; PRIOR APPLICATION NUMBER: 60/241,808  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,826  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,786  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,221  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/246,475  
; PRIOR FILING DATE: 2000-11-08  
; PRIOR APPLICATION NUMBER: 60/231,243  
; PRIOR FILING DATE: 2000-09-08  
; PRIOR APPLICATION NUMBER: 60/233,065

Query Match 92.2%; Score 2223.5; DB 6; Length 494;  
Best Local Similarity 93.0%; Pred No. 6.6e-109;  
Matches 422; Conservative 9; Mismatches 20; Indels 3; Gaps 2;

Qy 1 QVQLVQSGGGLVPGGSLRLSCAASGFTFRSNAMGVHVRQAPGKGLWVSGISGGSGTYY 60  
Db 41 EVQLVESGGGLVPGGSLRLSCAAAEFAFENYMMHWVRQAPGKGLWVSHLNSDGSSTRY 100  
Qy 61 ADSVKGRFTISRDNKNTLYLQMSLRAREDATVYYCAK--HTGGGVDP--IDYWGQGLV 117  
Db 101 ADSVKGRFTISRDNKNTLYLQMSLRVEDTAVYYCARGVKGTGSSWFSDFDYWGQGLV 160  
Qy 118 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 177  
Db 161 TVSSASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAV 220  
Qy 178 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRPSNTKYDKVEPKSCDKTHTCPCPAPE 237  
Db 221 LQSSGLYSLSSVTVTPSSSLGTQTYICNVNHRPSNTKYDKVEPKSCDKTHTCPCPAPE 280  
Qy 238 LLGGPSVFLPPPKDFTLMSRTPETVTVVVDVSHEDPEVKFNWYVDGVVEVHNAKTKPRE 297  
Db 281 LLGGPSVFLPPPKDFTLMSRTPETVTVVVDVSHEDPEVKFNWYVDGVVEVHNAKTKPRE 340  
Qy 298 EQYNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAAPLIEKTIISKAKGPQPVYTLPP 357  
Db 341 EQYNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKAAPLIEKTIISKAKGPQPVYTLPP 400  
Qy 358 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLIVD 417  
Db 401 SRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLIVD 460  
Qy 418 KSRWQQGNVFCSCVYHEALHNHYTQKSLSLSPGK 451  
Db 461 KSRWQQGNVFCSCVYHEALHNHYTQKSLSLSPGK 494

## RESULT 14

US-10-089-500-53

; Sequence 53, Application US/10089500

; GENERAL INFORMATION:

; APPLICANT: KYOWA HAKKO KOGYO CO., LTD

; TITLE OF INVENTION: Humanized anti-GD3 antibody and it's cytokine conjugate

```

; FILE REFERENCE: 11239W01
; CURRENT APPLICATION NUMBER: US/10/089,500
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: H11-278291
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 53
; LENGTH: 582
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic protein
US-10-089-500-53

Query Match 91.9%; Score 2216; DB 6; Length 582;
Best Local Similarity 92.7%; Pred. No. 1.9e-108;
Matches 418; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGSGSTYY 60
DB 1 EVQLVESGGDGVQPGGSLRVSCAASGFAFASHYAMSVRQAPGKGLWVAYISSGSGSTYY 60
QY 61 ADSVKGRFTISRDNKNTLYIQMNSLRRAEDTAVYYCAKHTGGVWDPIDYWGQGTLLTVS 120
DB 61 SDSVKGRFTISRDNKNTLYIQMNSLRRAEDSAVYFCTRVKLGTY--FDSWGQGTLLTVS 118
QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180
DB 119 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 178
QY 181 SGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
DB 179 SGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 238
QY 241 GPSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 300
DB 239 GPSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 298
QY 301 NSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 360
DB 299 NSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 358
QY 361 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDK 420
DB 359 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDK 418
QY 421 WQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 451
DB 419 WQOGNVFSCSVNHEALHNHYTQKSLSLSPGK 449

RESULT 15
US-09-304-465A-2
; Sequence 2, Application US/09304465A
; GENERAL INFORMATION:
; APPLICANT: BASEY, CAROL D.
; TITLE OF INVENTION: PROTEIN PURIFICATION
; FILE REFERENCE: P1241R1
; CURRENT APPLICATION NUMBER: US/09/304,465A
; CURRENT FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/084,459
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
US-09-304-465A-2

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Query Match 91.8%; Score 2214.5; DB 5; Length 449;
Best Local Similarity 92.7%; Pred. No. 1.8e-108;
Matches 417; Conservative 12; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKGLWVSGISGSGSTYY 60
DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFNIKDTYIHWVRQAPGKGLWVARIYPTNGYTRY 60
QY 61 ADSVKGRFTISRDNKNTLYIQMNSLRRAEDTAVYYCAKHTGGVWDPIDYWGQGTLLTVS 120
DB 61 ADSVKGRFTISRDNKNTLYIQMNSLRRAEDTAVYYCSRWGDGFY-AMDYWGQGTLLTVS 119
QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 180
DB 120 SASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 179
QY 181 SGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 240
DB 180 SGLYSLSVTVTPSSSLGTQTYICNVNHPKPSNTKVDKVEPKSCDKTHTCPPCPAPEL 239
QY 241 GPSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 300
DB 240 GPSVFLFPPPKPDKTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQ 299
QY 301 NSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 360
DB 300 NSTYRVSVSLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSR 359
QY 361 ELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDK 420
DB 360 EMTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDK 419
QY 421 WQOGNVFSCSVNHEALHNHYTQKSLSLSPG 450
DB 420 WQOGNVFSCSVNHEALHNHYTQKSLSLSPG 449

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Search completed: October 9, 2002, 19:21:24  
Job time : 60.8265 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:07:45 ; Search time 24.1607 Seconds  
(without alignments)  
1793.668 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 QVQLVQSGGGLVPGGSLRL.....MHEALHNHYTQKSLSLSPGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR-71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | DB ID    | Description         |
|------------|--------|-------------|--------|----------|---------------------|
| 1          | 1767   | 73.3        | 330    | 1 GHU    | Ig gamma-1 chain C  |
| 2          | 1630.5 | 67.6        | 377    | 2 A23511 | Ig gamma-3 chain C  |
| 3          | 1628.5 | 67.5        | 377    | 2 A60764 | Ig gamma-3 chain C  |
| 4          | 1604   | 66.5        | 326    | 1 G2HU   | Ig gamma-2 chain C  |
| 5          | 1590.5 | 66.0        | 327    | 1 G4HU   | Ig gamma-4 chain C  |
| 6          | 1513   | 62.8        | 470    | 2 G22080 | Ig heavy chain pre  |
| 7          | 1499.5 | 62.2        | 444    | 2 FC4436 | monoclonal antibody |
| 8          | 1451.5 | 60.2        | 469    | 2 S37483 | Ig gamma-2a chain   |
| 9          | 1435   | 59.5        | 446    | 2 S40295 | Ig gamma-2a chain   |
| 10         | 1433   | 59.4        | 374    | 2 S69339 | Ig heavy chain V r  |
| 11         | 1430   | 59.3        | 472    | 2 S31459 | Ig gamma-1 chain -  |
| 12         | 1382   | 57.3        | 474    | 1 G2MS11 | Ig gamma-2b chain   |
| 13         | 1376.5 | 57.1        | 475    | 2 S01321 | Ig gamma-2b chain   |
| 14         | 1263   | 52.4        | 328    | 2 I47159 | Ig gamma-2a chain   |
| 15         | 1260   | 52.3        | 255    | 4 S31866 | Ig gamma-1 chain C  |
| 16         | 1257   | 52.1        | 328    | 2 I47160 | Ig gamma-2b chain   |
| 17         | 1254   | 52.0        | 234    | 2 PT0207 | Ig gamma chain C r  |
| 18         | 1231   | 51.1        | 328    | 2 I47158 | Ig gamma-1 chain C  |
| 19         | 1230.5 | 51.0        | 323    | 1 GHRB   | Ig gamma chain C r  |
| 20         | 1227   | 50.9        | 328    | 2 I47161 | Ig gamma-3 chain C  |
| 21         | 1216.5 | 50.5        | 329    | 1 G2GP   | Ig gamma-2 chain C  |
| 22         | 1161.5 | 48.2        | 308    | 2 C30554 | Ig heavy chain C r  |
| 23         | 1152   | 47.8        | 326    | 2 FS0017 | Ig gamma-1 chain C  |
| 24         | 1151   | 47.7        | 289    | 1 G3HUI  | Ig gamma-1 chain c  |
| 25         | 1146.5 | 47.6        | 333    | 2 FS0018 | Ig gamma-2b chain   |
| 26         | 1142   | 47.4        | 324    | 1 G1MS   | Ig gamma-1 chain C  |
| 27         | 1141   | 47.3        | 329    | 1 G3MSC  | Ig gamma-3 chain C  |
| 28         | 1137   | 47.2        | 393    | 1 G1MSM  | Ig gamma-1 chain C  |
| 29         | 1130   | 46.9        | 398    | 1 G3MSM  | Ig gamma-3 chain C  |

#### ALIGNMENTS

##### RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence\_revision 18-Aug-1982 #text\_change 16-Jul-1999

C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A:Reference number: A93433; MUID:82274238

A:Accession: A93433

A:Molecule type: DNA

A:Residues: 1-330 <ELL>

A:Cross-references: EMBL:Z17370

A:Note: This sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) marker

A:Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A:Reference number: S33904

A:Accession: S36861

A:Molecule type: DNA

A:Residues: 2-330 <HAR>

A:Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of

A:Reference number: S33887; MUID:83001943

A:Accession: S33887

A:Molecule type: DNA

A:Residues: 88-113/235-330 <TAK>

A:Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman

Biochemistry 9, 3161-3170, 1970

A:Title: The covalent structure of a human gammagamma-immunoglobulin. VII. Amino acid seq

A:Reference number: A90563; MUID:71064024

A:Contents: myeloma protein Eu

A:Accession: B90563

A:Molecule type: protein

A:Residues: 1-96, 'R', 98-135 <CUN>

A:Note: this sequence has the G1m(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A:Title: The covalent structure of a human gammagamma-immunoglobulin. VIII. Amino acid se

A:Reference number: A90564; MUID:71064025

A:Contents: Eu

A:Accession: A90564

A:Molecule type: protein

A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 2

A:Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R:Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Ni



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Query Match 67.5%; Score 1628.5; DB 2; Length 377;
Best Local Similarity 82.0%; Pred. No. 1.5e-86;
Matches 309; Conservative 10; Mismatches 11; Indels 47; Gaps 1;

QY 122 ASTKGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 181
DQ 1 ASTKGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 182 GLYSLSVVTVPPSSSLGTFYICNVNKPSTNTKVDKKV----- 219
DQ 61 GLYSLSVVTVPPSSSLGTFYICNVNKPSTNTKVDKRLKPLGDTHTPCRPCKSC 120

QY 220 -----BPKSDKTHTCPPCPAPPELLGGPSVFLFPPPKPDT 254
DQ 121 DTPPC 180

QY 255 LMSIRTPVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLT 314
DQ 181 LMSIRTPVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYNSTYRVVSVLT 240

QY 315 QDWLNGKEYKCKVKNKALPAPIEKTIKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVK 374
DQ 241 QDWLNGKEYKCKVKNKALPAPIEKTIKAKGQPREPQVYTLPPSRDELTKNOVSLTCLVK 300

QY 375 GFYPDSIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC 434
DQ 301 GFYPDSIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFC 360

QY 435 ALHNHYTQKSLSLSPGK 451
DQ 361 ALHNRYTQKSLSLSPGK 377

RESULT 4
G4HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence-revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:J00230; MID:g32759; PIDN:CAB58438.1; PID:g6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and s
A:Reference number: A92809; MUID:81007873
A:Accession: A92809
A:Contents: myeloma protein T11
A:Molecule type: protein
A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357
A:Accession: A90752
A:Contents: myeloma protein Zie
A:Molecule type: protein
A:Residues: 1-24,'E',26-57,'EV',60-85;132-171,'222',175,'B',177-193,'D',195-196,'Q',198-
A:Note: This sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A:Reference number: A93132; MUID:80114419
A:Accession: A93132

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A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amid
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:133-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: Interchain (to light chain) #status experimental
F:27-83,140-200,245-304/Disulfide bonds: #status experimental
F:102,103,106,109/Disulfide bonds: Interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.5%; Score 1604; DB 1; Length 326;
Best Local Similarity 91.2%; Pred. No. 3.3e-85;
Matches 301; Conservative 12; Mismatches 13; Indels 4; Gaps 2;

QY 122 ASTKGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 181
DQ 1 ASTKGPSVFPLAPSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 182 GLYSLSVVTVPPSSSLGTFYICNVNKPSTNTKVDKSRWQQGNVFCSEYV 241
DQ 61 GLYSLSVVTVPPSSSLGTFYICNVNKPSTNTKVDKSRWQQGNVFCSEYV 116

QY 242 PSVFLFPPKPKDFTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 301
DQ 117 PSVFLFPPKPKDFTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 176

QY 302 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 361
DQ 177 STYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIKAKGQPREPQVYTLPPSRDE 236

QY 362 LTKNOVSLTCLVKGYPDSIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 421
DQ 237 LTKNOVSLTCLVKGYPDSIAVWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRW 296

QY 422 QCGNVFSCSVMEALHNHYTQKSLSLSPGK 451
DQ 297 QCGNVFSCSVMEALHNHYTQKSLSLSPGK 326

RESULT 5
G4HU
Ig gamma-4 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 02-Apr-1982 #sequence-revision 02-Apr-1982 #text_change 16-Jul-1999
C:Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A:Reference number: A90933; MUID:83157104

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A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <EL>

A:Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A:Reference number: A30249; MUID:70207560

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30; 81-326 <PIN>

C:Genetics:

A:Gene: IGH4

A:Cross-references: GDB:119340; OMTM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 95/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,141-201,247-305/Disulfide bonds: #status predicted

F:105,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 66.0%; Score 1590.5; DB 1; Length 327;

Best Local Similarity 90.9%; Pred. No. 2e-84;

Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;

QY 122 ASKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNNGALSTGVTTPAVLQSS 181

Db 1 ASKGPSVFLPAPSSKSTSGGTAALGCLVKDYFPEPTVSNNGALSTGVTTPAVLQSS 60

QY 182 GLYSLSVTVVPSVSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPELGG 241

Db 61 GLYSLSVTVVPSVSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPELGG 117

QY 242 PSVFLPAPSKPDLMISRTPEVTCVVDVSHEDPEVDFNMFVDCGVEVHNNAKTPREEQYN 301

Db 118 PSVFLPAPSKPDLMISRTPEVTCVVDVSHEDPEVDFNMFVDCGVEVHNNAKTPREEQYN 177

QY 302 STYRVSVTLVHQDLNKGKCKVSNKALPAPIETKISKAKQPREQVYTLPPSRDE 361

Db 178 STYRVSVTLVHQDLNKGKCKVSNKALPAPIETKISKAKQPREQVYTLPPSRDE 237

QY 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 421

Db 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFPLYSKLTVDKSRW 297

QY 422 QGNVFSCSVMEALHNHYTQKSLSLSPGK 451

Db 298 QGNVFSCSVMEALHNHYTQKSLSLSPGK 327

RESULT 6

S22080

Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine

N:Alternate names: Ig gamma-1 chain C region (clone 8.10)

C:Species: Bos primigenius taurus (cattle)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 23-Jul-1999

A:Accession: S22080; S06610; A31303

R:Sanders, P. G.

submitted to the EMBL Data Library, November 1991

A:Reference number: S22080

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-470 <SAN>

A:Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440

R:Symons, D.B.A.; Clarkson, C.A.; Beale, D.

Mol. Immunol. 26, 841-850, 1989

A:Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and g

A:Reference number: S06610; MUID:90097956

A:Accession: S06610

A:Molecule type: DNA

A:Residues: 142-470 <SYM>

A:Cross-references: EMBL:X16701

A:Note: the sequence was determined from the germline gene

C:Genetics:

A:Gene: Ig CH gamma-1

A:Introns: 98/1; 111/1; 221/1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein

F:161-225/Domain: immunoglobulin homology <IMM>

F:318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 62.8%; Score 1513; DB 2; Length 470;

Best Local Similarity 64.2%; Pred. No. 8.3e-80;

Matches 292; Conservative 55; Mismatches 100; Indels 8; Gaps 6;

QY 1 QVQLVQSGGGLVOPGGSLRLSCAASGFTFRSNAMGVRAQAPGKLEWVSGISGGSTYY 60

Db 20 QVQLRESGSLVKPSQTLTCTVSGFSLSYALTFWRAQAPGKLEWVGIT-SGGTTY 78

QY 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHTGGVMDP--IDYMGQGTLYT 118

Db 79 NPALKSRLSITKENSQVSLSVSSVTPEDTATYYCARSTYGEVGDGAIADAWGGLVLT 138

QY 119 VSSASTKGFSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNNGALSTGVTTPAVL 178

Db 139 VSSASTAPKVPYPLSCCCKSSSTVTLGCLVSSYMPFVTVVNSGALKSGVHTFPVL 198

QY 179 QSSGLYSLSSVTVVPSVSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPEL 238

Db 199 QSSGLYSLSSVTVVPSVSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPEL 255

QY 239 LGSPSVFLPAPSKPDLMISRTPEVTCVVDVSHEDPEVDFNMFVDCGVEVHNNAKTPREE 298

Db 256 PGGSPVFIFFPKPKDPLTISGTPPEVTCVVDVSHEDPEVDFNMFVDCGVEVHNNAKTPREE 315

QY 299 QYNSTYRVSVLTVLHQDLNKGKCKVSNKALPAPIETKISKAKQPREQVYTLPPS 358

Db 316 QFNSTYRVSVLTVLHQDLNKGKCKVSNKALPAPIETKISKAKQPREQVYTLPPS 375

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP--ENNYKTPPVLDSDGSFPLYSKLT 416

Db 376 QEELSKSTVSLTCLVKGFYPSDIAVEWESNGQPESDKYITPPOLDADSDSIFLYSKLRV 435

QY 417 DKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 451

Db 436 DRNSWQSGDYYTCVMHEALHNHYTQKSLSKSAK 470

RESULT 7

PC4436

monoclonal antibody 13-1 heavy chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 04-Feb-1998 #sequence\_revision 13-Mar-1998 #text\_change 21-Jan-2000

R:Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada,

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porp

A:Reference number: JC5810; MUID:98063277

A:Accession: PC4436

A:Molecule type: protein

A:Residues: 1-444 <AKA>

C:Comment: This catalytic antibody has peroxidase oxidase activity. It is directed ag

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:251-320/Domain: immunoglobulin homology <IMM>

F:22/Disulfide bonds: interchain (to 98) #status predicted

F:99/Disulfide bonds: interchain (to 109) #status predicted









R;Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.  
Nature 283, 786-789, 1980  
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from r  
A:Reference number: A02157; MUID:80120716  
A:Contents: a allele  
A:Accession: A02157  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>  
A:Cross-references: GB:J00461  
A:Note: the sequence was determined from the germline gene  
R;Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.  
Science 206, 1299-1303, 1979  
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b hea  
A:Reference number: A26235; MUID:80081501  
A:Contents: MPC 11  
A:Accession: A26235  
A:Molecule type: mRNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU1>  
A:Note: Lys-474 is probably removed posttranslationally  
R;Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.  
Science 206, 1303-1306, 1979  
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob  
A:Reference number: A26232; MUID:80081502  
A:Accession: A26232  
A:Molecule type: DNA  
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TU2>  
R;Ollio, R.; Rougeon, F.  
Nature 296, 761-763, 1982  
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamm  
A:Reference number: A26233; MUID:82173203  
A:Contents: b allele  
A:Accession: A26233  
A:Molecule type: DNA  
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OUL>  
A:Cross-references: GB:J00461  
R;Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahash  
J. Biol. Chem. 269, 12345-12350, 1994  
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.  
A:Reference number: A53598; MUID:94216359  
A:Accession: A53598  
A>Status: preliminary  
A:Molecule type: protein  
A:Residues: 234-251 <XIM>  
C:Comment: The a allele sequence is shown.  
C:Genetics: 138/1; 236/1; 258/1; 368/1  
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob  
F;157-222/Domain: immunoglobulin homology <IM1>  
F;236-257/Region: hinge  
F;281-350/Domain: immunoglobulin homology <IM2>  
F;387-454/Domain: immunoglobulin homology <IM3>  
F;152/Disulfide bonds: interchain (to light chain) #status predicted  
F;164-220, 288-348, 394-452/Disulfide bonds: #status predicted  
F;247, 250, 253, 256/Disulfide bonds: interchain (to heavy chain) #status predicted  
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 57.3%; Score 1382; DB 1; Length 474;  
Best Local Similarity 56.8%; Pred. No. 2.8e-72;  
Matches 260; Conservative 73; Mismatches 115; Indels 10; Gaps 3;  
Qy 1 QVOLVSGGLVOPGGSLRLSCAASGFTFRSNAMGWVROAPKGLVWVSGISGGSTYY 60  
Db 20 EVQLQSGPELVNPGASVKMSCKASGYTFTYVHHWKQKPGQGLEWIGVINPKDGTFR 79  
Qy 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVWDPIDYWGQGLTVTS 120  
Db 80 NEKFQKATLTSDKSNATYMEISLSTSDSAVYCARDYD--YDFAYWGQGLTVTS 136  
Qy 121 SASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 180

Db 137 AAKTTPSVYPLAPGCGDFTGSSVTSGCLVKGYPPEVTVTNWSSLSLSSSVHTLSQALLQ 196  
Qy 181 SGLYSLSVVTVPSSSLGRTQYICNVNHNKPSNTKVKKVPEKSCDKT-HTCPP-----C 233  
Db 197 SGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVTDKKLEPSGPISTINCPCKECHK 256  
Qy 234 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293  
Db 257 PARNLEGGPSVFLFPPNINIKDLMSLTPEKTVVVDSEDDPDVQISKFVNNEVHTAQT 316  
Qy 294 KPREEQYNSTYRVSVLTVHLHODWLNKGEYCKVSNKALPAPIEKTTISKAKGQPREPQVY 353  
Db 317 QTHREDYNSTIRVVSALPIQHODWNSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVY 376  
Qy 354 TLPPSRDELTKNOVSLTCLVKGYPSPDIKAVENESGQPNENYKTPPVLDSDGSFFLYSK 413  
Db 377 ILPPPAQLSRKDVSLTCLVGVNPGDISVEWTSNGHTEENYKDTAPVLDSDGSFYIYSK 436  
Qy 414 LTVDKSRWQGNVFCVSMHEALHNHYTQKSLSLSPGK 451  
Db 437 LNMKTSKWEKTDTSFSCNVRHEGLKNYILKTKTISRSPGK 474  
RESULT 13  
S01321  
Ig gamma-2b chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 30-Sep-1989 #sequence\_revision 30-Sep-1989 #text\_change 23-Jul-1999  
C:Accession: S01321  
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.  
Eur. J. Biochem. 176, 287-295, 1988  
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directe  
A:Reference number: S01320; MUID:883229081  
A:Accession: S01321  
A:Molecule type: mRNA  
A:Residues: 1-475 <DEL>  
A:Cross-references: EMBL:X13188; NID:q51780; PIDN:CAA31580.1; PID:q51781  
A:Note: this sequence was determined from the differentiated gene  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F;1-19/Domain: signal sequence #status predicted <SIG>  
F;20-475/Product: Ig gamma-2b chain #status predicted <MAT>  
F;159-223/Domain: immunoglobulin homology <IMM>  
Query Match 57.1%; Score 1376.5; DB 2; Length 475;  
Best Local Similarity 57.2%; Pred. No. 5.8e-72;  
Matches 262; Conservative 71; Mismatches 116; Indels 9; Gaps 4;  
Qy 1 QVOLVSGGLVOPGGSLRLSCAASGFTFRSNAMGWVROAPKGLVWVSGISGGSTYY 60  
Db 20 QVOLQSGAEIARPGASVKLSCKASGYTLTYSIGSWVKQRTGGLEWIGEYIPGSGNSYF 79  
Qy 61 ADSVKGRTISRDNKNTLYLQMSLRADTAIVYCAKHTGGVWDPIDYWGQGLTVTS 120  
Db 80 NEKFQKATLTVDKSSSTAYLHLSLTSDSAVYFCAGPRQVGLL-PFGYWGQGLTVTS 138  
Qy 121 SASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPEPTVYSWNSGALTSGVHTFPAVLQS 180  
Db 139 AAKTTPSVYPLAPGCGDFTGSSVTGCLVKGYPPEVTVTNWSSLSLSSSVHTPEALLQ- 197  
Qy 181 SGLYSLSVVTVPSSSLGRTQYICNVNHNKPSNTKVKKVPEKSCDKT-HTCPP-----C 233  
Db 198 SGLYTMSSSVTVPSSTWPSQTVTCVAHPASSTVTDKKLEPSGPISTINCPCKECHK 257  
Qy 234 PAPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKT 293  
Db 258 PARNLEGGPSVFLFPPNINIKDLMSLTPEKTVVVDSEDDPDVQISKFVNNEVHTAQT 317  
Qy 294 KPREEQYNSTYRVSVLTVHLHODWLNKGEYCKVSNKALPAPIEKTTISKAKGQPREPQVY 353  
Db 318 QTHREDYNSTIRVVSALPIQHODWNSGKEFKCKVNNKDLPSPIERTISKIKGLVRAPOVY 377  
Qy 354 TLPPSRDELTKNOVSLTCLVKGYPSPDIKAVENESGQPNENYKTPPVLDSDGSFFLYSK 413

Db 378 ILSPPEOLSRKVDLSLCLAVGSPEDISVETNSGHTTEENYKDTAPVLDSGSGFYISK 437  
QY 414 LTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 451  
Db 438 LNMKTSKWEKTDSCFVNRHGLKNYLLKTIISRSPGK 475  
RESULT 14  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03779; NID:g433123; PIDN:AAA52217.1; PID:g433124  
C:Gene: IgG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>  
Query Match 52.4%; Score 1263; DB 2; Length 328;  
Best Local Similarity 69.6%; Pred. No. 1.2e-65;  
Matches 231; Conservative 43; Mismatches 52; Indels 6; Gaps 2;  
QY 122 ASTKGPSVFPLAPSKSTSGTAAGLVKYDPEPVTVMNSGALTSVHTFPFVAVLQSS 181  
Db 1 APKTAPSVYPLACSRDTSQPNVALGCLASSYFPEPVTVMNSGALSSGVHTFPFVAVLQPS 60  
QY 182 GLYSLSSVTVVSSSLCTQYICNVNHPKSNKVDKKVEPKSCDKTHCCPPCPAPELGG 241  
Db 61 GLYSLSSMTVPASSLSKSYTCNVNHPATTTKVDKRVGKTKPPCPCPCAPCESP----G 116  
QY 242 PSVELFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 301  
Db 117 PSVFIFFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREQYN 176  
QY 302 STYRVSVLTVLQDHLNGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 361  
Db 177 STYRVSVLPIQHODWLNGLKEFKCKVNKKDLPAPIRIISKAKGQTPREPVYTLPPHAE 236  
QY 362 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDSDGSGFFLYSKLTVDKS 419  
Db 237 LRSKVSITCLVIGFYPPDIDVEMQRNGQPEPEGNVYRTTPQDDVDGYFLYSKFSVDKA 296  
QY 420 RWQGNVFCSCVMHEALHNHYTKSLSLSPGK 451  
Db 297 SWQGGIGFQCAVMHEALHNHYTKSLSLSPGK 328  
RESULT 15  
S31866  
Ig gamma-1 chain C region - synthetic  
C:Species: synthetic  
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli  
C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000  
C:Accession: S31866  
R:Filpula, D.  
submitted to the EMBL Data Library, February 1993  
A:Description: Screening method for protein-protein interactions of cloned gene products.  
A:Reference number: S31866  
A:Accession: S31866  
A:Molecule type: mRNA  
A:Residues: 1-255 <FIL>  
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069  
C:Keywords: immunoglobulin

F:1-22/Region: Escherichia coli outer membrane protein A precursor  
F:23-255/Region: human Ig gamma-1 chain C region  
Query Match 52.3%; Score 1260; DB 4; Length 255;  
Best Local Similarity 97.5%; Pred. No. 1.4e-65;  
Matches 233; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 213 TKVDKKVEPKSCDKTHCCPPCPAPELGGPSVFLFPPPKPDMLMISRTPEVTCVVVDVSH 272  
Db 17 TVAQADVESKSCDKTHCCPPCPAPELGGPSVFLFPPPKPDMLMISRTPEVTCVVVDVSH 76  
QY 273 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLDHDLNGKEYKCKVSNKAL 332  
Db 77 EDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLDHDLNGKEYKCKVSNKAL 136  
QY 333 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOE 392  
Db 137 PAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOE 196  
QY 393 NNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKSLSLSPGK 451  
Db 197 NNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKSLSLSPGK 255

Search completed: October 9, 2002, 19:13:20  
Job time : 25.1607 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:04:54 ; Search time 13.8061 Seconds  
(without alignments)  
1264.839 Million cell updates/sec

Title: US-09-822-698A-26

Perfect score: 2411

Sequence: 1 QVQLVQSGGGLVPGSSLR.....MHEALHNHYTKSLSPGK 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Query  | Score | Match | Length | DB         | ID | Description         |
|------------|--------|-------|-------|--------|------------|----|---------------------|
| 1          | 1767   | 73.3  | 330   | 1      | GC1_HUMAN  |    | P01857 homo sapien  |
| 2          | 1604   | 66.5  | 326   | 1      | GC2_HUMAN  |    | P01859 homo sapien  |
| 3          | 1590.5 | 66.0  | 327   | 1      | GC4_HUMAN  |    | P01861 homo sapien  |
| 4          | 1230.5 | 51.0  | 323   | 1      | GC_RABIT   |    | P01870 oryctolagus  |
| 5          | 1216.5 | 50.5  | 329   | 1      | GC2_CAVPO  |    | P01862 cavia porce  |
| 6          | 1156   | 47.9  | 290   | 1      | GC3_HUMAN  |    | P01860 homo sapien  |
| 7          | 1152   | 47.8  | 326   | 1      | GC1_RAT    |    | P20759 rattus norv  |
| 8          | 1146.5 | 47.6  | 333   | 1      | GCB_RAT    |    | P20761 rattus norv  |
| 9          | 1142   | 47.4  | 324   | 1      | GC1_MOUSE  |    | P01868 mus musculus |
| 10         | 1141   | 47.3  | 329   | 1      | GC3_MOUSE  |    | P22436 mus musculus |
| 11         | 1137   | 47.2  | 393   | 1      | GC1M_MOUSE |    | P01869 mus musculus |
| 12         | 1130   | 46.9  | 398   | 1      | GC3M_MOUSE |    | P03987 mus musculus |
| 13         | 1126   | 46.7  | 330   | 1      | GCA_MOUSE  |    | P01863 mus musculus |
| 14         | 1123.5 | 46.6  | 335   | 1      | GCAB_MOUSE |    | P01864 mus musculus |
| 15         | 1121   | 46.5  | 399   | 1      | GCAM_MOUSE |    | P01865 mus musculus |
| 16         | 1118.5 | 46.4  | 329   | 1      | GCC_RAT    |    | P20762 rattus norv  |
| 17         | 1112   | 46.1  | 322   | 1      | GCA_RAT    |    | P20760 rattus norv  |
| 18         | 1087   | 45.1  | 336   | 1      | GCB_MOUSE  |    | P01866 mus musculus |
| 19         | 1082   | 44.9  | 405   | 1      | GCBM_MOUSE |    | P01867 mus musculus |
| 20         | 492    | 20.4  | 428   | 1      | EPC_MOUSE  |    | P01854 homo sapien  |
| 21         | 483.5  | 20.1  | 429   | 1      | EPC_RAT    |    | P01855 rattus norv  |
| 22         | 471    | 19.5  | 117   | 1      | HV3C_HUMAN |    | P01764 homo sapien  |
| 23         | 468    | 19.4  | 421   | 1      | EPC_MOUSE  |    | P05336 mus musculus |
| 24         | 466.5  | 19.3  | 114   | 1      | HV3B_HUMAN |    | P01763 homo sapien  |
| 25         | 456.5  | 18.9  | 122   | 1      | HV3G_HUMAN |    | P01768 homo sapien  |
| 26         | 450.5  | 18.7  | 122   | 1      | HV3A_HUMAN |    | P01762 homo sapien  |
| 27         | 449.5  | 18.6  | 116   | 1      | HV3T_HUMAN |    | P01781 homo sapien  |
| 28         | 447    | 18.5  | 121   | 1      | HV3D_HUMAN |    | P01771 homo sapien  |
| 29         | 444    | 18.4  | 454   | 1      | MUC_HUMAN  |    | P01872 homo sapien  |
| 30         | 440    | 18.2  | 455   | 1      | MUC_MOUSE  |    | P01872 mus musculus |
| 31         | 439    | 18.2  | 458   | 1      | MUC_RABIT  |    | P03988 oryctolagus  |
| 32         | 438.5  | 18.2  | 116   | 1      | HV05_CARAU |    | P19181 carassius a  |
| 33         | 437.5  | 18.1  | 122   | 1      | HV3H_HUMAN |    | P01769 homo sapien  |

|    |       |      |     |   |            |  |                     |
|----|-------|------|-----|---|------------|--|---------------------|
| 34 | 437.5 | 18.1 | 126 | 1 | HV3K_HUMAN |  | P01772 homo sapien  |
| 35 | 435.5 | 18.1 | 136 | 1 | HV16_MOUSE |  | P01783 mus musculus |
| 36 | 435   | 18.0 | 115 | 1 | HV3D_HUMAN |  | P01765 homo sapien  |
| 37 | 432   | 17.9 | 117 | 1 | HV02_CANFA |  | P01785 canis famil  |
| 38 | 430   | 17.8 | 476 | 1 | MUCM_MOUSE |  | P01873 mus musculus |
| 39 | 429   | 17.8 | 479 | 1 | MUCM_RABIT |  | P04221 oryctolagus  |
| 40 | 428   | 17.8 | 119 | 1 | HV3I_HUMAN |  | P01770 homo sapien  |
| 41 | 427   | 17.7 | 115 | 1 | HV3F_HUMAN |  | P01767 homo sapien  |
| 42 | 422.5 | 17.5 | 120 | 1 | HV3O_HUMAN |  | P01782 homo sapien  |
| 43 | 422   | 17.5 | 457 | 1 | MUC_SUNMO  |  | P20768 suncus muri  |
| 44 | 419.5 | 17.4 | 119 | 1 | HV3M_HUMAN |  | P01774 homo sapien  |
| 45 | 419   | 17.4 | 120 | 1 | HV3E_HUMAN |  | P01766 homo sapien  |

# ALIGNMENTS

| RESULT 1 | GC1_HUMAN                                                             | STANDARD; | PRT; | 330 AA. |
|----------|-----------------------------------------------------------------------|-----------|------|---------|
| AC       | P01857;                                                               |           |      |         |
| DT       | 21-JUL-1986 (Rel. 01, Created)                                        |           |      |         |
| DT       | 21-JUL-1986 (Rel. 01, Last sequence update)                           |           |      |         |
| DT       | 16-OCT-2001 (Rel. 40, Last annotation update)                         |           |      |         |
| DE       | Ig gamma-1 chain C region.                                            |           |      |         |
| GN       | IGHG1.                                                                |           |      |         |
| OS       | Homo sapiens (Human).                                                 |           |      |         |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |           |      |         |
| OC       | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.            |           |      |         |
| OX       | NCBI_TaxID=9606;                                                      |           |      |         |
| RN       | [1]                                                                   |           |      |         |
| RP       | SEQUENCE FROM N.A.                                                    |           |      |         |
| RX       | MEDLINE=82274238; PubMed=6287432;                                     |           |      |         |
| RA       | Edlison J.W., Berson B.J., Hood L.E.;                                 |           |      |         |
| RT       | "The nucleotide sequence of a human immunoglobulin C gamma gene.";    |           |      |         |
| RL       | Nucleic Acids Res. 10:4071-4079(1982).                                |           |      |         |
| RN       | [2]                                                                   |           |      |         |
| RP       | SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).                               |           |      |         |
| RX       | MEDLINE=71064024; PubMed=5489771;                                     |           |      |         |
| RA       | Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,            |           |      |         |
| RT       | Waxdal M.J., Edelman G.M.;                                            |           |      |         |
| RT       | "The covalent structure of a human gamma G-immunoglobulin. VII. Amino |           |      |         |
| RL       | acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";      |           |      |         |
| RN       | Biochemistry 9:3161-3170(1970).                                       |           |      |         |
| [3]      |                                                                       |           |      |         |
| RP       | SEQUENCE OF 136-329 (EU).                                             |           |      |         |
| RX       | MEDLINE=71064025; PubMed=5530842;                                     |           |      |         |
| RA       | Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,         |           |      |         |
| RT       | Edelman G.M.;                                                         |           |      |         |
| RT       | "The covalent structure of a human gamma G-immunoglobulin. 8. Amino   |           |      |         |
| RL       | acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";      |           |      |         |
| RN       | Biochemistry 9:3171-3181(1970).                                       |           |      |         |
| [4]      |                                                                       |           |      |         |
| RP       | SEQUENCE (MYELOMA PROTEIN NIE).                                       |           |      |         |
| RX       | MEDLINE=77070269; PubMed=826475;                                      |           |      |         |
| RA       | Ponstingl H., Hilschmann N.;                                          |           |      |         |
| RT       | "The rule of antibody structure. The primary structure of a           |           |      |         |
| RT       | monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The        |           |      |         |
| RT       | chymotryptic peptides of the H-chain, alignment of the tryptic        |           |      |         |
| RL       | peptides and discussion of the complete structure.";                  |           |      |         |
| RN       | Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).                 |           |      |         |
| [5]      |                                                                       |           |      |         |
| RP       | SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.                  |           |      |         |
| RX       | MEDLINE=83289131; PubMed=6884994;                                     |           |      |         |
| RA       | Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;                     |           |      |         |
| RT       | "Three-dimensional structure determination of antibodies. Primary     |           |      |         |
| RT       | structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";    |           |      |         |
| RN       | Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).                   |           |      |         |
| [6]      |                                                                       |           |      |         |
| RP       | DISULFIDE BONDS.                                                      |           |      |         |
| RX       | MEDLINE=71064027; PubMed=4923144;                                     |           |      |         |
| RA       | Gall W.E., Edelman G.M.;                                              |           |      |         |
| RT       | "The covalent structure of a human gamma G-immunoglobulin. X.         |           |      |         |

RT Intrachain disulfide bonds.";  
RN Biochemistry 9:3188-3196(1970).  
RP [7]  
RX MEDLINE=77070267; PubMed=1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and  
RT characterization of the protein, the L- and H-chains, the  
RT cyanogen bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's 2. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RP MEDLINE=81208100; PubMed=7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";  
RL Biochemistry 20:2361-2370(1981).  
CC -!- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPE MARKER, 97-K, & THE  
CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)  
CC MARKER & THE GIM (NON-1) MARKERS.  
CC -!- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF  
CC 35,116,198,269 & 272.  
CC -!- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES  
CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES  
CC 268-272.  
CC -!- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF  
CC RESIDUES 198,267&272.  
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DR EMBL; J00228; AAC82527.1; ALT\_INIT.  
DR PIR; A02146; GHU.  
DR PDB; 1FC1; 15-JUL-92.  
DR PDB; 1FC2; 15-JUL-92.  
DR MIM; 147100; -  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_C1.  
DR InterPro; IPR003600; Ig\_Like.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00410; Ig\_Like; 1.  
DR SMART; SM00407; IG\_C1; 2.  
DR PROSITE; PS00290; IG\_MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW 3D-structure.  
FT NON\_TER 1  
FT DOMAIN 1 98  
FT HINGE. 99  
FT CH1. 110  
FT DOMAIN 111 223  
FT CH2. 224  
FT DOMAIN 224 330  
FT CH3. 330  
FT DISULFID 27 83  
FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).  
FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT CARBOHYD 180 180  
FT MOD\_RES 330 330  
FT VARIANT 97 97  
FT VARIANT 239 239  
FT VARIANT 241 241  
FT STRAND 123 126  
FT HELIX 130 134

FT TURN 136 137  
FT STRAND 141 148  
FT STRAND 158 162  
FT TURN 163 164  
FT STRAND 165 166  
FT STRAND 175 178  
FT STRAND 183 190  
FT HELIX 193 197  
FT TURN 198 199  
FT STRAND 202 206  
FT STRAND 215 219  
FT STRAND 227 227  
FT STRAND 230 234  
FT HELIX 238 240  
FT TURN 241 242  
FT STRAND 245 256  
FT STRAND 260 266  
FT TURN 267 268  
FT STRAND 269 270  
FT STRAND 274 276  
FT STRAND 280 281  
FT TURN 283 284  
FT STRAND 287 296  
FT HELIX 297 301  
FT TURN 302 303  
FT STRAND 306 312  
FT STRAND 313 314  
FT TURN 316 317  
FT STRAND 330 334  
SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;  
  
Query Match 73.3%; Score 1767; DB 1; Length 330;  
Best Local Similarity 100.0%; Pred. No. 7.7e-115;  
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 122 ASYKGSVPFLAPSSKSTSGGTAALCLVKDYFPEPVTVSNNSGALTSGVHTTTPAVLQSS 181  
Db 1 ASYKGSVPFLAPSSKSTSGGTAALCLVKDYFPEPVTVSNNSGALTSGVHTTTPAVLQSS 60  
Qy 182 GLXSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPELGG 241  
Db 61 GLXSLSSVTVTPSSSLGTQTYICNVNHRKPSNTKVDKVEPKSCDKTHTCPCPAPELGG 120  
Qy 242 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYN 301  
Db 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKENWYVDGVEVHNAKTKPREEQYN 180  
Qy 302 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 361  
Db 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYITLPPSRDE 240  
Qy 362 LTRKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 421  
Db 241 LTRKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300  
Qy 422 QQGNVFCSCVMHEALNHYTQKSLSLSPGK 451  
Db 301 QQGNVFCSCVMHEALNHYTQKSLSLSPGK 330  
  
RESULT 2  
GC2\_HUMAN  
ID GC2\_HUMAN STANDARD; PRT; 326 AA.  
AC P01859;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-2 chain C region.  
GN IGHG2  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OC NCBI\_TaxID=9606;  
OX



GN IGHG4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83157104; PubMed=6299662;  
RA Ellison J.W., Buxbaum J.N., Hood L.E.;  
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";  
RL DNA 1:11-18(1981).  
RN [2]  
RP MEDLINE=70207560; PubMed=4192699;  
RX Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;  
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the  
RT constant region of a gamma 4 chain.";  
RL Biochem. J. 117:33-47(1970).  
CC -----  
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CC -----  
DR EMBL; K01316; AAB59394.1; ALT\_INT.  
DR PIR; A02150; G4HU.  
DR HSP; P01842; 7FAB.  
DR MIM; 147130; -  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003600; Ig\_Like.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00410; Ig\_Like; 1.  
DR SMART; SM00407; IgC1; 2.  
DR PROSITE; PS00290; Ig\_MHC; 2.  
KW Immunoglobulin domain; Immunoglobulin C region.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CH1.  
FT DOMAIN 99 110 HINGE.  
FT DOMAIN 111 220 CH2.  
FT DOMAIN 221 327 CH3.  
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).  
FT DISULFID 27 83  
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).  
FT DISULFID 141 201  
FT DISULFID 247 305  
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;  
  
Query Match 66.08; Score 1590.5; DB 1; Length 327;  
Best Local Similarity 90.9%; Pred. No. 1:1e-102;  
Matches 300; Conservative 12; Mismatches 15; Indels 3; Gaps 1;  
  
QY 122 ASTKGSVFPLAPSSKSTSGTALGCLVKDYRPEPTVSWNSGALTSGVHTFPAVLQSS 181  
DB 1 ASTKGSVFPLAPSSKSTSGTALGCLVKDYRPEPTVSWNSGALTSGVHTFPAVLQSS 60  
QY 182 GLYSLSVVVTPSSSLGTTQYICNNVHKPSNTKVDKPKSCDKTHTCPCPAPPELLGG 241  
DB 61 GLYSLSVVVTPSSSLGTTQYICNNVHKPSNTKVDKPKSCDKTHTCPCPAPPELLGG 117  
QY 242 PSVFLFPKPKDTLMIKSTPVTCTVVDVDEDEPKVFNKYVDGVEVHNAKTKPREQYN 301  
DB 118 PSVFLFPKPKDTLMIKSTPVTCTVVDVDEDEPKVFNKYVDGVEVHNAKTKPREQYN 177  
QY 302 STYRVSVLTVLHQLWLNKGEYKCKVSKNAPAPIEKTIKAKGQPREPVYTLPPSRDE 361  
DB 178 STYRVSVLTVLHQLWLNKGEYKCKVSKNAPAPIEKTIKAKGQPREPVYTLPPSRDE 237  
QY 362 LTKNQVSLTCLVKGYFSPDIAVENESQGPENNYKTTTPVLDSDGSGFFLYSLTVDKSRW 421

DB 238 MTKNQVSLTCLVKGYFSPDIAVENESQGPENNYKTTTPVLDSDGSGFFLYSLTVDKSRW 297  
QY 422 QQGNVFCSCVMHEALHNYHTQKSLSLSPGK 451  
DB 298 QQGNVFCSCVMHEALHNYHTQKSLSLSLGK 327  
  
RESULT 4  
GC\_RABIT STANDARD; PRT; 323 AA.  
ID GC\_RABIT  
AC F01870;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 21-JUL-1986 (Rel. 01, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig gamma chain C region.  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=84030930; PubMed=6313520;  
RA Bernstein K.E., Alexander C.B., Mage R.G.;  
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant  
RT F-1 haplotype.";  
RL Immunogenetics 18:387-397(1983).  
RN [2]  
RP SEQUENCE OF 1-128.  
RX MEDLINE=76135469; PubMed=1243651;  
RA Pratt D.M., Mole L.E.;  
RT "Sequence studies on the constant region of the Fd sections of rabbit  
RT immunoglobulin G of different allotype.";  
RL Biochem. J. 151:337-349(1975).  
RN [3]  
RP SEQUENCE OF 88-266 FROM N.A.  
RX MEDLINE=83299917; PubMed=6193512;  
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;  
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma  
RT heavy chain and identification of two genomic C gamma genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).  
RN [4]  
RP SEQUENCE OF 132-161.  
RX MEDLINE=70110015; PubMed=5461106;  
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;  
RT "Sequence studies of the Fd section of the heavy chain of rabbit  
RT immunoglobulin G.";  
RL Biochem. J. 116:249-259(1970).  
RN [5]  
RP SEQUENCE OF 129-131 AND 155-322.  
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;  
RL (In) Killander J. (eds.);  
Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,  
Stockholm (1967).  
CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,  
CC 104-THR, AND THE E14 MARKER, 185-THR. REF.3 HAS THE D11 AND E15  
CC MARKERS, AND REF.5 THE E15 MARKER.  
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CC -----  
DR EMBL; M16426; AAA31289.1; -  
DR PIR; A02161; GHRB.  
DR HSP; P01857; 1FC1.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_c1.  
DR Pfam; PF00047; Ig; 3.  
DR SMART; SM00407; IgC1; 2.

```

DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 Q -> D (IN REF. 5).
FT CONFLICT 187 187 N -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SQ SEQUENCE 323 AA; 35404 MW; 69E8A118D579A8B CRC64;

Query Match 51.08; Score 1230.5; DB 1; Length 323;
Best Local Similarity 70.08; Pred. No. 6.8e-78;
Matches 229; Conservative 34; Mismatches 57; Indels 7; Gaps 2;

QY 125 KGPSVFPLAPSSKSTSGGTAALGLVQDYPEPVTVSWNSGALTSGVHTFPAVLQSSGLY 184
Db 4 KAPSVFPLAPCGDPTSPSTVTGLGVKGLPEPVTVTWNSGTLTNGVTFPSVQSSGLY 63

QY 185 SLSSVTVFSSSLGTTQYICNVNKPNTKVDKKEPKSCDKTHCTCPCPAPPELLGGPSV 244
Db 64 SLSSVTVFSSS--QPVTCNVAHPATNKVDKTVASTCSK---PTCPPELLGGPSV 116

QY 245 FLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNVDGVVEVHNAKTPREEQVNSTY 304
Db 117 FLPPPKPDTLMISRTPEVTCVVDVSHEDPEVKFNVDGVVEVHNAKTPREEQVNSTY 176

QY 305 RVSVLTVLHQLDNLGKRYKCKVSNKALPAPIETKISKAKGQPREQVYTLPPSRDELTK 364
Db 177 RVSVLTLPITHQDLNGLKRYKCKVSNKALPAPIETKISKARGQPLEKPVYTMGPPREELSS 236

QY 365 NOVSLTCLVKGYPSPDIAVENSGQPNENYKTPPVLDSDGSEFFLYSKLTVDKSKWQ 424
Db 237 RVSLTCLVKGYPSPDIAVENSGQPNENYKTPPVLDSDGSEFFLYSKLTVDKSKWQ 296

QY 425 NVFSCSVNHEALHNHYTKSLSPGK 451
Db 297 DVFTCSVNHEALHNHYTKSLSPGK 323

RESULT 5
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_Taxid=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshstein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
```

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RL Biochemistry 10:18-25(1971).
RN [3]
RX SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RL and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RX SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RX SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RX DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC 1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR HSP; P01772; 2F84.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00410; IG-like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202 INTERCHAIN (WITH A HEAVY CHAIN).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 50.58; Score 1216.5; DB 1; Length 329;
Best Local Similarity 70.48; Pred. No. 6.4e-77;
Matches 235; Conservative 28; Mismatches 62; Indels 9; Gaps 4;

QY 121 SASTKGPSVFPLAPSSKSTSGGTAALGLVQDYPEPVTVSWNSGALTSGVHTFPAVLQ 180
Db 1 SASTTAPSVFPLAASCVDPTSSMTLGLVKGYPPEPVTVKWSGALTSGVHTFPAVLQ- 59

QY 181 SGLYSLSVVTVFSSSLGTTQYICNVNKPNTKVDKKEPKSCDKTH--TCPCPAPEL 238
Db 60 SGLYSLSVTVFSSSOKAT---CNVAHPASTKVDKTVERTPTZPBCTCPKCPPEP 115

QY 239 LGGPSVFPLPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNVDGVVEVHNAKTPREE 298
Db 116 LGGPSVFIFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNVDGVVEVHNAKTPREE 175

QY 299 QYNSTYRVSVSLTVLHQLDNLGKRYKCKVSNKALPAPIETKISKAKGQPREQVYTLPPS 358
Db 176 QYNSTYRVSVSLTVLHQLDNLGKRYKCKVSNKALPAPIETKISKAKGQPREQVYTLPPS 235

QY 359 RDELTKNQVSLTCLVKGFYPSDIAVEVPSNQGP--ENNYKTPPVLDSDGSEFFLYSKLTV 416
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||||:||||:||||: ||:|||| ||| || | || ||||: ||:||||:|||||
Db 236 RDELSKSVSTCLINFFPADIHVWASNRVPVSEKYNTPPIEDADGSGVELYSKLTIV 295

Qy 417 DKSRRWQGNFVSCVMHEALHNHYTKOKLSLSPG 450
||| ||| |||:||||| |||: ||| |||
Db 296 DKSAMDQGTVTCSVMHEALHNHYTKOKAISRSPG 329

RESULT 6
GC3_HUMAN STANDARD; PRT; 290 AA.
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant:
RT gamma 3 heavy-chain disease protein wis.";
RL Biochemistry 19:4304-4308(1980).
RN [2]
RP REVISIONS TO 12-97 OF PROTEIN WIS.
RX MEDLINE=77118561; PubMed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable
RT quadruplication of a 15-amino acid residue basic unit.";
RL J. Biol. Chem. 252:883-889(1977).
RN [3]
RP REVISIONS TO 59-289 OF PROTEIN WIS (DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=6808505;
RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC.
RT Structure of the FC fragment of immunoglobulin G3.";
RL Biochem. Biophys. Res. Commun. 71:907-914(1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B.,
RA Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial
RT gene deletion model.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264(1982).
CC -|- SUBUNIT: DIMER LINKED BY 12 DISULFIDE BONDS; IT HAS AN EXTRA
CC INTERCHAIN DISULFIDE BOND AT POSITION 7 IN ADDITION TO THE 11
CC NORMALLY PRESENT IN THE HINGE REGION.
CC -|- MISCELLANEOUS: THE HEAVY CHAIN DISEASE PROTEIN WIS IS SHOWN.
CC -|- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 42-76 WAS TAKEN FROM THE
CC REF.2.
CC -|- MISCELLANEOUS: DISEASE PROTEIN WIS IS LACKING MOST OF THE V REGION
CC AND ALL OF THE CHI REGION.
CC -|- MISCELLANEOUS: DISEASE PROTEIN ZUC LACK MOST OF THE V REGION, ALL
CC OF THE CHI REGION, AND PART OF THE HINGE COMPARED WITH NORMAL
CC GAMMA-3 HEAVY CHAINS.
CC -|- MISCELLANEOUS: DISEASE PROTEIN OMM MAY REPRESENT AN ALLELIC FORM
CC OR ANOTHER GAMMA CHAIN SUBCLASS.
CC -|- MISCELLANEOUS: THE HINGE REGION IN GAMMA-3 CHAINS IS ABOUT FOUR
CC TIMES AS LONG AS IN OTHER GAMMA CHAINS AND CONTAINS THREE
CC IDENTICAL 15-RESIDUE SEGMENTS PRECEDED BY A SIMILAR 17-RESIDUE
CC SEGMENT (12-28).

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CC EMBL; J00231; AAA52805.1; ALT_SEQ.
DR PIR; A02149; G3HOW1.
DR HSSP; P01857; IFC1.
DR MIM; 147120; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00410; Ig_like; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat.
FT DOMAIN 12 73 HINGE.
FT 74 183 CH2.
FT 184 289 CH3.
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6
FT DISULFID 7 7
FT DISULFID 24 24
FT DISULFID 27 27
FT DISULFID 33 33
FT DISULFID 39 39
FT DISULFID 42 42
FT DISULFID 48 48
FT DISULFID 54 54
FT DISULFID 57 57
FT DISULFID 63 63
FT DISULFID 69 69
FT DISULFID 72 72
FT CARBOHYD 140 140
FT MOD_RES 290 290
FT VARIANT 126 127
FT VARIANT 134 134
FT VARIANT 139 139
FT VARIANT 182 182
FT VARIANT 227 227
FT VARIANT 227 227
FT VARIANT 279 279
FT SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;
Query Match 47.9%; Score 1156; DB 1; Length 290;
Best Local Similarity 90.5%; Pred. No. 8.1e-73;
Matches 210; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
Qy 220 EPKSCDKTHTCPGCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVKF 279
||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 59 EPKSCDTTPPCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVYVDSHEDPEVQF 118
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 280 NNYVDGVVHNAKTPRDEQYNSYRVSVLTVDHDLNGLNGKEYCKKVSNKALPAPIEKT 339
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 119 KKYVDGVGVHNAKTPRDEQYNSYRVSVLTVDHDLNGLNGKEYCKKVSNKALPAPIEKT 178
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 340 ISKAGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTP 399
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 179 ISKTKAGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSDIAVEWESNGQPENNYKTP 238
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 400 PYLSDSGSFFLYSKLTVDKSRWQQGNFYSCVMHEALHNHYTKOKLSLSPGK 451
|:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |:||||| |:|||||
Db 239 PMLSDSGSFFLYSKLTVDKSRWQQGNFYSCVMHEALHNHYTKOKLSLSPGK 290
```





DE Ig gamma-1 chain C region.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=80045036; PubMed=115593;  
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,  
RA Takahashi N., Mano Y.;  
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin  
RT gamma 1 chain gene";  
RL Cell 18:559-568(1979).  
RN [2]  
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).  
RX MEDLINE=80202559; PubMed=6769752;  
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,  
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;  
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences  
RT cloned in a bacterial plasmid";  
RL Gene 9:87-97(1980).  
RN [3]  
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).  
RX MEDLINE=80012837; PubMed=113776;  
RA Rogers J., Clarke P., Salser W.;  
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin  
RT heavy chain";  
RL Nucleic Acids Res. 6:3305-3321(1979).  
RN [4]  
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).  
RX MEDLINE=78242288; PubMed=98524;  
RA Adetugbo K.;  
RT "Evolution of immunoglobulin subclasses. Primary structure of a  
RT murine myeloma gammal chain";  
RL J. Biol. Chem. 253:6068-6075(1978).  
RN [5]  
RP DISULFIDE BONDS (MOPC 21).  
RX MEDLINE=73008889; PubMed=5073237;  
RA Swasti J., Milstein C.;  
RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";  
RL Biochem. J. 126:837-850(1972).  
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CC -----  
DR EMBL; V00793; CAA24172.1; -;  
DR EMBL; V00793; CAA24173.1; -;  
DR EMBL; V00793; CAA24174.1; -;  
DR EMBL; V00793; CAA24175.1; -;  
DR EMBL; V00795; CAA24176.1; -;  
DR PIR; A02159; GIMS.  
DR HSP; P01842; 7FAB.  
DR GlycoSuiteDB; P01868; -;  
DR MGD; MGI:96446; Igh-4.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003597; Ig\_c1.  
DR Pfam; PF00047; Ig\_3.  
DR SMART; SM00407; Igcl\_2.  
DR PROSITE; PS00290; IG\_MHC; 1.  
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;  
KW Alternative splicing.  
FT NON\_TER 1 1  
FT DOMAIN 1 97 CH1.  
FT HINGE. 97 97  
FT DOMAIN 98 110  
FT DOMAIN 111 217 CH2.  
FT DOMAIN 218 324 CH3.  
FT DISULFID 27 82  
FT DISULFID 102 102  
FT INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 104 104  
FT DISULFID 107 107  
FT DISULFID 109 109  
FT DISULFID 138 138  
FT CARBOHYD 174 174  
FT N-LINKED (GLCNAC. . .).  
FT /FTid=CAR\_000055.  
FT DISULFID 244 302  
FT MOD\_RES 324 324  
FT CONFLICT 276 276 N -> D (IN REF. 3).  
FT CONFLICT 278 278 N -> D (IN REF. 3).  
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;  
Query Match 47.4%; Score 1142; DB 1; Length 324;  
Best Local similarity 62.0%; Pred. NO. 8.6e-72;  
Matches 206; Conservative 56; Mismatches 60; Indels 10; Gaps 4;  
QY 122 ASITKGPSVFPPLAPSSKSTGGTAALGCLVKGDFPEPVTVSNNSGALTSVHTTFAVLQSS 181  
Db 1 AKTTPSVYPLAPGSAQAQNSMWTLCGLVGYFPEPVTVWNSGSLSSGVHTTFAVLQSD 60  
QY 182 GLYSLSSVTVPPSSSLGTQTYICNVNHNKPSNTKYDKKVEPKSCDKTHTCPP--CPAPELL 239  
Db 61 -LYTLSSVTVPPSSRPSETVTCNVAHPASSTKVDDKIVPRDCG----CKPCTCTVPEV- 114  
QY 240 GGSVFLFPEPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNKYVDGVEVHNATKPREEQ 299  
Db 115 --SSVFIFFPKPKDVLITLTPKVTGVVDISKDDPEVQFSFVDDVEVHTAQTQPREEQ 172  
QY 300 YNTRYRVSVLTVLHODWLNKYEKCKVSNKALPAPEKTISKAKGQPREPQVYTTLPSSR 359  
Db 173 FNSTERSVSELPIMHODWLNKYEKRCVNSAFAPEKTISKTKGRKAPQVYTTIPPK 232  
QY 360 DLTKNQVSLTCLVKGFPSPDIATVEWESNGOPENNYKTPPEVLDSDGSFFLYSKLTVDKS 419  
Db 233 EQMAKDKVSLTCMITDFPEDITVEWQNGQPAENYKNTQPIMNTNGSYFYVSKLVQKS 292  
QY 420 RWOQGVNFCVSNVHEALNHNHYTKQSLSLSPGK 451  
Db 293 NWEAGNTFTCSVLHLEGLHNHHTKSLSHSPGK 324  
RESULT 10  
GC3\_MOUSE STANDARD; PRT; 329 AA.  
ID GC3\_MOUSE  
AC P22436;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ig gamma-3 chain C region, secreted form.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=85027161; PubMed=6092053;  
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,  
RA Tucker P.W., Blattner F.R.;  
RT "Structural analysis of the murine IgG3 constant region gene";  
RL EMBO J. 3:2041-2046(1984).  
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CC -----  
DR EMBL; J00451; -; NOT\_ANNOTATED\_CDS.  
DR PIR; B02156; G3MSC.  
DR HSP; P01857; IFCL.  
DR InterPro; IPR003006; Ig\_MHC.

```
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003600; Ig-like.
DR Pfam: PF00047; Ig_3.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match
Best Local Similarity 64.08; Pred. No. 1e-71; Length 329;
Matches 212; Conservative 47; Mismatches 68; Indels 4; Gaps 3;

QY 123 STKGSPVPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSSG 182
Db 1 TTAPSVPLVPGCDTSGSVTLGCLVKGYFPEPTVKWNYGALSGVHTFPAVLQSSG 59

QY 183 LXSLSVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCP--PCPAPELLG 240
Db 60 FYSLSLVTVFSSSTWPSQTVICNVNHNKPSNTKVDKVEPKSCDKTHTCP--PCPAPELLG 118

QY 241 GRSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 300
Db 119 GRSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQY 178

QY 301 NSTYRVSVLTVLHODWLNGLKEKYSKSNKALPAPIETKISKAKGROPQVYTLPPSRD 360
Db 179 NSTYRVSVLTVLHODWLNGLKEKYSKSNKALPAPIETKISKAKGROPQVYTLPPSRD 238

QY 361 ELTKNQVSLTCLVKGFYPSDIAVEGSENGQPPENPKYTPPVLDSDGFFLYSKLTVDKSR 420
Db 239 QMSKKVSLTCLVNTFFSEATISVWERNGLEQDYKNTPPILDSGTYFLYSLKLTVDTS 298

QY 421 WQQGVFSCSVNMEALHNHYTKSLSPGK 451
Db 299 WQQGVFSCSVNMEALHNHYTKSLSPGK 329

RESULT 11
GC1M_MOUSE STANDARD; PRT; 393 AA.
AC P01869;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-1 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=80045036; PubMed=115593;
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
RT gamma 1 chain gene.";
RL Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 323-393 FROM N.A.
RX MEDLINE=82197626; PubMed=6804950;
RA Tyler B.M., Cowan A.F., Gerondakis S.D., Adams J.M., Bernard O.;
RT "mRNA for surface immunoglobulin gamma chains encodes a highly
RT conserved transmembrane sequence and a 28-residue intracellular
RT domain.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
RN [3]

SEQUENCE OF 323-366 FROM N.A.
MEDLINE=82115295; PubMed=6799207;
Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
Eisenberg D., Wall R.;
"Gene segments encoding transmembrane carboxyl termini of
Immunoglobulin gamma chains.";
Cell 26:19-27(1981).
[4]

SEQUENCE OF 1-44 FROM N.A.
MEDLINE=8222190; PubMed=6283537;
Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
"Nucleotide sequences of gene segments encoding membrane domains of
Immunoglobulin gamma chains.";
Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

-1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
SEGMENT OF MU CHAINS.

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EMBL; V00793; CAA24172.1; -
EMBL; V00793; CAA24173.1; -
EMBL; V00793; CAA24174.1; -
PIR; B02159; G1MSM.
HSP; P01842; 7FAB.
MG; MG1:96446; Igh-4.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003597; Ig_c1.
Pfam: PF00047; Ig_3.
SMART; SM00407; IGc1; 2.
PROSITE; PS00290; IG_MHC; 1.
Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
Alternative splicing; Transmembrane.
NON_TER 1 97 CH1.
DOMAIN 98 110 HINGE.
DOMAIN 111 217 CH2.
DOMAIN 218 324 CH3.
DISULFID 27 82
DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
DISULFID 138 198
CARBOHYD 174 174 N-LINKED (GLCNAC...).
DISULFID 244 302 POTENTIAL.
TRANSMEM 340 357 CYTOPLASMIC (POTENTIAL).
DOMAIN 358 393
SEQUENCE 393 AA; 43386 MW; 4CC8834387AICE27 CRC64;

Query Match
Best Local Similarity 47.2%; Score 1137; DB 1; Length 393;
Matches 205; Conservative 56; Mismatches 60; Indels 10; Gaps 4;

QY 122 ASTKGPSVEPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 181
Db 1 AKTTPSVVPLAPSSKSTSGGTAALGCLVKGYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 182 GLYSLSVTVFSSSLGTQTYICNVNHNKPSNTKVDKVEPKSCDKTHTCP--CPAPELL 239
Db 61 -LYTSSSVTVFSSSPRSETVTCNVNHNKPSNTKVDKVEPKSCDKTHTCP--CPAPELL 114

QY 240 GGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQ 299
Db 119 GGSVFLFPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATKPREQ 299
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Db 115 --SSVFPPPKDVLITITLTPKVTCTVVVDISKDDPEVQFSWFDVDDVEVHTAQTPREEQ 172
QY 300 YNSYRVRVSVLTVLHQDLWNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 359
Db 173 FNSFRSVSELPINHQDLWNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSR 232
QY 360 DELTKNOVSLTCLVKGFPYSDIAVEVESNGQPNENYKTPPPVLDSDSGSFFLYSKLTVDKS 419
Db 233 EQMAKDKVSLTCTMTDFPEPDIIVENQWNGQPAENYKNTQPIIMNNGSYFYVSKLNVQKS 292
QY 420 RWQGNVFCSSVMHEALHNHYTKSLSLSP 450
Db 293 NWEAGNTFTCSVLHGLHNHHTKSLSPG 323

RESULT 12
GC3M_MOUSE
ID GC3M_MOUSE STANDARD; PRT; 398 AA.
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Konaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
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DR EMBL; J00451; BAB59655.1; -
DR EMBL; V01526; CAA24767.1; ALT_SEQ.
DR PIR; A02155; GJMSL.
DR HSSP; P01857; IFC1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_like.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT TRANSMEM 346 362
FT DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
FT CONFLICT 333 333 E -> G (IN REF. 2).
FT CONFLICT 342 342 E -> Q (IN REF. 2).
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FT CONFLICT 388 388 P -> F (IN REF. 2).
SQ SEQUENCE 398 AA; 43929 MW; CF7E264B50A41B95 CRC64;

Query Match 46.9%; Score 1130; DB 1; Length 398;
Best Local Similarity 63.8%; Pred. No. 7.5e-71;
Matches 210; Conservative 47; Mismatches 68; Indels 4; Gaps 3;

QY 123 STGKPSVFLPAPSSKTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSSG 182
Db 1 TTTAPSVYPLVPGCSDTISGSSVTLGCLVKGYFPEPTVKNNYKALSSGVRTVSSVLQ-SG 59
QY 183 LYSLSVVTVPSSSLGQTQYICNNHKNPSNTKVDKVEPKSCDKTHTCP--PCPAPELLG 240
Db 60 FYSLSLVTVPSSTWPSQTWCNVAHPASKTELKRIEPR-IPKSTPPGSSCPGNTLG 118
QY 241 GPSVFLPFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQ 300
Db 119 GPSVFIFPPPKDALMISLTPEKTCVVVDVSEDDPDVHVSFWEVDKNEVHTAWTQPREAQ 178
QY 301 NSTRVSVLTVLHQDLWNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRD 360
Db 179 NSTFRVVSALPIQHDWMRGKEPKCKVNNKALPAPIERTISKPKGRAQTPQVYTIPTPRE 238
QY 361 ELTKNOVSLTCLVKGFPYSDIAVEVESNGQPNENYKTPPPVLDSDSGSFFLYSKLTVDKSR 420
Db 239 QMSKKKVSILTCLVTFSEALSVWEERNGELEDYKNTPPILDSGDTFLYSLKLVDTDS 298
QY 421 WQGNVFCSSVMHEALHNHYTKSLSLSP 449
Db 299 WLOGEIFTCSVYHEALHNHHTKSLSRP 327

RESULT 13
GCAA_MOUSE
ID GCAA_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Ig gamma-2A chain C region, A allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81076554; PubMed=6777755;
RA Sikorav J.-L., Auffray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA.";
RL Nucleic Acids Res. 8:3143-3155(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=81198976; PubMed=6262729;
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer.";
RL Nucleic Acids Res. 9:1365-1381(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81223894; PubMed=6787604;
RA Ollio R., Auffray C., Morthams C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN [4]
RP MYELOMA PROTEIN MOPC 173.
RX MEDLINE=74175517; PubMed=4831970;
RA Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
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RT for the evolution of immunoglobulin structure and function.";
RL Eur. J. Biochem. 43:423-435(1974).
RN [5]
RP DISULFIDE BONDS.
RX MEDLINE=73056887; PubMed=4565406;
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RL immunoglobulin. Identification of the disulfide bridges.";
RN Eur. J. Biochem. 30:452-462(1972).
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DR EMBL; V00798; CAA24178.1; .
DR PIR; A02152; G2MSA.
DR HSP; P01842; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT DISULFID 330 330
FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 46.7%; Score 1126; DB 1; Length 330;
Best Local Similarity 63.6%; Pred. NO. 1.1e-70;
Matches 211; Conservative 44; Mismatches 73; Indels 4; Gaps 3;

QY 122 ASTKGSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNHGALTSVGHVTPAVLQSS 181
Db 1 AKTAPSVPLAPVCGDGTGSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFPALLQSD 60

QY 182 GLYSLSVSVTPSSSLGTQTYICNVNHNKPSNFKVDKVEPKSCDKTHTCTCPP--CPAPELI 239
Db 61 -LYTLSSSVTVTSWPQSITCNVAHPASSTKVDKIEPRG-FTIKPCPCCKPAPNLL 118

QY 240 GGSVFLFPKPKDGLMISRPETVCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQ 299
Db 119 GGSVFLFPKPKDGLMISRPETVCVVDVSHEDPEVKFNWYDGVGVHNAKTKPREQ 178

QY 300 YNSTYRVSVTLVHLDWLNKGEYKCKVSNKALPAPIEKTISKAKGPRPQVYVTLPPSR 359
Db 179 YNSTLRVVSALPIQHQQDWSGKEFKCKVNNKDLPAPIERTISKPKSVRAPQVYVLPPE 238

QY 360 DELTKNOVSLTCLVKGYFSDTAWEWSNGQENNYKTTTPVLDSDGSFYLKSLTVDKS 419
Db 239 EEMTKKQVITTCVMVTFMPEDIVENTNNGKTELNYKNTPEVLDSDGSFYFMYSLRYEKK 298

QY 420 RWQGNVFCSCVMHEALHNHYTKLSLSPGK 451
Db 299 NWVERNSYSCSVVHEGLNHHHTKFSRTPGK 330

RESULT 14
GCAB_MOUSE STANDARD; PRT; 335 AA.
ID GCAB_MOUSE
AC P01864;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2A chain C region, B allele.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eumalia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT Ig2a and Ig2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499(1981).
RN [2]
RP SEQUENCE.
RC MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Strosberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain C regions of Igla and Ig1b allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -1- MISCELLANEOUS: THE SEQUENCE DIFFERS FROM THAT OF THE A ALLELE,
CC FROM BALB/C MICE, AT 15% OF THE POSITIONS.
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DR EMBL; J00479; .; NOT_ANNOTATED_CDS.
DR PIR; A02153; G2MSAB.
DR HSP; P01857; 1FCI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig-cl.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00410; Ig-like; 1.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
SQ SEQUENCE 335 AA; 36596 MW; FA3382792CBB13C6 CRC64;

Query Match 46.6%; Score 1123.5; DB 1; Length 335;
Best Local Similarity 61.3%; Pred. NO. 1.7e-70;
Matches 206; Conservative 53; Mismatches 70; Indels 7; Gaps 2;

QY 122 ASTKGSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNHGALTSVGHVTPAVLQSS 181
Db 1 AKTAPSVPLAPVCGDGTGSSVTLGCLVKGYFPEPTVLTWNSGSLSSGVHTFPALLQ-S 59

QY 182 GLYSLSVSVTPSSSLGTQTYICNVNHNKPSNFKVDKVEPK-----SCDKTHTCTCPPA 235
Db 60 GLYTLSSSVTVTSWPQSITCNVAHPASSTKVDKIEPRVPTQNCPPHQVPPCAA 119

QY 236 PELLGGSPVFLFPKPKDGLMISRPETVCVVDVSHEDPEVKFNWYDGVGVHNAKTKP 295
Db 120 PDLGGSPVFLFPKPKDGLMISRPETVCVVDVSHEDPEVKFNWYDGVGVHNAKTKP 179

QY 296 REOYNSTYRVSVTLVHLDWLNKGEYKCKVSNKALPAPIEKTISKAKGPRPQVYVTL 355
Db 180 HREDYNSTLRVVSALPIQHQQDWSGKEFKCKVNNKDLPAPIERTISKPKSVRAPQVYV 239

QY 356 PPSRDELTKNOVSLTCLVKGYFSDTAWEWSNGQENNYKTTTPVLDSDGSFYLKSLT 415
Db 240 PPAEEMTKKQVITTCVMVTFMPEDIVENTNNGKTELNYKNTPEVLDSDGSFYFMYSKLR 299

QY 416 VDKSRWQGNVFCSCVMHEALHNHYTKLSLSPGK 451

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Qy 62 DSVKGRFTISRDNKNTLYLQMSNLRADETAVYYCAKHTGGVWDPIDYWGQGLTVTVSS 121
Db 60 DSVKGRFTYKDKDRNLSLQMSLSRSEDATAMYYCAR-----GDYSAYWGPGLTVTVSA 113
Qy 122 ASYKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTTFAVLQSS 181
Db 114 AKTTPPSVPLAPGSAQNTSMVTLGCLVKGYFPEPTVTVNWSGLSSGVHTTFAVLQSD 173
Qy 182 GLYSLSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPP--CPAPEL 239
Db 174 -LVTLSSTVTPSSSTWPSSTVTCNVAHPASSTKVDKIVPRDCG---CKPCICTVPEV- 227
Qy 240 GGPSTVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNATKKREEQ 299
Db 228 --SSVFIFFPKPKDVLITLTTPKVTCTVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQ 285
Qy 300 YNSTYRVSVLTVLHODWLNKNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYITLPPSR 359
Db 286 FNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGPKAPQVYITPPPK 345
Qy 360 DELTKNOVSLTCLVKGYFSPDITAVESWGQPENNYKTTTPVLDSDGSFELYSLIVDKS 419
Db 346 EQMAKQVSLTCLVITDFFEDITVDMQNGQPAENYKNTQPMIDTDSGYFVYSLNIVQKS 405
Qy 420 RWQOGNVFSCVMHEALHNHYTKQSLSPGK 451
Db 406 NWEAGNTFTCSVLHGLHNHHTTEKLNHSHPGK 437

RESULT 2
Q91205
ID Q91205 PRELIMINARY; PRT; 473 AA.
AC Q91205;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 51.9 KDA PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH0327.1; -.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;

Query Match 63.1%; Score 1522.5; DB 11; Length 473;
Best Local Similarity 63.0%; Pred. No. 1.3e-116;
Matches 289; Conservative 64; Mismatches 93; Indels 13; Gaps 5;

Qy 1 QVQLVQSGGGLVQPGGSLRLSAAAGFTFSRNAMGWVRQAPKGLWVSGISGGSTYY 60
Db 20 EVQLVESGGGLVQPGGSLRLSAAAGFTFSYGMHWVRQAPKGLWVAVINSGSTIYY 79
Qy 61 ADSVKGRFTISRDNKNTLYLQMSNLRADETAVYYCAKHTGGVWDPIDYWGQGLTVTV 119
Db 80 ADTVKGRFTISRDNKNTLYLQMSNLRADETAVYYCAKHTGGVWDPIDYWGQGLTVTV 135
Qy 120 SSASTKGPSVFPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTTFAVLQ 179
Db 136 SSARTTPPSVPLAPGCGDITGSSVTLGCLVKGYFPEPTVTVNWSGLSSGVHTTFAVLQ 195
Qy 180 SSGISLSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPP----- 232
Db 196 -SGLIYTHSSSVTVTPSSSTWPSSTVTCNVAHPASSITVDKLEFSPGIPSTINCPCKECHK 254
Qy 233 CPAPELLGGPSVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAT 292
Db 255 CPAPNLEGGPSVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNAT 314
```

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Qy 293 TKPREQYNSTYRVSVLTVLHODWLNKNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQV 352
Db 315 TOTREDYNSTYRVSVLTVLHODWLNKNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQV 374
Qy 353 YTLPPSDELTKNOVSLTCLVKGYFSPDITAVESWGQPENNYKTTTPVLDSDGSFELY 412
Db 375 YILPPPAEQLSRKDVSLTCLVGVFNPGDISVETNNGHTTEENYKDTAPVLDSDGSFY 434
Qy 413 KLTVDKSRWQOGNVFSCVMHEALHNHYTKQSLSPGK 451
Db 435 KLDIKTSKWEKTDSEFSCNVNHEGLKXNYLKKTISRSPGK 473

RESULT 3
Q99LC4
ID Q99LC4 PRELIMINARY; PRT; 463 AA.
AC Q99LC4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SIMILAR TO RIKEN CDNA 1810060009 GENE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003435; AAH03435.1; -.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003600; Ig_Like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IgC1; 2.
DR SMART; SM00406; IgV; 1.
DR SMART; SM00410; Ig_Like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN.1.
SQ SEQUENCE 463 AA; 51007 MW; EAA674C6B8C30783 CRC64;

Query Match 61.5%; Score 1483.5; DB 11; Length 463;
Best Local Similarity 59.6%; Pred. No. 2e-113;
Matches 270; Conservative 78; Mismatches 94; Indels 11; Gaps 5;

Qy 1 QVQLVQSGGGLVQPGGSLRLSAAAGFTFSRNAMGWVRQAPKGLWVSGISGGSTYY 60
Db 20 QVQLVQSGGGLVQPGGSLRLSAAAGFTFSRNAMGWVRQAPKGLWVSGISGGSTYY 79
Qy 61 ADSVKGRFTISRDNKNTLYLQMSNLRADETAVYYCAKHTGGVWDPIDYWGQGLTVTV 120
Db 80 SEKFKGKATLTITDKSSSTAYMHLSSLTSEDVAYFCARSSYYV-YDLPAYWGQGLTVTV 138
Qy 121 SASYKGSVPFLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTTFAVLQ 180
Db 139 AAKTTPPSVPLAPGSAQNTSMVTLGCLVKGYFPEPTVTVNWSGLSSGVHTTFAVLQ 198
Qy 181 SGLYSLSVTVTPSSSLGTQYICNVNHNKPSNTKVDKVEPKSCDKTHTCPP--CPAPEL 238
Db 199 D-LYTLSSSVTVTPSSSTWPSSTVTCNVAHPASSITVDKLEFSPGIPSTINCPCKECHK 253
Qy 239 LGGPSVFLPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVVHNATKKREE 298
Db 254 ---SSVFIFFPKPKDVLITLTTPKVTCTVVDISKDDPEVQFSWFVDDVEVHTAQTQPRE 310
Qy 299 QYNSTYRVSVLTVLHODWLNKNGKEYCKVSNKALPAPIEKTISKAKGQPRFPQVYITLPP 358
Db 311 OFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEKTISKTKGPKAPQVYITPP 370
```







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RESULT 8
Q96P08
ID Q96P08 PRELIMINARY; PRT; 701 AA.
AC Q96P08;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FACTOR VII ACTIVE SITE MUTANT IMMUNOCONJUGATE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21477448; PubMed=11593034;
RA Hu Z., Garen A.;
RT "targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
DR EMBL: AF272774; AAK58686.1;
SQ SEQUENCE 701 AA; 77826 MW; 94AC6CEB42CC992F CRC64;

Query Match 52.4%; Score 1264.5; DB 4; Length 701;
Best Local Similarity 70.1%; Pred. No. 3.3e-95;
Matches 255; Conservative 8; Mismatches 52; Indels 49; Gaps 5;

QY 91 TAVYYCAKHTGGVNDPIDYWGQGLTVTVSSASTKGPSVFPPLAPSSKSTSGTAAAGCLV 150
DB 384 TEYMFCAGYSDG-----SKDSCAGDSGGPHATHYRGTYLTG----- 420
QY 151 KDYFPEPTVSNWNGALTSVHTFPAVLQSSGLYSLSSVTVTPSSSLGTQTVICNVNHPK 210
DB 421 -----IVSWGQCAIVG-----HFGVY-----TRVSQYIEWLQKMRSERP 457
QY 211 S---NTKVDKKVEPKSCDKHTPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCW 267
DB 458 GYLLRAPFEGSAERKSCDKHTPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCW 517
QY 268 VDVSHPEDPKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHODWLNQGEYKCKV 327
DB 518 VDVSHPEDPKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLHODWLNQGEYKCKV 577
QY 328 SNKALPAPIEKTISKAKGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 387
DB 578 SNKALPAPIEKTISKAKGPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWES 637
QY 388 NGQPNENYKTPPPVLDSDGFFLYSKLTVDKSRWQGNVFCVSNMHEALHNHYTKQSLSL 447
DB 638 NGQPNENYKTPPPVLDSDGFFLYSKLTVDKSRWQGNVFCVSNMHEALHNHYTKQSLSL 697
QY 448 SPCK 451
DB 698 SPCK 701

RESULT 9
Q96BB9
ID Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 65.0 KDA PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1;
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 40.2%; Score 968.5; DB 4; Length 597;
Best Local Similarity 38.7%; Pred. No. 5e-71;
Matches 218; Conservative 77; Mismatches 153; Indels 115; Gaps 16;

QY 1 QVQLVQSGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
DB 20 EVQLLEGGGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSAISGGSTYY 79
QY 61 ADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYYCAK-----HTGGCVWDPIDYWGQGL 116
DB 80 ADSVKGRFTISRDNSKNTLYLQMSLRAEDTAVYYCAKPRGYSAGSNYTREDYWGQGL 139
QY 117 VTSSASTKGPSVFPPLAPSSKSTSG-GTAAAGCLVLDYFPEPTVSN--NSGALTSGVHT 173
DB 140 VTVSSGSASAPTLFPLVSCENSPDTSVAVAGCLAQDFLPDSITFSWKYKNSDISSTRG 199
QY 174 FPAVLQSSGLYSLSSVTVFPSSSL--GTQYI-TCNVNHPKSN-----TKVD 216
DB 200 FPSVLR-GGKYAATSQVLLPSPKDMQGTDEHVYCKVQHPNGNKEKNVPLPVIAPLPKVS 258
QY 217 KKVPEKS-----CDKTHTCP-----PCPAPELLGGPS 243
DB 259 VFVPRDGFNGNPKRKLICQATGFSRQVSWLREGKQVGSVTTDQVQAKESGPT 318
QY 244 -----VFLPFPKPKDT 254
DB 319 TYKVTSLTIKESDWLSQSMFCTCRVDHRGLTFQGNASSMCPVQDPAIRVFAIPPS-FAS 377
QY 255 LMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNATKPREQYNSTYRVVSVLTVLH 314
DB 378 IFLTKSKLCLVTDLTLYD-SVTISWTRQNGEAVKTHNTISEHPNATFSAVGEASICE 436
QY 315 QDWLNGKEYCKCKVSKNALKAPAEIKTISKAKGQ-REPOVYTLPPSRDELTKNQVSLTCL 372
DB 437 DQWNSGERFTCTVHTDLPPLKQTSRPGKVALHPDVLPPAREQLNRESATITCL 496
QY 373 VKGFYPSDIAVEWESNGQ-ENNYKTPPVLV--SDGSFFLYSKLTVDKSRWQGNVFS 428
DB 497 VTGSPADVFQWMRGOPLSPEKYITVSAPMPPEQAPGRVFAHSILTVSEENNTGETYT 556
QY 429 CSMVHEALHNHYTKQSLSPGK 451
DB 557 CVVAHEALPNRVTERVTVDKSTGK 579

RESULT 10
Q96K68
ID Q96K68 PRELIMINARY; PRT; 494 AA.
AC Q96K68;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CDNA FLJ14473 FIS, CLONE MAMMA1001080, HIGHLY SIMILAR TO HOMO
DE SAPIENS SNC73 PROTEIN (SNC73) MRNA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MAMMARY GLAND;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
RA Ninomiya K., Iwanagaki T.;
```

RT "NEDO human cDNA sequencing project."  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AK027379; BAB55072.1; -  
SQ SEQUENCE 494 AA; 53088 MW; 9A1D7AE5AE4C0E CRC64;

Query Match 34.6%; Score 834; DB 4; Length 494;  
Best Local Similarity 41.8%; Pred. No. 4.2e-60;  
Matches 199; Conservative 62; Mismatches 171; Indels 44; Gaps 16;

```
QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 EVOLVESGGGLVKPGGSLRLSCAASGLSFSTYAMWVRQAPGKLEWVSSISRSYIY 79
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 ADSVKGRTISRDNKNTLYLOMNSLRADTAAYVYCAKHT -GGVWDPIDYWGQGLTV 119
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 RDSVKGRTISRDNKNTLYLOMNSLRADTAAYVYCARDSCNGAICYCFGWQGLTV 139
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 120 SSASTKGPSVFELAPSSKSTSGGTAALGCLVKDYFP -EPVTVMNSGALTSGVHTFPAVL 178
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 140 SSASPTSPKVPFLSICS -TOPDGNWVIACLVQGFQEPQLSVTWSESGQGVARNPPSQ 198
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 179 QSSG-LYSLSSVIVPSS-LGTQTYICNVNHNKPSNTKVDKKVEPKSCDKTHCPCPAP 236
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 199 DASGDLVTTSQLTPATQCLAGKSVTCHVKHY -TNPSQDVTV-----PCPVP 245
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 237 ELLGGPSVFLPFPKPK-----DTLMISRTPEVTCVVVDVSHEDPEVKFNW 281
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 246 STPTTPSPST -PPTSPSCCHPRLSLRPALEDLLLGSEANLCTLGL -RDASGVTFW 303
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 282 YVDGVEVHNATKPREQYNSTYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 341
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 304 TPSSGK--SAVGQPPERLDCGYSSVSLPGCAEPFNHGKTFCTAAAPESKTPLTATLS 361
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 342 KAKGPREPOVYTLPPSRDELTKNQ-VSLTCLVKGYFSPDAVAVESNGO--PENNYKTT 398
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 362 KS -GNTFPEVHLPPPESEALNELVTLTCLARGFSPKDVLVKWLQSGQELPREKYLTV 420
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 399 PPVLD -SDG--SFTLYSKLTVDKRWQGNVFCVSMHEALHNHYTKQSLSPGK 451
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 421 ASRQPSQGTTFVAVTSILRAEDWKKGDTFSCMGVHGHEALPLAFTQKTIIDRLAGK 476
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

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RESULT 11

Q99KA4 ID Q99KA4 PRELIMINARY; PRT; 487 AA.  
AC Q99KA4;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 52.6 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Strausberg R.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC004786; AAH04786.1; -  
DR HSSP: P01810; 2FBJ

DR InterPro: IPR003599; Ig.  
DR InterPro: IPR003597; Ig\_cl.  
DR InterPro: IPR003600; Ig\_like.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR003596; Ig\_v.  
DR Pfam: PF00047; Ig\_4.  
DR SMART: SM00409; IG; 3.  
DR SMART: SM00407; IGcl; 3.  
DR SMART: SM00406; IGv; 1.  
DR SMART: SM00410; IG\_like; 1.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein  
SQ SEQUENCE 487 AA; 52554 MW; 7DC8E96DB333077B CRC64;

Query Match 34.0%; Score 820.5; DB 11; Length 487;  
Best Local Similarity 40.4%; Pred. No. 5.3e-59;  
Matches 188; Conservative 78; Mismatches 170; Indels 29; Gaps 15;

```
QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 EVOLVESGGGLVKPGGSLRLSCAASGFTFSYAMSWVRQTPKRLIEWATISDGGSTYY 79
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 ADSVKGRTISRDNKNTLYLOMNSLRADTAAYVYCAKHTGG--GVWDPIDYWGQGLTV 117
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 PDNVKGRFTISRDNKNTLYLOMNSLRADTAAYVYCARDMGSPYGGYSRFDYWGQGTI 139
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 118 TVSSASTKGPSVFELAPSSKSTSGGTAALGCLVKDYFPE -PVTVMNSGALTSGVHTFPA 176
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 140 TVSSASARNPTIYPLT -LPRALSSDPVIGLCLHDYFPSTGNVTWGRSGKDIITVTFPP 198
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 177 VLQSSGLYSLSSVIVPSSSLGT-QTYICNVNHNKPSNTKVDKKVEPKSCDKTHCPCPA 235
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 199 ALASGGYTMSSQLTLPAVECPGESVKCSVQH--DSNAVQELDVKCGPPPPCPCP- 254
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 236 PELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNHYDGEVHNATKP 295
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 255 PSC--HPSLSLORPALED-LLLGSDASLTCTLNGURNPEGAV -FTW----EPSTGKDAV 305
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 296 REBOYNST---YRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPV 352
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 306 QKAVQNSCGCYSSVSLPGCAERNWNSGAFKCTVTHPESDT -LGTIAKITVTFPPQV 364
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 353 YTLPPSRDELTKNQ-VSLTCLVKGYFSPDAVAVESNGO---PENNYKTPPVLDSDG-- 406
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 365 HLLPPESEALNELVSLTCLVRAFPKPVLRWLHNGNEELSPESYLVFPELKEFEGEGAT 424
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 407 SFFLYSKLTVDKRWQGNVFCVSMHEALHNHYTKQSLSPGK 451
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 425 TYLVTSVLRVSAETWKGQDYQSCMGVHGHEALPMNFTQKTIIDRLSGK 469
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

RESULT 12

Q91WP5 ID Q91WP5 PRELIMINARY; PRT; 479 AA.  
AC Q91WP5;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE HYPOTHETICAL 51.6 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=COLON;  
RA Strausberg R.;  
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC013656; AAH13656.1; -  
KW Hypothetical protein.  
SQ SEQUENCE 479 AA; 51603 MW; ECB2D0877748584F CRC64;

Query Match 32.3%; Score 778.5; DB 11; Length 479;  
Best Local Similarity 39.5%; Pred. No. 1.4e-55;  
Matches 183; Conservative 80; Mismatches 167; Indels 33; Gaps 16;

```
QY 1 QVOLVQSGGLVQPGGSLRLSCAASGFTFRSNAMGWVRQAPGKLEWVSGISGGSTYY 60
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 20 EVOLVESGGGLVKPGGSLRVSCAASGLTFSYAMSWVRQSPKRLIEWAAVAINSGNTYY 79
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 ADSVKGRTISRDNKNTLYLOMNSLRADTAAYVYCAKHTGGGVWDPIDYWGQGLTVTVS 120
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 80 SDTMKGRFTISRDNKNTLYLOMNSLRADTAAYVYCAKHTGGGVWDPIDYWGQGLTVTVS 133
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 121 SASTKGPSVFELAPSSKSTSGGTAALGCLVKDYFPE -PVTVMNSGALTSGVHTFPAVLQ 179
 :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```



```
Q91XE1
ID Q91XE1 PRELIMINARY; PRT; 480 AA.
AC Q91XE1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR IMAGE:4224494) (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=COLON;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010798; AAH10798.1; -.
FT NON_TER 1
SQ SEQUENCE 480 AA; 51936 MW; 20B9234EEF2B41ED CRC64;

Query Match 31.3%; Score 755.5; DB 11; Length 480;
Best Local Similarity 39.6%; Pred. No. 1.1e-53;
Matches 183; Conservative 73; Mismatches 175; Indels 31; Gaps 16;

QY 2 VQLVQSGGLVQPGSLRLSCAASGTFERSNAGWVRQAPGKLEWVSGISGGSTYYA 61
Db 20 VKLVESGGGLVKPGSLRLSCAASGTFISNSYMSWVRQTPKRLWVATISNGYATHYP 79
QY 62 DSVKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGGVWDPIDYWGOGTLTVSS 121
Db 80 DSMKGRFTISRDNKNTLYLQMNLSRAEDTAVYCAKHTGGGVWDPIDYWGOGTLTVSS 135
QY 122 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYPE-PVTVSWNSGALTSGVHTFPAVLQS 180
Db 136 EPAREPTIYPLT-PPQALSSDPVLIIGLIHDYFPGTMTVNTGCKSGKDITTVNFPALAS 194
QY 181 SGLYSLSSVTVFSSSLGT-OTYICNVNHPKSNKVDKVPKSCDKTHTCPPCPAPELL 239
Db 195 GGRTYMSQLTLPAVECEGESYKCSVQH-DSNPVQELNVNCPGICSPPTTPPPSCQ-- 251
QY 240 GGPSVFLFPKPKDITLMISRTPEVTCVVDVSHEDPE-VKFNWYVDGVEVHNAKTPREE 298
Db 252 --PFLSLQRPALSD-LLLSGDSAITCTLNL--RDPEGAVFTW-----EPSTCKDAVQKK 301
QY 299 QYNST---YRWVSVLTVLHODMLNGKEYCKKVSNNKALPAPIEKTISKAKGQPREPQVYTL 355
Db 302 AVQNSCGCYSVSSVLPGCAERNWNGASFKCTVTHPESDT-LTGTTAKVTNTVPPQVHLL 360
QY 356 PPSRDELTKNQ-VSLTCLVKGYFIPSDIAVEWESNGQ---PENNYKTPPVLDSDG---SFF 409
Db 361 PPPSEELALNELLSLTCLVRAFNPKPELVLRHLHNEELSPESYLVEPLKEPGEGATYTL 420
QY 410 LYSKLTVDKSRWQGGNVFSCSVMHREALHNYHTOKSLSLSPGK 451
Db 421 VTSVLRVSAEINWKGQDQYSCWNGHEALPMNFTOKTIDRLSGK 462
```

Search completed: October 9, 2002, 19:12:26  
Job time : 39.5421 secs

Gentcore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:05:30 ; Search time 18.801 Seconds  
(without alignments)  
2024.299 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSLPLVTPGEPAS.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: SPTREMBL\_19.\*
- 2: sp\_archaea.\*
- 3: sp\_bacteria.\*
- 4: sp\_fungi.\*
- 5: sp\_human.\*
- 6: sp\_invertebrate.\*
- 7: sp\_mhc.\*
- 8: sp\_mhc.\*
- 9: sp\_organelle.\*
- 10: sp\_phase.\*
- 11: sp\_plant.\*
- 12: sp\_rodent.\*
- 13: sp\_virus.\*
- 14: sp\_vertebrate.\*
- 15: sp\_unclassified.\*
- 16: sp\_rvirus.\*
- 17: sp\_bacteriaph.\*
- 18: sp\_archaea.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Query Match | Length | ID            | Description         |
|------------|-------------|--------|---------------|---------------------|
| 1          | 795.5       | 69.4   | 238 11 Q99M37 | Q99M37 mus musculus |
| 2          | 635         | 55.4   | 214 11 Q9RIA5 | Q9RIA5 mus musculus |
| 3          | 628         | 54.8   | 211 11 Q9IXL0 | Q9IXL0 mus musculus |
| 4          | 624.5       | 54.5   | 235 11 Q9IWF8 | Q9IWF8 mus musculus |
| 5          | 621         | 54.2   | 234 11 Q9IWF8 | Q9IWF8 mus musculus |
| 6          | 609         | 53.1   | 233 11 Q9IWS9 | Q9IWS9 mus musculus |
| 7          | 428.5       | 37.4   | 114 4 Q9UL80  | Q9UL80 homo sapien  |
| 8          | 407         | 35.5   | 236 4 Q96E61  | Q96E61 homo sapien  |
| 9          | 406         | 35.4   | 104 11 Q9UL82 | Q9UL82 mus musculus |
| 10         | 376.5       | 32.9   | 235 11 Q99M11 | Q99M11 mus musculus |
| 11         | 373         | 32.5   | 109 4 Q9UL78  | Q9UL78 homo sapien  |
| 12         | 370.5       | 32.3   | 233 11 Q9IV32 | Q9IV32 m adult mal  |
| 13         | 369         | 32.2   | 109 4 Q9UL86  | Q9UL86 homo sapien  |
| 14         | 364.5       | 31.8   | 233 4 Q96I69  | Q96I69 homo sapien  |
| 15         | 351.5       | 30.7   | 108 4 Q9UL83  | Q9UL83 homo sapien  |
| 16         | 340.5       | 29.7   | 111 11 Q920E9 | Q920E9 mus musculus |

|    |       |      |               |                     |
|----|-------|------|---------------|---------------------|
| 17 | 325.5 | 28.4 | 107 11 Q9ER29 | Q9ER29 mus musculus |
| 18 | 322   | 28.1 | 107 4 Q9UL81  | Q9UL81 homo sapien  |
| 19 | 322   | 28.1 | 109 4 Q9UL85  | Q9UL85 homo sapien  |
| 20 | 316.5 | 27.6 | 108 4 Q9UL77  | Q9UL77 homo sapien  |
| 21 | 316   | 27.6 | 116 4 Q96PF6  | Q96PF6 homo sapien  |
| 22 | 313   | 27.3 | 106 5 Q9U410  | Q9U410 schistosoma  |
| 23 | 309.5 | 27.0 | 108 4 Q9UL79  | Q9UL79 homo sapien  |
| 24 | 308   | 26.9 | 107 4 Q96SA9  | Q96SA9 homo sapien  |
| 25 | 307.5 | 26.8 | 298 11 Q9QIF0 | Q9QIF0 mus musculus |
| 26 | 303.5 | 26.7 | 108 4 Q9UL70  | Q9UL70 homo sapien  |
| 27 | 296.5 | 25.6 | 109 11 Q920E6 | Q920E6 mus musculus |
| 28 | 284.5 | 24.8 | 103 11 Q9JL80 | Q9JL80 mus musculus |
| 29 | 283.5 | 24.7 | 99 11 Q9JL74  | Q9JL74 mus musculus |
| 30 | 276.5 | 24.1 | 101 11 Q9JL78 | Q9JL78 mus musculus |
| 31 | 265.5 | 23.2 | 97 11 Q9JL76  | Q9JL76 mus musculus |
| 32 | 255.5 | 22.3 | 127 11 Q925S9 | Q925S9 mus musculus |
| 33 | 249.5 | 21.8 | 109 6 Q9N0W5  | Q9N0W5 oryctolagus  |
| 34 | 240.5 | 21.0 | 107 11 Q9JL84 | Q9JL84 mus musculus |
| 35 | 234   | 20.4 | 130 11 Q9D8W4 | Q9D8W4 mus musculus |
| 36 | 223   | 19.5 | 108 4 Q96S80  | Q96S80 homo sapien  |
| 37 | 222   | 19.4 | 241 11 Q92IA6 | Q92IA6 mus musculus |
| 38 | 217   | 18.9 | 268 13 Q90524 | Q90524 ginglymosto  |
| 39 | 213.5 | 18.6 | 107 4 Q9UL82  | Q9UL82 homo sapien  |
| 40 | 211.5 | 18.5 | 218 11 Q925S1 | Q925S1 mus musculus |
| 41 | 204.5 | 17.8 | 267 13 Q90529 | Q90529 ginglymosto  |
| 42 | 202.5 | 17.7 | 112 4 Q96JD1  | Q96JD1 homo sapien  |
| 43 | 201   | 17.5 | 107 4 Q9NSD6  | Q9NSD6 mus musculus |
| 44 | 201   | 17.5 | 509 11 Q9QX57 | Q9QX57 mus musculus |
| 45 | 201   | 17.5 | 513 11 P97797 | P97797 mus musculus |

# ALIGNMENTS

RESULT 1

Q99M37 ID Q99M37 PRELIMINARY: PRT; 238 AA.

AC Q99M37; DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE HYPOTHETICAL 26.3 KDA PROTEIN.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, CROSS  
RC TISSUE.;  
RA Strausberg R.;  
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC002035; AA02035.1; -  
DR HSSP; P01679; 2FBJ.  
DR InterPro; IPR003599; Ig.  
DR InterPro; IPR003597; Ig\_c1.  
DR InterPro; IPR003600; Ig\_like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_LV.  
DR Pfam; PF00047; Ig; 2.  
DR SMART; SM00409; IG; 2.  
DR SMART; SM00407; IGc1; 1.  
DR SMART; SM00406; IGV; 1.  
DR SMART; SM00410; IG\_like; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
KW Hypothetical protein.

SQ SEQUENCE 238 AA; 26344 MW; F82B06A0B801330A CRC64;

Query Match 69.4%; Score 795.5; DB 11; Length 238;  
Best Local Similarity 67.7%; Pred No. 1e-67;  
Matches 149; Conservative 31; Mismatches 39; Indels 1; Gaps 1;  
QY 1 EIVLTQSLPLVTPGEPASISCRSSQSLLSNGVYTYLDWYLOKPGQSPQLLYSGSHRA 60

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20 DVVWTCPTLSLPSVLGDDQASISCRSSQSIHVHSGNTYLEWYLOKPGSPKLLIYKVSNNR 79
 ::||:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:
61 SGVDPDRFSGSGVSGDTFTLRISRVEADGVYCYCMGQLSPFTFGPCTKVDIKRGTVAAPS 120
 ||:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:
80 SGVDPDRFSGSGSGDTFTLRISRVEADGVYCYFQGSHPYTFGSGTKLEIKRAD-AAPT 138
 ||:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:
121 VFIFPPSDQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS 180
 |||||:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:
139 VSIFPPSSQSLTSGGASVVCFLNNFYPKDINVKKWIDGSRQGVLSWTDQDSKDSYSTS 198
 |||||:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:
181 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 220
 :||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
199 MSSTLTLTKDEVERHNSYTCEATHKSTSTSPVTKSFNRNEC 238
 :||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:

RESULT 2
Q9RIA5 PRELIMINARY: PRT; 214 AA.
ID Q9RIA5
AC Q9RIA5;
DC Q9RIA5;
DD 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotated)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RS SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RP "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RT Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AF152371; AAD40242.1; -.
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR SMART; SM00410; Ig_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
FT NON_TER 214
SQ SEQUENCE 214 AA; 52922 MW; 52BA205FDE995E2A CRC64;

Query Match 55.4%; Score 635; DB 11; Length 214;
Best Local Similarity 55.0%; Pred. No. 1.6e-52;
Matches 121; Conservative 37; Mismatches 56; Indels 6; Gaps

QY 1 EVLTQSPSLSPVTPGPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 60
 :|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:
DB 1 DIQLTQSPSSMYASLGERTVITCKASQDI----NSYLSWFQQRPGKSPKTLIYRANRLV 55
 :|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:
QY 61 SGVDPDRFSGSVGDTFTLRISRVEADGVYCYCMGQLSPFTFGPCTKVDIKRGTVAAPS 120
 ||:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:
DB 56 DGVPRFSGSGGSDGYSLTISSEYEDNGIYYCLOYDFEPTFGSGTKLEIKRAD-AAPT 114
 |||||:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:
QY 121 VFIFPPSDQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYSTS 180
 |||||:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:
DB 115 VSIFPPSSQSLTSGGASVVCFLNNFYPKDINVKKWIDGSRQGVLSWTDQDSKDSYSTS 174
 |||||:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:||||:|:|:|:
QY 181 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 220
 :||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
DB 175 MSSTLTLTKDEVERHNSYTCEATHKSTSTSPVTKSFNRNEC 214

RESULT 3
Q91XLO PRELIMINARY: PRT; 211 AA.
ID Q91XLO
AC Q91XLO;

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Db 197 RAASSYLSLTPQMKSHRSYCQVTHGEG--STVEKTVAPTEC 235
 : || ||| : : || ||| : | ||| : | ||| : | ||| :
RESULT 9
Q9JL82 PRELIMINARY; PRT; 104 AA.
Q9JL82;
AC Q9JL82;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=2044942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin."
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206024; AAF69322.1; -.
DR HSSP; P01607; IREI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1
FT TER 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AA1AE CRC64;

Query Match 35.4%; Score 406; DB 11; Length 104;
Best Local Similarity 75.0%; Pred. No. 3.8e-31;
Matches 78; Conservative 12; Mismatches 14; Indels 0; Gaps

QY 9 LSUPVTGPPEASICRQSLLHNSGYTLDWLYLKPGSPQLLIYSGSHRASGVPDFRS 68
||| : | ||||| ||||| : || ||||| ||||| : ||||| ||||| : |||||
Db 1 LSUPVLGSQDASICRQSGLVHTNGNTYLHWLYLKPGSPKLLIYKYSNRFSGVPDFRS 60
||| : | ||||| ||||| : || ||||| ||||| : ||||| ||||| : |||||
QY 69 GSYSGTDFLTRISRYEAEDVGVIYCMOGLQSPFTFGPGTKVDIK 112
|| ||||| ||||| ||||| ||||| : ||| : | ||||| ||||| : |||
Db 61 GSGSGTDFTLKISRVEAEDLGVYFCSTHTVPYTFGGGTKLEIK 104
|| ||||| ||||| ||||| ||||| ||||| : ||| : | ||||| ||||| : |||

RESULT 10
Q99M11 PRELIMINARY; PRT; 235 AA.
AC Q99M11;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOPHETICAL 25.4 KDa PROTEIN.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN RP SEQUENCE FROM N.A.
RC STRAIN=R.j;
RX Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC001219; AH02129.1; -.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig_2.
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DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR SMART; SM00410; IGv; 1.
DR SMART; SM00410; IGv; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25403 MW; 39807BFE6782A3FB CRC64;

Query Match 32.98; Score 376.5; DB 11; Length 235;
Best Local Similarity 38.88; Pred. No. 7.3e+28;
Matches 87; Conservative 39; Mismatches 85; Indels 13; Gaps 6;

QY 1 EIVLQSPFLSPVTPGEPASISCRSSQSLHNSNGYVLDWYLOKPGSQSPQLLIYSGSHRA 60
Db :||||| :
20 QLVLTQ-PSSVSTSLGSAKLPCRSTGNI--GDSVNNYQYMGSRPTNMIYGDLLRP 75
QY 61 SGVPRFSGSV--SGTDFTLIRISVEAEADVGVVYCMQGLQSPFTFGPKVKDIKRGTVAA 118
Db :||||| :
76 SGVDRFSGSIDSSNSAFLTIQVQADDEADYVCSYSGIRVFGGKTLVLSPQPKTS 135
QY 119 PSVFIFFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSK--D 176
Db :||||| :
136 PSVTLFPSPSRELEFNKATLVCTISDFYPGVTVDMKADG---TPVTQGVETTPQSKQNN 192
QY 177 STYSLSSTLTLSKADYEHKKHYACEVTHQGLSLSPVTKSFNRGEC 220
Db : ||||| :
193 NKYMASSTLTAKAWETHSSYSCQVTHEG--HTVEKSLSRADC 234

RESULT 12
Q9UL78 PRELIMINARY; PRT; 109 AA.
AC Q9UL78;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RL fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035036; AAD56272.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
FT NON_TER 1
FT NON_TER 109
SQ SEQUENCE 109 AA; 11646 MW; 5F675C52EC7EE197 CRC64;

Query Match 32.58; Score 373; DB 4; Length 109;
Best Local Similarity 66.48; Pred. No. 5.6e+28;
Matches 75; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

QY 1 EIVLQSPFLSPVTPGEPASISCRSSQSLHNSNGYVLDWYLOKPGSQSPQLLIYSGSHRA 60
Db :||||| :
1 EIVLQSPCTLSLSPGERATLSCRASQSVSS---YLAWYQOKPGCAPRELLIYGASSRA 56

QY 61 SGVPRFSGSVSGTDFTLIRISVEAEADVGVVYCMQGLQSPFTFGPKVKVDIKR 113
Db :||||| :
57 TGIPDRFSGSGSTDFTLIRSLRPEDCANYYCQYQYMGSSPLTFGGTKVKEIKR 109
```

```
Query Match 32.3%; Score 370.5; DB 11; Length 233;
Best Local Similarity 38.3%; Pred. No. 2.7e-27;
Matches 85; Conservative 42; Mismatches 84; Indels 11; Gaps 6;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLIIYSGSHRA 60
DB 20 QAVVTOGES-ALTTSPGETVTLTCSRSTGAVTTSNYA--NMVQKPDHLFTGLIGGTNNRA 76
QY 61 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVGYCMQGLQSPFTFGPGKVDIKRGTVAAPS 120
DB 77 PGVPARESGSLIGDKAAALITGAQTEDEAIFCALWYSS-WFEGGCTKLVLGPKSPSPS 135
QY 121 VFIPPSDQLKSGTASVCLLNNEYPREAKVQWKVDNALQSGNSQSVTEQDSKST-- 178
DB 136 VTLPSPSELETKATLVCTITDFYGVGVVDWVKDVG--TPVTQGMETQPSKOSNNK 192
QY 179 YLSSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 220
DB 193 YMASSTLTLTARAWERHSSYSCQVTHEG--HTVEKSLSRADC 232

RESULT 13
Q9UL86 PRELIMINARY; PRT; 109 AA.
ID Q9UL86
AC Q9UL86;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1;
DR HSSP; P80362; IWLTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 109
FT SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 32.2%; Score 369; DB 4; Length 109;
Best Local Similarity 67.3%; Pred. No. 1.3e-27;
Matches 76; Conservative 11; Mismatches 22; Indels 4; Gaps 1;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLIIYSGSHRA 60
DB 1 EIVLTQSPVLPVTPGERATLSRASQSVSSS----YLAWYQKPGQAPRLIIYGTSSRA 56
QY 61 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVGYCMQGLQSPFTFGPGKVDIKR 113
DB 57 TGIPDRFSGSGSETDFTLTIRLEPEDFAVYICQYQSGSIITFGPGTKVDIKR 109

RESULT 14
Q96169 PRELIMINARY; PRT; 233 AA.
ID Q96169
AC Q96169;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UNKNOWN (PROTEIN FOR MGC:12849).
```

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=PRIMARY B-CELLS FROM TONSILS;
RA Strausberg R.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC007782; AAH07782.1;
SQ SEQUENCE 233 AA; 24802 MW; C694F8397B27650B CRC64;

Query Match 31.8%; Score 364.5; DB 4; Length 233;
Best Local Similarity 36.7%; Pred. No. 9.9e-27;
Matches 81; Conservative 44; Mismatches 83; Indels 13; Gaps 6;

QY 3 VLQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLIIYSGSHRASG 62
DB 22 VLQV-PASVSVAPGQTARTICGS-----NLGSKSVNMYQLRPGQAPLVVYENKERPA 75
QY 63 VPDPRFSGSVSGTDFTLRISRVEAEDGVGYCM--OGLQSPFTFGPGTKVDIKRGTVAAP 120
DB 76 IPERLSALTSEETATLTISVWAGDEADYFCQVWDTTQQYVFGTGTQTVLGPKANPT 135
QY 121 VFIPPSDEOLKSGTASVCLLNNEYPREAKVQWKVDNA-LQSGNSQSVTEQDSKSTY 179
DB 136 VTLPSPSELETKATLVCLISDFYPGAVYAWKADGSPVKAG--VETTKPSQSNKY 193
QY 180 SLSTLTLSKADYEHKVKYACEVTHQGLSSPVTKSFNRGEC 220
DB 194 AASSYLSLTPEQWKSHRSYSCQVTHEG--STVEKTVAPTEC 232

RESULT 15
Q9UL83 PRELIMINARY; PRT; 108 AA.
ID Q9UL83
AC Q9UL83;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1;
DR HSSP; P80362; IWLTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
FT NON_TER 108
FT SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 30.7%; Score 351.5; DB 4; Length 108;
Best Local Similarity 63.7%; Pred. No. 6.1e-26;
Matches 72; Conservative 14; Mismatches 22; Indels 5; Gaps 2;

QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLDWYLOKPGSPOLLIIYSGSHRA 60
DB 1 EIVMTQSPATLSVSPGERATLSRASQSVSSN----LAWYQKPGQAPRLIIYCASTR 55
QY 61 SGVDPFRFSGSVSGTDFTLRISRVEAEDGVGYCMQGLQSPFTFGPGTKVDIKR 113
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Db 56 TGIPARESGSGCTEFTLTIISSLQFEDEFAVYYCQHYNWPFTEGPGTKYDIKR 108

Search completed: October 9, 2002, 19:12:25  
Job time : 19.801 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:12:30 ; Search time 23.5714 Seconds  
(without alignments)  
1036.689 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 220

Sequence: 1 EIVLTQSLPLPVTGPAPAS.....EVTHQGLSPVTKSFNRGFC 220

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 747574 seqs, 111073796 residues

Word size : 0

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A\_Geneseq\_032802.\*

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
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- 11: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1990.DAT.\*
- 12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT.\*
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- 21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description                 |
|------------|-------|-------------|--------|-------|-----------------------------|
| 1          | 220   | 100.0       | 220    | 22    | AAE12714 Human recombinant  |
| 2          | 114   | 51.8        | 381    | 22    | AAE12707 Human blypH1-IL-2  |
| 3          | 113   | 51.4        | 113    | 22    | AAE12705 Human PHL Fab anti |
| 4          | 110   | 50.0        | 236    | 21    | AAV56286 HCAT1 clone 25 ant |
| 5          | 107   | 48.6        | 107    | 22    | AAE62265 Light chain constr |
| 6          | 107   | 48.6        | 108    | 20    | AAW06002 Amino acid sequenc |
| 7          | 107   | 48.6        | 108    | 21    | AAV92191 Human IgG1 kappa d |
| 8          | 107   | 48.6        | 234    | 15    | AAAS2951 Human anti-IgE Mab |
| 9          | 107   | 48.6        | 468    | 21    | AAV92196 Human IL-6R-alpha- |
| 10         | 107   | 48.6        | 727    | 21    | AAV92192 Human gp130-kappa  |
| 11         | 106   | 48.2        | 106    | 9     | AAE81028 C region of L chai |

|    |     |      |     |    |          |                    |
|----|-----|------|-----|----|----------|--------------------|
| 12 | 106 | 48.2 | 106 | 14 | AAE1687  | Undefined ORF1 enc |
| 13 | 106 | 48.2 | 106 | 14 | AAE43686 | Human kappa consta |
| 14 | 106 | 48.2 | 106 | 18 | AAW37347 | Immunoglobulin C-k |
| 15 | 106 | 48.2 | 106 | 19 | AAW59622 | Anti-RSV F protein |
| 16 | 106 | 48.2 | 106 | 19 | AAW48649 | Constant region of |
| 17 | 106 | 48.2 | 106 | 22 | AAW04072 | Interleukin recept |
| 18 | 106 | 48.2 | 107 | 19 | AAW40578 | Human kappa CL dom |
| 19 | 106 | 48.2 | 107 | 20 | AAV50152 | Human kappa light  |
| 20 | 106 | 48.2 | 107 | 20 | AAV08745 | Human kappa-CL dom |
| 21 | 106 | 48.2 | 107 | 20 | AAW92425 | Human kappa protei |
| 22 | 106 | 48.2 | 107 | 21 | AAE27000 | Human kappa CL dom |
| 23 | 106 | 48.2 | 143 | 10 | AAE93559 | Sequence of human  |
| 24 | 106 | 48.2 | 193 | 22 | AAE52145 | Humanised HmFGL 11 |
| 25 | 106 | 48.2 | 201 | 20 | AAV29770 | P-selectin ligand  |
| 26 | 106 | 48.2 | 213 | 17 | AAW04301 | Antibody fusion pr |
| 27 | 106 | 48.2 | 213 | 17 | AAW05830 | Humanised M291 ant |
| 28 | 106 | 48.2 | 213 | 22 | AAE10510 | Humanised high pot |
| 29 | 106 | 48.2 | 213 | 22 | AAE10512 | Humanised high pot |
| 30 | 106 | 48.2 | 213 | 22 | AAE10514 | Humanised high pot |
| 31 | 106 | 48.2 | 213 | 22 | AAE10516 | Humanised high pot |
| 32 | 106 | 48.2 | 213 | 22 | AAE10518 | Humanised high pot |
| 33 | 106 | 48.2 | 213 | 22 | AAE10520 | Humanised high pot |
| 34 | 106 | 48.2 | 213 | 22 | AAE10522 | Humanised high pot |
| 35 | 106 | 48.2 | 213 | 22 | AAE10524 | Humanised high pot |
| 36 | 106 | 48.2 | 213 | 22 | AAE10526 | Humanised high pot |
| 37 | 106 | 48.2 | 213 | 22 | AAE83157 | Humanised high pot |
| 38 | 106 | 48.2 | 214 | 14 | AAE30776 | Ganglioside GM2 an |
| 39 | 106 | 48.2 | 214 | 14 | AAE30776 | H52L6-158 murine a |
| 40 | 106 | 48.2 | 214 | 14 | AAE33338 | Completely humanis |
| 41 | 106 | 48.2 | 214 | 17 | AAW05828 | Humanised ID10 ant |
| 42 | 106 | 48.2 | 214 | 18 | AAW45517 | NANUC-2 light chai |
| 43 | 106 | 48.2 | 214 | 18 | AAW34504 | Light chain of hum |
| 44 | 106 | 48.2 | 214 | 18 | AAW34506 | Light chain of ful |
| 45 | 106 | 48.2 | 214 | 18 | AAW07615 | Ulcerative colitis |
|    |     |      | 214 | 19 | AAW64671 | Human UC PANCA mon |

## ALIGNMENTS

|          |                                                                         |                                     |
|----------|-------------------------------------------------------------------------|-------------------------------------|
| RESULT 1 | AAE12714                                                                | AAE12714 standard; Protein; 220 AA. |
| ID       | AAE12714                                                                | standard; Protein; 220 AA.          |
| XX       |                                                                         |                                     |
| AC       | AAE12714;                                                               |                                     |
| XX       |                                                                         |                                     |
| DT       | 04-JAN-2002                                                             | (first entry)                       |
| XX       |                                                                         |                                     |
| DE       | Human recombinant immunoglobulin (Ig) light chain region.               |                                     |
| XX       |                                                                         |                                     |
| KW       | Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;        |                                     |
| KW       | light chain region; cancer; breast; lung; bladder;                      |                                     |
| KW       | cytostatic; therapy; immunoglobulin; Ig.                                |                                     |
| XX       |                                                                         |                                     |
| OS       | Homo sapiens.                                                           |                                     |
| XX       |                                                                         |                                     |
| PN       | WO200175110-A2.                                                         |                                     |
| XX       |                                                                         |                                     |
| PD       | 11-OCT-2001.                                                            |                                     |
| XX       |                                                                         |                                     |
| PF       | 30-MAR-2001; 2001WO-US10589.                                            |                                     |
| XX       |                                                                         |                                     |
| PR       | 30-MAR-2000; 2000US-0538913.                                            |                                     |
| XX       |                                                                         |                                     |
| PA       | (DYAX-) DYAX CORP.                                                      |                                     |
| XX       |                                                                         |                                     |
| PI       | Hoogenboom HRJM, Henderikx MPG;                                         |                                     |
| XX       |                                                                         |                                     |
| DR       | WPI; 2001-626437/72.                                                    |                                     |
| DR       | N-PSDB; AAD20744.                                                       |                                     |
| XX       |                                                                         |                                     |
| PT       | Novel isolated tumor-associated antigen mucin-1-specific binding member |                                     |
| PT       | for diagnosing and treating cancer, comprises mucin-1 binding domain or |                                     |
| PT       | its portion for binding to an epitope of the protein core of mucin-1    |                                     |

```

XX PS Claim 12; Page 103; 126pp; English.
XX CC
XX CC The invention relates to an isolated tumour-associated antigen mucin-1
XX CC (MUC-1)-specific binding member comprising an antigen binding domain
XX CC region having an antibody variable light (VL) or heavy (VH) region,
XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
XX CC MUC1-specific binding member is useful for treating cancer, preferably
XX CC adenocarcinoma, in an individual, where the cancer is present in tissue
XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX CC binding member is useful for diagnosing and imaging MUC1-expressing
XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,
XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX CC containing molecules, and for therapeutically or prophylactically
XX CC treating cancer. The present sequence is human recombinant immunoglobulin
XX CC (Ig) light chain region (variable VL and CL constant kappa light chain).
XX SQ Sequence 220 AA;
Query Match 100.0%; Score 220; DB 22; Length 220;
Best Local Similarity 100.0%; Pred. No. 1.6e-197;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGOSPLLIIYSGSHRA 60
DB 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGOSPLLIIYSGSHRA 60
QY 61 SGVPDRFSGSVSGTDFTLIRSRVEAEDGVYVYCMQGLQSPFTFGPTGKVDIKRGTVAAAPS 120
DB 61 SGVPDRFSGSVSGTDFTLIRSRVEAEDGVYVYCMQGLQSPFTFGPTGKVDIKRGTVAAAPS 120
QY 121 VFIFPPSDEQLKSGTASVYVCLLNPNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS 180
DB 121 VFIFPPSDEQLKSGTASVYVCLLNPNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSITYS 180
QY 181 LSSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 220
DB 181 LSSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 220
RESULT 2
AAE12707
ID AAE12707 standard; Protein; 381 AA.
XX AC AAE12707;
XX DT 04-JAN-2002 (first entry)
XX DE Human bivPH1-IL-2 immunocytokine protein.
XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; cancer;
XX KW breast; ovary; lung; bladder; cytostatic; therapy; immunocytokine.
XX OS Homo sapiens.
XX PN WO200175110-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US10589.
XX PR 30-MAR-2000; 2000US-0538913.
XX PA (DYAX-) DYAX CORP.
XX PI Hoogenboom HRJM, Henderikx MPG;
XX DR WPI: 2001-626437/72.
XX DR N-PSDB; AAD20732.

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```

XX PT Novel isolated tumor-associated antigen mucin-1-specific binding member
XX PT for diagnosing and treating cancer, comprises mucin-1 binding domain or
XX PT its portion for binding to an epitope of the protein core of mucin-1 -
XX PS Claim 9; Page 95-97; 126pp; English.
XX CC The invention relates to an isolated tumour-associated antigen mucin-1
XX CC (MUC-1)-specific binding member comprising an antigen binding domain
XX CC region having an antibody variable light (VL) or heavy (VH) region,
XX CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific
XX CC binding member is useful for diagnosing cancer, preferably adenocarcinoma
XX CC The binding of MUC1-specific binding member to MUC1 is detected by a
XX CC detection method selected from enzyme-linked immunosorbent assay,
XX CC magnetic resonance imaging, scintillation counting, and X-ray film.
XX CC MUC1-specific binding member is useful for treating cancer, preferably
XX CC adenocarcinoma, in an individual, where the cancer is present in tissue
XX CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific
XX CC binding member is useful for diagnosing and imaging MUC1-expressing
XX CC cancer cells and tissues, for purifying or isolating non-glycosylated,
XX CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-
XX CC containing molecules, and for therapeutically or prophylactically
XX CC treating cancer. The present sequence is human bivPH1-IL-2
XX CC immunocytokine protein. bivPH1 is mucin specific binding portion.
XX SQ Sequence 381 AA;
Query Match 51.8%; Score 114; DB 22; Length 381;
Best Local Similarity 100.0%; Pred. No. 3.1e-98;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGOSPLLIIYSGSHRA 60
DB 127 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGOSPLLIIYSGSHRA 186
QY 61 SGVPDRFSGSVSGTDFTLIRSRVEAEDGVYVYCMQGLQSPFTFGPTGKVDIKRG 114
DB 187 SGVPDRFSGSVSGTDFTLIRSRVEAEDGVYVYCMQGLQSPFTFGPTGKVDIKRG 240
RESULT 3
AAE12705
ID AAE12705 standard; Protein; 113 AA.
XX AC AAE12705;
XX DT 04-JAN-2002 (first entry)
XX DE Human PH1 Fab antibody variable light chain region (VL).
XX KW Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma; VL;
XX KW variable light chain region; cancer; breast; ovary; lung; bladder;
XX KW cytostatic; therapy; PH1 antibody.
XX OS Homo sapiens.
XX PN WO200175110-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US10589.
XX PR
XX PA
XX PI
XX DR

```



PR 30-MAR-2000; 2000US-0538913.  
 PA (DYAX-) DYAX CORP.  
 XX  
 XX  
 PI Hoogenboom HRJM, Henderikx MPG;  
 XX  
 XX WPI; 2001-626437/72.  
 DR N-PSDB; AAD20730.  
 XX  
 XX Novel isolated tumor-associated antigen mucin-1-specific binding member  
 PT for diagnosing and treating cancer, comprises mucin-1 binding domain or  
 PT its portion for binding to an epitope of the protein core of mucin-1 -  
 XX  
 XX Claim 3; Page 93; 126pp; English.  
 XX  
 XX The invention relates to an isolated tumour-associated antigen mucin-1  
 CC (MUC-1)-specific binding member comprising an antigen binding domain  
 CC region having an antibody variable light (VL) or heavy (VH) region,  
 CC or a complementarity determining region (CDR) of VL or VH. MUC1-specific  
 CC binding member is useful for diagnosing cancer, preferably adenocarcinoma  
 CC The binding of MUC1-specific binding member to MUC1 is detected by a  
 CC detection method selected from enzyme-linked immunosorbent assay,  
 CC magnetic resonance imaging, scintillation counting, and x-ray film.  
 CC MUC1-specific binding member is useful for treating cancer, preferably  
 CC adenocarcinoma, in an individual, where the cancer is present in tissue  
 CC of the breast, ovary, lung, or bladder of the individual. MUC1-specific  
 CC binding member is useful for diagnosing and imaging MUC1-expressing  
 CC cancer cells and tissues, for purifying or isolating non-glycosylated,  
 CC underglycosylated or cancer-associated forms of MUC1 or MUC1 epitope-  
 CC containing molecules, and for therapeutically or prophylactically  
 CC treating cancer. The present sequence is anti-MUC1 human PhI Fab  
 CC antibody VL region.  
 XX  
 XX Sequence 113 AA;  
 SQ  
 Query Match 51.4%; Score 113; DB 22; Length 113;  
 Best Local Similarity 100.0%; Pred. No. 8.9e-98;  
 Matches 113; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EIVLTQSPLSLPTGEPASISCRSSQLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60  
 DB 1 EIVLTQSPLSLPTGEPASISCRSSQLHNSGYTLDWYLOKPGQSPQLLIYSGSHRA 60  
 QY 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVYCMQGLQSPFTFGPTKVDIKR 113  
 DB 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVYCMQGLQSPFTFGPTKVDIKR 113  
 RESULT 4  
 AAY56286  
 ID AAY56286 standard; Protein; 236 AA.  
 XX  
 XX AAY56286;  
 XX  
 XX 08-FEB-2000 (first entry)  
 XX  
 XX HCAT1 clone 25 antibody variable light chain protein sequence.  
 DE  
 XX Human cationic amino acid transporter; hCAT1; targeted delivery;  
 KW gene delivery; virus-like particle; retroviral envelope molecule;  
 KW infection; gene therapy; restenosis; balloon angioplasty;  
 KW smooth muscle cell; transduction.  
 XX  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX EP959136-A1.  
 XX  
 XX 24-NOV-1999.  
 PD  
 XX 20-MAY-1998; 98EP-0201693.  
 PF  
 XX 20-MAY-1998; 98EP-0201693.  
 PR

XX (INTR-) INTROGENE BV.  
 PA  
 XX WPI: 2000-001283/01.  
 DR N-PSDB; AA238770.  
 XX  
 XX New virus-like particle or gene delivery vehicle, useful for gene  
 PT therapy -  
 PT  
 XX Claim 13; Fig 16; 66pp; English.  
 PS  
 XX The present invention describes a virus-like particle or gene delivery  
 CC vehicle comprising a ligand capable of binding to a human amino acid  
 CC transporter. The method is useful for the target delivery of substances  
 CC to cells e.g. gene therapy. A human cationic amino acid transporter  
 CC (hCAT1) targeted adenovirus is useful for local applications of  
 CC adenoviral vector e.g. in patients with restenosis following balloon  
 CC angioplasty where smooth muscle cells need to be transduced with an  
 CC adenoviral vector carrying the cENOS cDNA. More efficient transduction  
 CC of tissues can be carried out therefore resulting in lower  
 CC multiplicity's of infections that can be used and therefore less vector  
 CC associated toxicity to the tissues surrounding the target cells. AA238737  
 CC to AA238770, and AAY56264 to AAY56287 represent sequences used in the  
 CC exemplification of the present invention.  
 XX  
 XX Sequence 236 AA;  
 SQ  
 Query Match 50.0%; Score 110; DB 21; Length 236;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-94;  
 Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 111 IRKGTVAAPSVTFPPSDQLKSGTASVVCLLNLFYPREAKVQWKVDNALQSGNSQESVT 170  
 DB 127 IRKGTVAAPSVTFPPSDQLKSGTASVVCLLNLFYPREAKVQWKVDNALQSGNSQESVT 186  
 QY 171 EQDSKDYSLSTLTLSKADYEKHVKVACEVTHOGLSSPVTKSFNRGEC 220  
 DB 187 EQDSKDYSLSTLTLSKADYEKHVKVACEVTHOGLSSPVTKSFNRGEC 236  
 RESULT 5  
 AAB62265  
 ID AAB62265 standard; Protein; 107 AA.  
 XX  
 XX AAB62265;  
 XX  
 XX 11-JUN-2001 (first entry)  
 DT  
 XX Light chain construct 431A amino acid fragment.  
 DE  
 XX Fusion protein; cell surface antigen; cancer; monoclonal antibody;  
 KW light chain construct; carcinoembryonic.  
 KW  
 XX Mammalia.  
 OS  
 XX WO200119842-A1.  
 PN  
 XX 22-MAR-2001.  
 PD  
 XX 18-SEP-2000; 2000WO-US25558.  
 PF  
 XX 17-SEP-1999; 99US-0399079.  
 PR  
 XX (GENZ ) GENZYME TRANSGENICS CORP.  
 PA  
 XX Pollock D, Meade HM, Bosslet K;  
 XX  
 XX WPI: 2001-257871/26.  
 DR N-PSDB; AAF57571.  
 DR  
 XX New fusion protein, useful for killing diseased cells e.g. cancer  
 PT cells, comprises fused first and second units, such that the protein  
 PT assembles into complex which optimizes activity of multimeric form of

PT second unit -  
XX Example 1; Fig 1B; 88pp; English.  
XX  
CC The invention relates to a fusion protein (I) comprising a first member  
CC fused to a second member, where the first and second members are chosen  
CC such that (I) assembles into a complex having a number of subunits which  
CC optimizes activity of the multimeric form of the second member. (I) is  
CC useful for selectively killing an aberrant or diseased cell which  
CC expresses a target antigen on its surface, e.g., a cancer cell expressing  
CC a cell surface antigen. (I) is also useful for detecting in vitro or in  
CC vivo the presence of target antigen in a sample, e.g., for diagnosing a  
CC disease, by contacting a sample or a control sample that allows  
CC interaction of (I) which is labeled, and detecting formation of a  
CC complex. (I) is also useful for selectively directing (e.g., localizing)  
CC the second unit of (I) to the vicinity of an undesirable cell. The  
CC present sequence represents a fragment of a light chain construct 431A  
CC that was generated using the light chain sequence from a humanised Mab  
CC against carcinoembryonic antigen (431).  
XX  
SQ Sequence 107 AA;  
Query Match 48.6%; Score 107; DB 22; Length 107;  
Best Local Similarity 100.0%; Pred. No. 3.4e-92;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 114 GTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 173  
DB 1 GTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 60  
QY 174 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
DB 61 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
RESULT 6  
AAW70802  
ID AAW70802 standard; protein; 108 AA.  
XX  
AC AAW70802;  
XX  
DT 03-FEB-1999 (first entry)  
DE Amino acid sequence of the kappa domain.  
XX  
KW gp130; cytokine antagonist; interleukin; gamma-interferon;  
KW granulocyte macrophage colony-stimulating factor; J peptide;  
KW transforming growth factor-beta.  
XX  
OS Synthetic.  
XX  
PN US5844099-A.  
XX  
PD 01-DEC-1998.  
XX  
PF 27-NOV-1995; 95US-0563105.  
XX  
PR 27-NOV-1995; 95US-0563105.  
PR 20-OCT-1993; 93US-0140222.  
XX  
PA (REGE-) REGENERON PHARM INC.  
XX  
PI Economides A, Stahl N, Yancopoulos GD;  
XX  
DR WPI; 1999-044669/04.  
XX  
PT Cytokine antagonists - comprising extracellular domains of  
PT specificity-determining and signal-transducing components of  
PT cytokine receptor  
XX  
PS \*Example, 4; Fig 13; 46pp; English.  
XX  
CC The present sequence represents the amino acid sequence of

CC kappa domain. The protein is used in the course of the invention.  
CC The specification describes cytokine antagonists comprising only the  
CC extracellular domain of the specificity-determining component of  
CC the cytokine receptor and the extracellular domain of a  
CC signal-transducing component of the cytokine receptor. The cytokine  
CC is an interleukin (IL-1, IL-2, IL-3, IL-4, IL-5 or IL-15),  
CC granulocyte macrophage colony-stimulating factor (GM-CSF),  
CC gamma-interferon or transforming growth factor-beta (TGF-beta). The  
CC antagonist is capable of binding the cytokine to form a nonfunctional  
CC complex. The compounds have therapeutic activity as cytokine antagonists  
CC and can also be used in assays for identifying novel agonists and  
CC antagonists of cytokines.  
XX  
SQ Sequence 108 AA;  
Query Match 48.6%; Score 107; DB 20; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.5e-92;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 114 GTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 173  
DB 2 GTVAAPSVFIFFPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQD 61  
QY 174 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
DB 62 SKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGEC 108  
RESULT 7  
AA92191  
ID AAY92191 standard; protein; 108 AA.  
XX  
AC AAY92191;  
XX  
DT 01-AUG-2000 (first entry)  
DE Human IgG1 kappa domain.  
XX  
KW gp130-C-gamma-1; cytokine; antagonist; CNTF; receptor; fusion protein;  
KW cytostatic; immunomodulator; osteopathic.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..2  
FT /note= "Ser-Gly bridge"  
FT Domain 3..107  
FT /label= kappa\_domain  
XX  
FN WO200018932-A2.  
XX  
PD 06-APR-2000.  
XX  
PF 22-SEP-1999; 99WO-US22045.  
XX  
PR 25-SEP-1998; 98US-0101858.  
PR 19-MAY-1999; 99US-0313942.  
XX  
PA (REGE-) REGENERON PHARM INC.  
XX  
PI Stahl N, Yancopoulos GD;  
XX  
DR WPI; 2000-293165/25.  
XX  
PT Isolated nucleic acid molecule for treating cytokine-related diseases  
PT or disorders encodes a fusion polypeptide capable of binding a cytokine  
PT to form a nonfunctional complex  
XX  
PS Example 4; Fig 13; 152pp; English.  
XX  
CC The invention concerns production of antagonists to any cytokine that  
CC utilizes an alpha specificity determining component, which when combined

CC with the cytokine, binds to a first beta signal transducing component to  
CC form a non-functional intermediate which then binds to a second beta  
CC signal transducing component causing beta-receptor dimerization, the  
CC soluble alpha specificity determining component of the receptor  
CC (SR-alpha) and the extracellular domain of the first beta signal  
CC transducing component of the cytokine receptor (beta-1) are combined to  
CC form heterodimers (SR-alpha:beta-1) that act as antagonist to the  
CC cytokine by binding the cytokine to form a non-functional complex. The  
CC receptor components are shared by cytokines such as the CNTF (ciliary  
CC neurotrophic factor) family of cytokines. The invention provides the  
CC basis for the development of IL-6 antagonists, as they show that if, in  
CC the presence of a ligand, a non-functional intermediate complex,  
CC consisting of the ligand, its alpha receptor and its beta-1 receptor  
CC component, can be formed, it will effectively block the action of the  
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers  
CC of the extracellular domains of the alpha specificity determining  
CC components of their receptors and the extracellular domain of gp130.  
CC The resultant heterodimers, function as high-affinity traps, rendering  
CC the cytokine inaccessible to form a signal transducing complex with the  
CC native membrane-bound forms of their receptor. The nucleic acids and  
CC polypeptides are useful for treating cytokine-related diseases or  
CC disorders such as osteoporosis and primary and secondary effects of  
CC cancer including multiple myeloma or cachexia.

XX Sequence 108 AA;

Query Match 48.6%; Score 107; DB 21; Length 108;  
Best Local Similarity 100.0%; Pred. No. 3.5e-92;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 114 GTVAAPSVFIIPPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 173  
DB 2 GTVAAPSVFIIPPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 61  
QY 174 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 220  
DB 62 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 108

RESULT 8  
AAR52951  
ID AAR52951 standard; Protein; 234 AA.  
XX  
AC AAR52951;  
XX  
DT 27-OCT-1994 (first entry)  
XX  
DE Human anti-IgE MAb light chain.  
XX  
KW Human IgE; CH4 region; triggers mediator release;  
KW Mast cells; Monoclonal antibody; allergy.  
XX  
OS Homo sapiens.

XX Key Location/Qualifiers  
XX Region 21..128  
XX /label= light chain variable region

XX EP592230-A.  
XX 13-APR-1994.  
XX  
XX 07-OCT-1993; 93EP-0308006.  
XX  
XX 07-OCT-1992; 92JP-0293800.  
XX  
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.  
XX  
XX Goto M, Kobayashi F, Mizuno A, Morinaga T, Washida N;  
XX Yoshida T;  
XX WPI; 1994-120330/15.  
XX  
XX N-PSDB; AAQ71872.

XX Human monoclonal anti-IgE peptide antibody - inhibits histamine  
PT release from mast cells by allergen stimulation, useful for  
PT preventing allergies  
XX  
XX Claim 3; Page 12; 21pp; English.  
XX  
XX AAR52951 shows the light chain of a human type anti-IgE peptide  
CC monoclonal antibody which inhibits the signal transmission for  
CC the release of chemical mediator from mast cells and basophils  
CC stimulated with allergen. The antibody can be used for the  
CC prophylaxis and the therapy of allergy.  
XX

XX Sequence 234 AA;

Query Match 48.6%; Score 107; DB 15; Length 234;  
Best Local Similarity 100.0%; Pred. No. 7e-92;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 114 GTVAAPSVFIIPPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 173  
DB 128 GTVAAPSVFIIPPDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 187  
QY 174 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 220  
DB 188 SKDSTYLSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNREGC 234

RESULT 9  
AAY92196  
ID AAY92196 standard; protein; 468 AA.

XX  
AC AAY92196;  
XX  
DT 01-AUG-2000 (first entry)  
XX  
DE Human IL-6R-alpha-kappa fusion protein.  
XX  
KW IL-6R-alpha-C-gamma-1; cytokine; antagonist; CNTF; receptor;  
KW fusion protein; cytostatic; immunomodulator; osteopathic.  
XX  
OS Synthetic.

XX OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
XX FT Protein 1..358  
XX /label= IL-6R-alpha  
XX FT Peptide 359..360  
XX /note= "Ala-Gly bridge"  
XX FT Protein 361..468  
XX /label= kappa\_domain

XX WO200018932-A2.  
XX  
XX PD 06-APR-2000.  
XX  
XX PF 22-SEP-1999; 99WO-US22045.  
XX  
XX 25-SEP-1998; 98US-0101858.  
XX 19-MAY-1999; 99US-0313942.  
XX  
XX (REGE-) REGENERON PHARM INC.  
XX  
XX Stahl N, Yancopoulos GD;  
XX  
XX WPI; 2000-293165/25.

XX Isolated nucleic acid molecule for treating cytokine-related diseases  
PT or disorders encodes a fusion polypeptide capable of binding a cytokine  
PT to form a nonfunctional complex  
XX  
XX Example 4; Page -; 152pp; English.

CC The invention concerns production of antagonists to any cytokine that  
CC utilizes an alpha specificity determining component, which when combined  
CC with the cytokine, binds to a first beta signal transducing component to  
CC form a non-functional intermediate which then binds to a second beta  
CC signal transducing component causing beta-receptor dimerization, the  
CC soluble alpha specificity determining component of the receptor  
CC (sr-alpha) and the extracellular domain of the first beta signal  
CC transducing component of the cytokine receptor (beta-1) are combined to  
CC form heterodimers (sr-alpha:beta-1) that act as antagonist to the  
CC cytokine by binding the cytokine to form a non-functional complex. The  
CC receptor components are shared by cytokines such as the CNTF (ciliary  
CC neurotrophic factor) family of cytokines. The invention provides the  
CC basis for the development of IL-6 antagonists, as they show that if, in  
CC the presence of a ligand, a non-functional intermediate complex,  
CC consisting of the ligand, its alpha receptor and its beta-1 receptor  
CC component, can be formed, it will effectively block the action of the  
CC ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers  
CC of the extracellular domains of the alpha specificity determining  
CC components of their receptors and the extracellular domain of gp130.  
CC The resultant heterodimers, function as high-affinity traps, rendering  
CC the cytokine inaccessible to form a signal transducing complex with the  
CC native membrane-bound forms of their receptor. The nucleic acids and  
CC polypeptides are useful for treating cytokine-related diseases or  
CC disorders such as osteoporosis and primary and secondary effects of  
CC cancer including multiple myeloma or cachexia.  
XX  
SQ Sequence 468 AA;  
  
Query Match 48.6%; Score 107; DB 21; Length 468;  
Best Local Similarity 100.0%; Pred. No. 1.3e-91;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 114 GTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 173  
Db 362 GTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 421  
  
Qy 174 SKDSTYSLSTLTLSKADYEHKHYACEVTHOGLSSPVTKSFNRGEC 220  
Db 422 SKDSTYSLSTLTLSKADYEHKHYACEVTHOGLSSPVTKSFNRGEC 468  
  
RESULT 10  
AA92192  
ID AA92192 standard; protein; 727 AA.  
XX  
AC AA92192;  
XX  
DT 01-AUG-2000 (first entry)  
XX  
DE Human gp130-kappa domain fusion protein.  
XX  
DE gp130-kappa domain; cytokine; antagonist; CNTF; receptor; fusion protein;  
KW cytostatic; immunomodulator; osteopathic.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Protein 1..619  
FT /label= gp130  
FT Peptide 620..621  
FT /note="Ser-Gly bridge"  
FT Protein 622..727  
FT /label= IgG1\_kappa\_domain  
XX  
XX WO200018932-A2.  
PN  
XX  
XX 06-APR-2000.  
PD  
XX 22-SEP-1999; 99WO-US22045.  
PF  
XX 25-SEP-1998; 98US-0101858.  
PR  
XX 19-MAY-1999; 99US-0313942.

XX (REGE-) REGENERON PHARM INC.  
PA  
XX Stahl N, Yancopoulos GD;  
PI  
XX WPI; 2000-293165/25.  
DR  
XX Isolated nucleic acid molecule for treating cytokine-related diseases  
XX or disorders encodes a fusion polypeptide capable of binding a cytokine  
XX to form a nonfunctional complex  
XX  
XX Example 4; Page -: 152pp; English.  
XX  
XX The invention concerns production of antagonists to any cytokine that  
XX utilizes an alpha specificity determining component, which when combined  
XX with the cytokine, binds to a first beta signal transducing component to  
XX form a non-functional intermediate which then binds to a second beta  
XX signal transducing component causing beta-receptor dimerization, the  
XX soluble alpha specificity determining component of the receptor  
XX (sr-alpha) and the extracellular domain of the first beta signal  
XX transducing component of the cytokine receptor (beta-1) are combined to  
XX form heterodimers (sr-alpha:beta-1) that act as antagonist to the  
XX cytokine by binding the cytokine to form a non-functional complex. The  
XX receptor components are shared by cytokines such as the CNTF (ciliary  
XX neurotrophic factor) family of cytokines. The invention provides the  
XX basis for the development of IL-6 antagonists, as they show that if, in  
XX the presence of a ligand, a non-functional intermediate complex,  
XX consisting of the ligand, its alpha receptor and its beta-1 receptor  
XX component, can be formed, it will effectively block the action of the  
XX ligand. Effective antagonists of IL-6 or CNTF consist of heterodimers  
XX of the extracellular domains of the alpha specificity determining  
XX components of their receptors and the extracellular domain of gp130.  
XX The resultant heterodimers, function as high-affinity traps, rendering  
XX the cytokine inaccessible to form a signal transducing complex with the  
XX native membrane-bound forms of their receptor. The nucleic acids and  
XX polypeptides are useful for treating cytokine-related diseases or  
XX disorders such as osteoporosis and primary and secondary effects of  
XX cancer including multiple myeloma or cachexia.  
XX  
XX NB. This sequence was constructed from the gp130 and kappa domain  
XX sequences given in Figures 9 and 13 of the specification.  
XX  
SQ Sequence 727 AA;  
  
Query Match 48.6%; Score 107; DB 21; Length 727;  
Best Local Similarity 100.0%; Pred. No. 1.9e-91;  
Matches 107; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 114 GTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 173  
Db 621 GTVAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQD 680  
  
Qy 174 SKDSTYSLSTLTLSKADYEHKHYACEVTHOGLSSPVTKSFNRGEC 220  
Db 681 SKDSTYSLSTLTLSKADYEHKHYACEVTHOGLSSPVTKSFNRGEC 727  
  
RESULT 11  
AAP81028  
ID AAP81028 standard; protein; 106 AA.  
XX  
AC AAP81028;  
XX  
DT 17-OCT-1990 (first entry)  
XX  
XX C region of L chain (chi) of human antibody.  
XX  
XX mouse-human chimeric antibody ; anticancer agent;  
KW human common acute lymphocytic leukaemia; ss.  
XX  
XX Homo sapiens.  
OS  
XX EP255694-A.  
PN  
XX

PD 10-FEB-1988.  
 XX 29-JUL-1987; 87EP-0110994.  
 XX 30-JUL-1986; 86JP-0177809.  
 XX (TEIJ ) TEIJIN KK.  
 XX Nishimura Y, Ichikawa Y, Kudo A, Watanabe T;  
 XX WPI; 1988-037653/06.  
 XX Mouse-human chimera antibody -  
 PT used for diagnosis and therapy of human common acute lymphocytic  
 PT leukaemia  
 XX Disclosure; ; p; English.  
 XX The chimeric antibody comprises a C region of human origin linked  
 CC to a V region of mouse origin in both the L and H chains. The mouse  
 CC -derived V region is opt. reactive with human common lymphocytic  
 CC leukaemia antigen.  
 CC See also AAN81358-9, AAN81360, AAN81362-6 and AAP81025-7.  
 XX Sequence 106 AA;  
 SQ  
 Query Match 48.2%; Score 106; DB 9; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 115 TVAAPSVFIFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
 DB 1 TVAAPSVFIFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
 QY 175 KDSYSLSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
 DB 61 KDSYSLSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 106  
 RESULT 12  
 AAR41687  
 ID AAR41687 standard; Protein; 106 AA.  
 AC AAR41687;  
 XX 20-OCT-1993 (first entry)  
 XX Undefined ORF1 encoded by plasmid pAH4611.  
 XX Polymerase chain reaction; primer; PCR; amplify; murine; heavy; light;  
 KW chain; variable; constant; region; anti-human; transferrin; receptor;  
 KW antibody; brain; capillary; endothelial cell; conjugate; epilepsy;  
 KW neuropharmaceutical; diagnostic; agent; tumour; AIDS; stroke;  
 KW Parkinsons disease; Alzheimers disease.  
 XX Synthetic.  
 XX WO9310819-A.  
 XX 10-JUN-1993.  
 XX 24-NOV-1992; 92WO-US10206.  
 XX 26-NOV-1991; 91US-0800458.  
 XX (ALKE-) ALKERMES INC.  
 XX Friden PW;  
 XX WPI; 1993-196742/24.  
 XX N-PSDB; AAQ43845.  
 XX Antibody conjugates specific for transferrin receptor - used

PT for diagnosis and treatment of cancer, AIDS and neurological  
 PT disorders  
 XX Disclosure; Fig 13H; 151pp; English.  
 XX The sequences given in AAR41686-87 represent proteins encoded by the  
 CC expression vector pAH4611. This vector was produced from the plasmid  
 CC pAG4270. pAG4270 is the expression vector for the light chain  
 CC variable region (VL) of the antibody 128.1 which was obtained by PCR  
 CC with leader/J region priming (see also AAQ43842). The vector also  
 CC contains an ampicillin resistance gene, a qpt (mycophenolic acid  
 CC resistance) selected marker, an immunoglobulin H enhancer and an  
 CC intron for V-constant region splicing. Transcription of the CH gene  
 CC is from the VH promoter of the murine 27.44 gene. The cloning of  
 CC the 128.1 VL region was accomplished in two stages with the production  
 CC of plasmid pSV4271 as an intermediate vector which lacks the promoter  
 CC region. This plasmid was used in conjunction with pAH4602 in the  
 CC production of the chimeric antibody 128.1. 128.1 is an anti-human  
 CC transferrin receptor antibody which binds to the transferrin receptor  
 CC on brain capillary endothelial cells. This antibody may be used in a  
 CC conjugate in which it is linked to a neuropharmaceutical or diagnostic  
 CC agent. The conjugate may be used to treat or prevent neurological  
 CC disorders eg. brain tumours, AIDS, stroke, epilepsy, Parkinsons and  
 CC Alzheimers disease. It may also be used for diagnostic methods.  
 XX Sequence 106 AA;  
 SQ  
 Query Match 48.2%; Score 106; DB 14; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 115 TVAAPSVFIFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
 DB 1 TVAAPSVFIFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
 QY 175 KDSYSLSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
 DB 61 KDSYSLSLSTLTLSKADYEKHKVYACEVTHOGLSSPVTKSFNRGEC 106  
 RESULT 13  
 AAR43686  
 ID AAR43686 standard; Protein; 106 AA.  
 XX AAR43686;  
 AC AAR43686;  
 XX 25-MAY-1994 (first entry)  
 XX Human kappa constant domain as encoded by pHCMV-KR.  
 XX Human; immunoglobulin; constant; region; humanised; P-selectin; light;  
 KW blocking; antibody; heavy; chain; variable; murine; thrombotic disease;  
 KW monoclonal; PBL 3; CDR; complementarity determining region; leukocyte;  
 KW expression vector; coexpression; pHCMV-1748RHA-gamma1CI-dhfr; epitope;  
 KW pHCMV-1748RLA-KR-neo; PBL 3/Humanised version A; vascular endothelium;  
 KW pHCMV-1747CH-gamma1CI-neo; pHCMV-1747-CL-KR-neo; PBL 3 chimera;  
 KW acute lung injury; ischaemia reperfusion injury; inflammation.  
 XX Homo sapiens.  
 XX WO9321956-A.  
 XX 11-NOV-1993.  
 XX 04-MAY-1993; 93WO-US04274.  
 XX 05-MAY-1992; 92US-0880196.  
 XX (CYTE-) CYTEL CORP.  
 XX Chestnut RW, Paulson JC, Polley MJ;  
 XX WPI; 1993-368423/46.

DR N-PSDB; AAQ51548.  
 XX  
 XX Anti-P-selectin antibody for ischaemia acute lung injury treatment -  
 PT useful to treat inflammation and pathological conditions of  
 PT Inter cellular adhesion by competitive inhibition assays  
 XX  
 PS Example 10; Fig 10; 82pp; English.  
 XX  
 XX The sequences given in AAR43685-86 represent human immunoglobulin  
 CC constant regions which were used in the production of the humanised  
 CC P-selectin blocking antibody, along with the heavy and light chain  
 CC variable region coding sequences of the murine monoclonal antibody  
 CC PBL.3, given in AAR43687-88. The CDRs from PBL.3 heavy and light  
 CC chains were substituted for the CDRs of human heavy and light chains.  
 CC The humanised variable regions were inserted into expression vectors.  
 CC By coexpression of appropriate combinations of heavy and light  
 CC chains, several humanised antibodies can be expressed. Coexpression  
 CC of pHCMV-1748RIA-gamma1C1-dhfr and pHCMV-1748RLA-KR-neo gives rise  
 CC to the PBL.3/Humanised version A. Coexpression of pHCMV-1747CH-  
 CC gamma1C1-neo and pHCMV-1747-CL-KR-neo gives rise to the PBL.3 chimera.  
 CC These humanised antibodies selectively bind epitopes on P-selectin and  
 CC block adhesion of leukocytes to the vascular endothelium. They may be  
 CC used to treat inflammatory and thrombotic diseases and other  
 CC pathological conditions involving P-selectin and antibodies to it, esp.  
 CC acute lung injury and ischaemia reperfusion injury.  
 XX  
 SQ Sequence 106 AA;  
 Query Match 48.2%; Score 106; DB 14; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 115 TVAAPSVFIFFPPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 174  
 DB 1 TVAAPSVFIFFPPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 60  
 QY 175 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
 DB 61 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106  
 RESULT 14  
 AAW37347  
 ID AAW37347 standard; Protein; 106 AA.  
 AC AAW37347;  
 XX  
 XX 11-MAY-1998 (first entry)  
 DT  
 DE Immunoglobulin C-kappa region.  
 XX Vaccine; B-cell malignancy; lymphoma; leukaemia; tumour;  
 KW gene amplification; immunotherapy; therapy; immunoglobulin;  
 KW C-kappa; constant region.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9741244-A1.  
 PN  
 XX  
 PD 06-NOV-1997.  
 XX  
 XX 25-APR-1997; 97WO-US07039.  
 PF  
 XX  
 XX 06-DEC-1996; 96US-0761277.  
 PR  
 XX 01-MAY-1996; 96US-0644664.  
 XX  
 XX (GENI-) GENITOPE CORP.  
 PA  
 XX Denney DW;  
 PI  
 XX  
 XX WPI; 1997-549743/50.  
 DR N-PSDB; AAT97190.  
 XX

PT Multivalent vaccine to treat B cell lymphoma or leukaemia -  
 PT comprises at least 2 different recombinant variable regions of  
 PT immunoglobulin molecules derived from B cell lymphoma cells  
 PS Example 10; Page 127-128; 177pp; English.  
 XX  
 XX This protein comprises an immunoglobulin (Ig) C-kappa region.  
 CC The invention provides a method for the production of tumour-  
 CC specific Ig derived from a B-cell lymphoma patient. In the novel  
 CC method, expression plasmids containing the patient's VH region(s)  
 CC joined to either a C-gamma-3 (see AAT97188) or C-gamma-4 (see AAT97189)  
 CC sequence and expression plasmids containing the patient's VL  
 CC region(s) joined to either a C-kappa (see AAT97190) or C-lambda-2  
 CC (see AAT97191) sequence are cotransfected along with a selectable and  
 CC amplifiable marker into a cell line (e.g. BW5147.G.1.4), and  
 CC transfected cells are then subjected to selection and amplification.  
 CC The method permits the production of a multivalent vaccine which  
 CC reflects the degree of somatic variation found within the patient's  
 CC tumour. These novel multivalent vaccines provide superior vaccines  
 CC for the treatment of B-cell lymphoma.  
 XX  
 SQ Sequence 106 AA;  
 Query Match 48.2%; Score 106; DB 18; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 115 TVAAPSVFIFFPPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 174  
 DB 1 TVAAPSVFIFFPPDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 60  
 QY 175 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
 DB 61 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106  
 RESULT 15  
 AAW59622  
 ID AAW59622 standard; Protein; 106 AA.  
 XX  
 AC AAW59622;  
 XX  
 XX 12-OCT-1998 (first entry)  
 DT  
 DE Anti-RSV F protein Hu19 MAB light chain constant region.  
 XX  
 XX Monoclonal antibody; human; Hu19C; Hu19D; engineered antibody; RSV;  
 KW respiratory syncytial virus; complementarity determining region;  
 KW CDR; infection; immunotherapy; therapy; diagnosis.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO9819704-A1.  
 PN  
 XX  
 PD 14-MAY-1998.  
 XX  
 XX 23-OCT-1997; 97WO-US19203.  
 PF  
 XX  
 XX 01-NOV-1996; 96US-0030149.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA  
 XX Deen KC, Dillon SB, Porter TG, Sweet RW;  
 PI  
 XX WPI; 1998-286600/25.  
 DR  
 XX Monoclonal antibodies reactive with Respiratory Syncytial Virus -  
 PT useful for detection, prevention and treatment of RSV infections  
 PT  
 XX Disclosure; Fig 3; 109pp; English.  
 PS  
 XX This is the amino acid sequence of the light chain constant region  
 CC (C kappa) of constructs 19C and 19D of novel human monoclonal  
 CC

CC antibodies (Mabs) reactive with the fusion (F) protein of  
 CC respiratory syncytial virus (RSV). Hu19A, Hu19B, Hu19C and Hu19D  
 CC Mabs are claimed. These are reshaped human antibodies comprising a  
 CC heavy chain selected from 19A, 19B, 19C or 19D (see AAW59615-18), and  
 CC a light chain selected from 19A, 19B, 19C or 19D (see AAW59620-21).  
 CC Such engineered antibodies are neutralising; they inhibit virus  
 CC growth in vitro and in vivo in animal models of RSV infection.  
 CC They can be used in the detection, prevention and passive  
 CC immunotherapy of RSV infection. Nucleic acids encoding the human  
 CC Mabs, recombinant plasmids (see AAV41427-33) and host cells (e.g.  
 CC COS, CHO, myeloma) are provided.  
 xx  
 SQ Sequence 106 AA;

Query Match 48.2%; Score 106; DB 19; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-91;  
 Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFTFPSPDQLKSGTASVYVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
 Db 1 TVAAPSVFTFPSPDQLKSGTASVYVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60

QY 175 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220  
 Db 61 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 106

Search completed: October 9, 2002, 19:23:00  
 Job time : 24.5714 secs





GenCore version 5.1.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:21:30 ; Search time 8.9759 Seconds  
(without alignments)  
598.427 Million cell updates/sec

Title: US-09-822-698A-24  
Perfect score: 220  
Sequence: 1 EIVLTQSLPLVPVTPGEPAS.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size : 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PC1US\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 106   | 48.2        | 106    | 2  | US-08-378-939-40  |
| 2          | 106   | 48.2        | 106    | 2  | US-08-761-277A-49 |
| 3          | 106   | 48.2        | 106    | 3  | US-08-444-644-26  |
| 4          | 106   | 48.2        | 106    | 4  | US-08-232-246A-26 |
| 5          | 106   | 48.2        | 107    | 1  | US-08-422-101-8   |
| 6          | 106   | 48.2        | 107    | 1  | US-08-422-091-8   |
| 7          | 106   | 48.2        | 107    | 2  | US-08-422-092-8   |
| 8          | 106   | 48.2        | 107    | 2  | US-08-788-800-5   |
| 9          | 106   | 48.2        | 107    | 3  | US-08-422-093-8   |
| 10         | 106   | 48.2        | 107    | 3  | US-08-422-112-8   |
| 11         | 106   | 48.2        | 213    | 3  | US-08-630-820-6   |
| 12         | 106   | 48.2        | 213    | 3  | US-08-397-411-12  |
| 13         | 106   | 48.2        | 214    | 1  | US-08-458-516-12  |
| 14         | 106   | 48.2        | 214    | 2  | US-07-934-373C-24 |
| 15         | 106   | 48.2        | 214    | 2  | US-07-934-373C-39 |
| 16         | 106   | 48.2        | 214    | 2  | US-07-934-373C-40 |
| 17         | 106   | 48.2        | 214    | 2  | US-08-480-753-6   |
| 18         | 106   | 48.2        | 214    | 2  | US-08-788-800-11  |
| 19         | 106   | 48.2        | 214    | 3  | US-09-041-889-11  |
| 20         | 106   | 48.2        | 214    | 3  | US-08-437-642B-24 |
| 21         | 106   | 48.2        | 214    | 3  | US-08-437-642B-39 |
| 22         | 106   | 48.2        | 214    | 3  | US-08-437-642B-40 |
| 23         | 106   | 48.2        | 214    | 3  | US-08-837-058-11  |
| 24         | 106   | 48.2        | 214    | 3  | US-09-097-309-2   |
| 25         | 106   | 48.2        | 214    | 3  | US-08-397-411-5   |
| 26         | 106   | 48.2        | 214    | 4  | US-09-097-171A-2  |
| 27         | 106   | 48.2        | 214    | 4  | US-09-247-352-4   |

|    |     |      |     |   |                   |                   |
|----|-----|------|-----|---|-------------------|-------------------|
| 28 | 106 | 48.2 | 214 | 4 | US-09-679-397-1   | Sequence 1, Appli |
| 29 | 106 | 48.2 | 214 | 5 | PCT-US93-07832-24 | Sequence 24, Appl |
| 30 | 106 | 48.2 | 214 | 5 | PCT-US93-07832-39 | Sequence 39, Appl |
| 31 | 106 | 48.2 | 214 | 5 | PCT-US93-07832-40 | Sequence 40, Appl |
| 32 | 106 | 48.2 | 215 | 2 | US-08-480-753-8   | Sequence 8, Appli |
| 33 | 106 | 48.2 | 218 | 2 | US-08-887-352B-13 | Sequence 13, Appl |
| 34 | 106 | 48.2 | 218 | 2 | US-08-887-352B-15 | Sequence 15, Appl |
| 35 | 106 | 48.2 | 218 | 2 | US-08-887-352B-17 | Sequence 17, Appl |
| 36 | 106 | 48.2 | 218 | 2 | US-08-887-352B-19 | Sequence 19, Appl |
| 37 | 106 | 48.2 | 218 | 2 | US-08-887-352B-24 | Sequence 24, Appl |
| 38 | 106 | 48.2 | 218 | 3 | US-08-466-151-9   | Sequence 9, Appli |
| 39 | 106 | 48.2 | 218 | 4 | US-09-109-207C-13 | Sequence 13, Appl |
| 40 | 106 | 48.2 | 218 | 4 | US-09-109-207C-15 | Sequence 15, Appl |
| 41 | 106 | 48.2 | 218 | 4 | US-09-109-207C-17 | Sequence 17, Appl |
| 42 | 106 | 48.2 | 218 | 4 | US-09-109-207C-19 | Sequence 19, Appl |
| 43 | 106 | 48.2 | 218 | 4 | US-09-109-207C-24 | Sequence 24, Appl |
| 44 | 106 | 48.2 | 218 | 4 | US-09-282-505-1   | Sequence 1, Appli |
| 45 | 106 | 48.2 | 218 | 4 | US-09-054-255-1   | Sequence 1, Appli |

## ALIGNMENTS

RESULT 1  
US-08-378-939-40  
; Sequence 40, Application US/08378939  
; Patent No. 5876961  
; GENERAL INFORMATION:  
; APPLICANT: CROWE, JAMES SCOTT  
; APPLICANT: LEWIS, ALAN PETER  
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ  
; STREET: 555 THIRTEENTH ST. N.W.  
; CITY: WASHINGTON  
; STATE: D. C.  
; COUNTRY: U.S.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA: US/08/378,939  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/952640  
; FILING DATE: 01-DEC-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ERNST, BARBARA G  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1808-118  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 783-6040  
; TELEFAX: (202) 783-6031  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 106 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-378-939-40

Query Match 48.2%; Score 106; DB 2; Length 106;

Best Local Similarity 100.0%; Pred. No. 9e-91;

Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TAAAPSVFIFFPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDS 174

Db 1 TAAAPSVFIFFPSDQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDS 60

Qy 175 KDSYSLSLTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 61 KDSYSLSLTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

## RESULT 2

US-08-761-277A-49  
; Sequence 49, Application US/08761277A  
; Patent No. 5972334  
; GENERAL INFORMATION:  
; APPLICANT: Denney Jr., Dan W.  
; TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And  
; TITLE OF INVENTION: Leukemia  
; NUMBER OF SEQUENCES: 80  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Medlen & Carroll, LLP  
; STREET: 220 Montgomery Street, Suite 2200  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States Of America  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/761.277A  
; FILING DATE: 06-DEC-1996  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/644,664  
; FILING DATE: 01-MAY-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MacKnight, Kamrin T.  
; REGISTRATION NUMBER: 38,230  
; REFERENCE/DOCKET NUMBER: GENITOPE-02406  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 49:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 106 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-761-277A-49

Query Match 48.2%; Score 106; DB 2; Length 106;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TVAAPSVFIPPSPDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDS 174  
Db 1 TVAAPSVFIPPSPDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDS 60

## RESULT 3

US-08-444-644-26  
; Sequence 26, Application US/08444644  
; Patent No. 6015555  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173

; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/444,644  
; FILING DATE:  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/232,246  
; FILING DATE: 07-JUL-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/800,458  
; FILING DATE: 26-NOV-1991  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US90/05077  
; FILING DATE: 07-SEP-1990  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/404,089  
; FILING DATE: 07-SEP-1989  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Wagner, Richard W.  
; REGISTRATION NUMBER: 34,480  
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (617) 861-6240  
; TELEFAX: (617) 861-9540  
; INFORMATION FOR SEQ ID NO: 26:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 106 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-08-444-644-26

Query Match 48.2%; Score 106; DB 3; Length 106;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TVAAPSVFIPPSPDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDS 174  
Db 1 TVAAPSVFIPPSPDEQLKSGTASVCLNNFYPRKQVQKVDNALQSGNSQESVTEQDS 60

Qy 175 KDSYSLSLTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 61 KDSYSLSLTLTKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 106

## RESULT 4

US-08-232-246A-26  
; Sequence 26, Application US/08232246A  
; Patent No. 6329508  
; GENERAL INFORMATION:  
; APPLICANT: Friden, Phillip M.  
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC  
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
; STREET: Two Militia Drive  
; CITY: Lexington  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02173

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232.246A  
FILING DATE: 04-MAY-1994  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/800,458  
FILING DATE: 26-NOV-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US90/05077  
FILING DATE: 07-SEP-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/404,089  
FILING DATE: 07-SEP-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Wagner, Richard W.  
REGISTRATION NUMBER: 34,480  
REFERENCE/DOCKET NUMBER: ALK88-15AAA  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 861-6240  
TELEFAX: (617) 861-9540  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-232-246A-26

Query Match 48.2%; Score 106; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 115 TAAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
DB 1 TAAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
QY 175 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220  
DB 61 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 106

RESULT 5  
US-08-422-101-8  
Sequence 8, Application US/08422101  
Patent No. 5739277  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
TITLE OF INVENTION: Half-Life  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,101  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 530

PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932-3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-422-101-8  
Query Match 48.2%; Score 106; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 115 TAAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
DB 2 TAAAPSVFIFFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
QY 175 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 220  
DB 62 KDSTYSLSTLTLSKADYKHKYACEVTHQGLSSPVTKSFNRGEC 107  
RESULT 6  
US-08-422-091-8  
Sequence 8, Application US/08422091  
Patent No. 5747035  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
TITLE OF INVENTION: Half-Life  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,091  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932-6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear

US-08-422-091-8

Query Match 48.2%; Score 106; DB 1; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
Db 2 TAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
|||||

Qy 175 KDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
|||||  
Db 62 KDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
|||||

RESULT 7

US-08-422-092-8  
; Sequence 8, Application US/08422092  
; Patent No. 5869046  
; GENERAL INFORMATION:  
; APPLICANT: Leonard Presta  
; APPLICANT: Brad Snedecor  
; TITLE OF INVENTION: Altered Polypeptides with Increased  
; TITLE OF INVENTION: Half-Life  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/422,092  
; FILING DATE: 14-APR-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 932-4  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-422-092-8

Query Match 48.2%; Score 106; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
Db 2 TAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
|||||

Qy 175 KDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
|||||  
Db 62 KDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
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RESULT 8

US-08-422-093-8  
; Sequence 8, Application US/08422093  
; Patent No. 6096871  
; GENERAL INFORMATION:  
; APPLICANT: Leonard Presta  
; APPLICANT: Brad Snedecor  
; TITLE OF INVENTION: Altered Polypeptides with Increased  
; TITLE OF INVENTION: Half-Life  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible

US-08-788-800-5

; Sequence 5, Application US/08788800  
; Patent No. 5914112  
; GENERAL INFORMATION:  
; APPLICANT: Bednar, Martin M.  
; APPLICANT: Thomas, G. Roger  
; APPLICANT: Gross, Cordell E.  
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080

COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WinPatIn (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/788,800  
; FILING DATE: 22-Jan-1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lee, Wendy M.  
; REGISTRATION NUMBER: 40,378  
; REFERENCE/DOCKET NUMBER: P0987r1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1994  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 107 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear

US-08-788-800-5

Query Match 48.2%; Score 106; DB 2; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 TAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
Db 2 TAAPSVFIFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
|||||

Qy 175 KDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
|||||  
Db 62 KDSTYLSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 107  
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RESULT 9

US-08-422-093-8  
; Sequence 8, Application US/08422093  
; Patent No. 6096871  
; GENERAL INFORMATION:  
; APPLICANT: Leonard Presta  
; APPLICANT: Brad Snedecor  
; TITLE OF INVENTION: Altered Polypeptides with Increased  
; TITLE OF INVENTION: Half-Life  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,093  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICANT: patin  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-422-093-8

Query Match 48.2%; Score 106; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 115 TVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
DB 2 TVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
QY 175 KDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220  
DB 62 KDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107

RESULT 10  
US-08-422-112-8  
Sequence 8, Application US/08422112  
Patent No. 6121022  
GENERAL INFORMATION:  
APPLICANT: Leonard Presta  
APPLICANT: Brad Snedecor  
TITLE OF INVENTION: Altered Polypeptides with Increased  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/422,112  
FILING DATE: 14-APR-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICANT: patin  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 932-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881

TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 107 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-422-112-8  
Query Match 48.2%; Score 106; DB 3; Length 107;  
Best Local Similarity 100.0%; Pred. No. 9e-91;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 115 TVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
DB 2 TVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 61  
QY 175 KDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 220  
DB 62 KDSTYLSLSTLTLSKADYERKHVYACEVTHQGLSSPVTKSFNRGEC 107  
RESULT 11  
US-08-630-820-6  
Sequence 6, Application US/08630820  
Patent No. 6008023  
GENERAL INFORMATION:  
APPLICANT: Oppen, Martin  
APPLICANT: Bosslet, Klaus  
APPLICANT: Czech, Joerg  
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,  
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES  
TITLE OF INVENTION: IN E. COLI  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/630,820  
FILING DATE: 10-APR-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19513676.4  
FILING DATE: 11-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/306  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 213 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-630-820-6  
Query Match 48.2%; Score 106; DB 3; Length 213;  
Best Local Similarity 100.0%; Pred. No. 1.7e-90;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 115 TVAAPSVFIFFPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174



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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-24

Query Match 48.2%; Score 106; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.7e-90;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TAAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174
Db 109 TAAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 168

QY 175 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
Db 169 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

Search completed: October 9, 2002, 19:26:36
Job time : 8.97959 secs

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; US-07-934-373C-39
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-39

Query Match 48.2%; Score 106; DB 2; Length 214;
Best Local Similarity 100.0%; Pred. No. 1.7e-90;
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TAAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174
Db 109 TAAAPSVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 168

QY 175 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
Db 169 KDSTYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 214

Search completed: October 9, 2002, 19:26:36
Job time : 8.97959 secs

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RESULT 15
US-07-934-373C-39
; Sequence 39, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:19:35 ; Search time 11.7857 Seconds  
(without alignments)  
1793.668 Million cell updates/sec

Title: US-09-822-698A-24  
Perfect score: 220  
Sequence: 1 EIVLTQSLPLVPTGPAS.....EVTHQGLSSPVTKSFNRGEC 220

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 106   | 48.2        | 106    | 1 K3HU   | Ig kappa chain C r |
| 2          | 106   | 48.2        | 215    | 2 JE0244 | Ig kappa chain NIG |
| 3          | 106   | 48.2        | 215    | 2 JE0242 | Ig kappa chain NIG |
| 4          | 106   | 48.2        | 215    | 2 JE0243 | Ig kappa chain C r |
| 5          | 99    | 45.0        | 99     | 2 S26053 | JC-kappa protein - |
| 6          | 82    | 37.3        | 135    | 2 S52059 | Ig kappa chain C r |
| 7          | 75    | 34.1        | 99     | 2 A37927 | Ig kappa chain C r |
| 8          | 70    | 31.8        | 216    | 2 JE0241 | Ig kappa chain An3 |
| 9          | 59    | 26.8        | 215    | 2 A23746 | Ig kappa chain V-I |
| 10         | 31    | 14.1        | 112    | 2 S58207 | Ig light chain V r |
| 11         | 31    | 14.1        | 112    | 2 S58206 | Ig light chain V r |
| 12         | 31    | 14.1        | 117    | 1 K2HUGM | Ig kappa chain pre |
| 13         | 31    | 14.1        | 123    | 2 S40319 | Ig kappa chain V r |
| 14         | 31    | 14.1        | 132    | 2 S26882 | Ig kappa chain V r |
| 15         | 31    | 14.1        | 135    | 2 S40342 | Ig kappa chain - h |
| 16         | 31    | 14.1        | 136    | 2 S40357 | Ig kappa chain V-I |
| 17         | 30    | 13.6        | 114    | 2 S40375 | Ig kappa chain - h |
| 18         | 28    | 12.7        | 113    | 1 K2HUTW | Ig kappa chain V-I |
| 19         | 27    | 12.3        | 100    | 2 S24681 | Ig kappa chain - h |
| 20         | 27    | 12.3        | 125    | 2 S40356 | Ig kappa chain - h |
| 21         | 27    | 12.3        | 126    | 2 S40339 | Ig kappa chain - h |
| 22         | 26    | 11.8        | 112    | 1 K2HUML | Ig kappa chain V-I |
| 23         | 26    | 11.8        | 121    | 2 S40371 | Ig kappa chain V r |
| 24         | 24    | 10.9        | 120    | 2 A49043 | Ig kappa chain V-I |
| 25         | 23    | 10.5        | 115    | 1 K2HUCM | Ig kappa chain V-I |
| 26         | 23    | 10.5        | 121    | 2 S24205 | Ig kappa chain V r |
| 27         | 23    | 10.5        | 127    | 2 S40323 | Ig kappa chain - h |
| 28         | 23    | 10.5        | 130    | 2 S40321 | Ig kappa chain - h |
| 29         | 22    | 10.0        | 87     | 2 S34091 | Ig kappa chain V r |

ALIGNMENTS

RESULT 1  
K3HU

Ig kappa chain C region - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Dec-1980 #sequence\_revision 02-Jul-1998 #text\_change 21-Jul-2000  
C:Accession: B90562; A91651; A90806; A94417; A91639; A92047; A94242; B37927; A02116;  
R:Gottlieb, P.D.; Cunningham, B.A.; Rutishauser, U.; Edelman, G.M.  
Biochemistry 9, 3155-3161, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. VI. Amino acid sequ  
A:Reference number: A90562; MUID:71064023  
A:Contents: myeloma protein Eu  
A:Accession: B90562  
A:Molecule type: protein  
A:Residues: 1-106 <GOR>  
A:Note: this sequence has the Inv (3) allotypic marker, 45-Ala and 83-Val  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disul  
A:Reference number: A90565; MUID:71064027  
A:Contents: annotation; Eu, disulfide bonds  
R:Suter, L.; Barnikol, H.U.; Watanabe, S.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 353, 189-208, 1972  
A:Title: Die Primaerstruktur einer monoklonalen Immunglobulin-L-Kette vom kappa-Typ,  
A:Reference number: A91651; MUID:72188439  
A:Contents: Bence Jones protein Ti  
A:Accession: A91651  
A:Molecule type: protein  
A:Residues: 1-106 <SVT>  
R:Hieter, P.A.; Max, E.E.; Seidman, J.G.; Maizel Jr., J.V.; Leder, P.  
Cell 22, 197-207, 1980  
A:Title: Cloned human and mouse kappa immunoglobulin constant and J region genes cons  
A:Reference number: A90806; MUID:81042304  
A:Accession: A90806  
A:Molecule type: DNA  
A:Residues: 1-106 <HIE>  
A:Cross-references: GB:J00241; NID:g33140; PIDN:CAA23823.1; PID:g1335148  
A:Note: the sequence was determined from the germline gene  
R:Hilschmann, N.; Barnikol, H.U.; Hess, M.; Langer, B.; Ponstingl, H.; Steinmetz-Kayn  
In Gamma Globulins: Structure and Function, Franek, F., and Shugar, D., eds., pp.57-7  
A:Reference number: A94417  
A:Contents: Bence Jones protein Roy  
A:Accession: A94417  
A:Molecule type: protein  
A:Residues: 1-44, A',46-56, 'Q',58-82, 'L',84-106 <HIL>  
A:Note: this sequence has the Inv (1.2) allotypic marker, 45-Ala and 83-Leu  
R:Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 348, 1718-1722, 1967  
A:Title: Die volstaendige Aminosaeuresequenz des Bence-Jones-Proteins Cum. (kappa-Typ  
A:Reference number: A91639; MUID:68242259  
A:Contents: Bence Jones protein Cum  
A:Accession: A91639  
A:Molecule type: protein

30 22 10.0 100 2 H3730 Ig kappa chain V r  
31 22 10.0 112 1 KVMSS1 Ig kappa chain V r  
32 22 10.0 112 2 S38716 Ig light chain V r  
33 22 10.0 113 1 KVM517 Ig kappa chain V r  
34 22 10.0 116 2 S20708 Ig kappa chain V r  
35 22 10.0 119 2 B27588 Ig kappa chain pre  
36 22 10.0 119 2 A27588 Ig kappa chain pre  
37 22 10.0 124 2 S03876 Ig kappa chain V-I  
38 20 9.1 112 2 I26317 Ig kappa chain V r  
39 20 9.1 112 2 E26317 Ig kappa chain V r  
40 20 9.1 112 2 G26317 Ig kappa chain V r  
41 20 9.1 112 2 B26317 Ig kappa chain V r  
42 20 9.1 112 2 A26317 Ig kappa chain V r  
43 20 9.1 112 2 D26317 Ig kappa chain V r  
44 20 9.1 112 2 F26317 Ig kappa chain V r  
45 20 9.1 112 2 PL0275 Ig kappa chain V r

A:Residues: 1-56,'O',58-106 <H12>  
R:Tritani, K.; Shinoda, T.; Putnam, F.W.  
J. Biol. Chem. 244, 3550-3560, 1969  
A:Title: The amino acid sequence of a kappa type Bence-Jones protein. III. The complete  
A:Reference number: A92047; MUID:69234734  
A:Contents: Bence Jones protein Ag  
A:Accession: A92047  
A:Molecule type: protein  
A:Residues: 1-13,'N',15-106 <TIT>  
R:Kohler, H.; Shimizu, A.; Paul, C.; Putnam, F.W.  
Science 169, 56-59, 1970  
A:Title: Macroglobulin structure: variable sequence of light and heavy chains.  
A:Reference number: A94242; MUID:70201507  
A:Contents: Waldenstrom's macroglobulin Ou  
A:Accession: A94242  
A:Molecule type: protein  
A:Residues: 1-13,'N',15-106 <KOH>  
R:Kurtz, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772  
A:Accession: B37927  
A:Status: not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 8-106 <KUR>  
A:Note: allotype Inv(3)  
R:Steiner, Y.; Chang, J.Y.  
FEBS Lett. 222, 6-10, 1987  
A:Title: Chemical modification of the carboxyl groups of protein substrates enhances the  
A:Reference number: S02572; MUID:88005152  
A:Contents: annotation  
C:Genetics:  
A:Gene: GDB:IGKC  
A:Cross-References: GDB:120088; OMIM:147200  
A:Map position: 2p12-2p12  
C:Complex: an immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
chain disulfide bonds; in some cases, such as IgA and IgM, the subunits associate into la  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:19-88/Domain: immunoglobulin homology <IMM>  
F:26-86/Disulfide bonds: #status experimental  
F:106/Disulfide bonds: interchain (to heavy chain) #status experimental

Query Match 48.2%; Score 106; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 5e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 1 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 60  
|||||

QY 175 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 220  
|||||  
DB 61 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 106  
|||||

RESULT 2  
JE0244  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0244  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (Vkv) identified in cases of AL amy  
A:Reference number: JE0243  
A:Accession: JE0244  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 48.2%; Score 106; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 9.1e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 110 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 169  
|||||

QY 175 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 220  
|||||  
DB 170 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 215  
|||||

RESULT 4  
JE0243  
Ig kappa chain NIG93 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0243  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (Vkv) identified in cases of AL  
A:Reference number: JE0243  
A:Accession: JE0243  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 48.2%; Score 106; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 9.1e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 110 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 169  
|||||

QY 175 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 220  
|||||  
DB 170 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 215  
|||||

RESULT 5  
S26653  
Ig kappa chain C region - chimpanzee (fragment)

Best Local Similarity 100.0%; Pred. No. 9.1e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 110 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 169  
|||||

QY 175 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 220  
|||||  
DB 170 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 215  
|||||

RESULT 3  
JE0242  
Ig kappa chain NIG26 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0242  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:  
A:Reference number: JE0241  
A:Accession: JE0242  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 48.2%; Score 106; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 9.1e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 110 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 169  
|||||

QY 175 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 220  
|||||  
DB 170 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 215  
|||||

RESULT 4  
JE0243  
Ig kappa chain NIG93 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0243  
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.  
submitted to JIPID, November 1998  
A:Description: A new subgroup of k type light chains (Vkv) identified in cases of AL  
A:Reference number: JE0243  
A:Accession: JE0243  
A:Molecule type: protein  
A:Residues: 1-215 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 48.2%; Score 106; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 9.1e-98;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 174  
|||||  
DB 110 TVAAPSVFIPTSPDQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSGNSQESVTEQDS 169  
|||||

QY 175 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 220  
|||||  
DB 170 KDSTYLSLSTLTLSKADYEKKHYACEVTHQGLSPVTKSFNRGEC 215  
|||||

RESULT 5  
S26653  
Ig kappa chain C region - chimpanzee (fragment)

C:Species: Pan troglodytes (chimpanzee)  
C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 21-Jan-2000  
C:Accession: S26653  
R:Ehrlich, P.H.; Moustafa, Z.A.; Harfeldt, K.E.; Isaacson, C.; Oestberg, L.  
Hum. Antibodies Hybridomas 1, 23-26, 1990  
A:Title: Potential of primate monoclonal antibodies to substitute for human antibodies:  
A:Reference number: S26652; MUID:91355693  
A:Accession: S26653  
A:Status: translation not shown  
A:Molecule type: mRNA  
A:Residues: 1-99 <EHR>  
A:Cross-references: EMBL:X65287  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: immunoglobulin  
F:19-88/Domain: immunoglobulin homology <IMM>

Query Match 45.0%; Score 99; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 4.5e-91;  
Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
Db 1 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60  
QY 175 KDSTYLSSTLTLSKADYEKHKVACEVTHQGLSSPVTK 213  
Db 61 KDSTYLSSTLTLSKADYEKHKVACEVTHQGLSSPVTK 99

RESULT 6  
S52059  
JC-kappa protein - human  
C:Species: Homo sapiens (man)  
C:Date: 14-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 08-Sep-2000  
C:Accession: S52059  
R:Frances, V.; Pandrau-Garcia, D.; Guret, C.; Ho, S.; Wang, Z.; Duvert, V.; Sacland, S.;  
EMBO J. 13, 5937-5943, 1994  
A:Title: A surrogate 15 kDa JC-kappa protein is expressed in combination with mu heavy chain  
A:Reference number: S52059; MUID:95112804  
A:Accession: S52059  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-135 <FRA>  
C:Superfamily: pre-B cell omega light chain; immunoglobulin homology

Query Match 37.3%; Score 82; DB 2; Length 135;  
Best Local Similarity 100.0%; Pred. No. 5.2e-74;  
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
Db 30 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 89  
QY 175 KDSTYLSSTLTLSKADYEKHK 196  
Db 90 KDSTYLSSTLTLSKADYEKHK 111

RESULT 7  
A37927  
Ig kappa chain C region (allotype Inv(1.2)) - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 28-Feb-1992 #sequence\_revision 28-Feb-1992 #text\_change 21-Jan-2000  
C:Accession: A37927  
R:Kurth, J.H.; Bowcock, A.M.; Erlich, H.A.; Nevo, S.; Cavalli-Sforza, L.L.  
Am. J. Hum. Genet. 48, 613-620, 1991  
A:Title: Km typing with PCR: application to population screening.  
A:Reference number: A37927; MUID:91150772  
A:Accession: A37927  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: DNA  
A:Residues: 1-99 <KUR>  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin  
F:12-81/Domain: immunoglobulin homology <IMM>

Query Match 34.1%; Score 75; DB 2; Length 99;  
Best Local Similarity 100.0%; Pred. No. 3.8e-67;  
Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 122 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 181  
Db 1 FIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSL 60  
QY 182 SSTLTLSKADYEKHK 196  
Db 61 SSTLTLSKADYEKHK 75

RESULT 8  
JE0241  
Ig kappa chain Am37 precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000  
C:Accession: JE0241  
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda  
submitted to JIPID, November 1998  
A:Description: Structure relationship of kappa type light chains with AL amyloidosis:  
A:Reference number: JE0241  
A:Accession: JE0241  
A:Molecule type: protein  
A:Residues: 1-216 <ALI>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 31.8%; Score 70; DB 2; Length 216;  
Best Local Similarity 100.0%; Pred. No. 7.1e-62;  
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174  
Db 111 TVAAPSVFIFPPSDEQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 170  
QY 175 KDSTYLSST 184  
Db 171 KDSTYLSST 180

RESULT 9  
A23746  
Ig kappa chain V-III (KAU cold agglutinin) - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Dec-1991 #sequence\_revision 30-Dec-1991 #text\_change 21-Jan-2000  
C:Accession: A23746  
J:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.  
J. Biol. Chem. 266, 2836-2842, 1991  
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immun  
A:Reference number: A23746; MUID:91131575  
A:Accession: A23746  
A:Status: preliminary  
A:Molecule type: protein  
A:Residues: 1-215 <LEO>  
C:Superfamily: immunoglobulin V region; immunoglobulin homology  
C:Keywords: heterotetramer; immunoglobulin  
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 26.8%; Score 59; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 6.6e-51;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 LLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLSKADYEKHKVYA 199  
Db 136 LLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSTLSKADYEKHKVYA 194

RESULT 10

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;1-4/Domain: signal sequence (fragment) #status predicted <SIG>  
F;5-117/Product: Ig kappa chain V-II region (GM607) #status predicted <MAT>  
F;20-99/Domain: immunoglobulin homology <IMM>  
F;27-97/Disulfide bonds: #status predicted

Query Match 14.1%; Score 31; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 3.2e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPLSLPVTPGEPASICRSSQSLLHNGY 35  
|||||  
DB 9 TQSPLSLPVTPGEPASICRSSQSLLHNGY 39  
|||||

RESULT 13  
S40319  
Ig kappa chain V region - human  
C;Species: Homo sapiens (man)  
C;Date: 19-May-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000  
C;Accession: S40319  
R;Kleip, R.; Jaenichen, R.; Zachau, H.G.  
Eur. J. Immunol. 23, 3248-3273, 1993  
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.  
A;Reference number: S40312; MUID:94080891  
A;Accession: S40319  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-123 <LE>  
A;Cross-references: EMBL:X72429; NID:g441326; PIDN:CAA51097.1; PID:g441327  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;26-105/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 31; DB 2; Length 123;  
Best Local Similarity 100.0%; Pred. No. 3.4e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPLSLPVTPGEPASICRSSQSLLHNGY 35  
|||||  
DB 15 TQSPLSLPVTPGEPASICRSSQSLLHNGY 45  
|||||

RESULT 14  
S26882  
Ig kappa chain V region (V607) - human  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 20-Jun-2000  
C;Accession: S26882  
R;Weichold, G.M.; Klobbeck, H.G.; Ohnheiser, R.; Combratio, G.; Zachau, H.G.  
Nature 347, 90-92, 1990  
A;Title: Megabase inversions in the human genome as physiological events.  
A;Reference number: S26882; MUID:90370099  
A;Accession: S26882  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-132 <WEI>  
A;Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:gl335367  
C;Genetics:  
A;Introns: 17/1  
C;Superfamily: immunoglobulin V region; immunoglobulin homology  
C;Keywords: heterotetramer; immunoglobulin  
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 31; DB 2; Length 132;  
Best Local Similarity 100.0%; Pred. No. 3.6e-23;  
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPLSLPVTPGEPASICRSSQSLLHNGY 35  
|||||

Db 25 TQSPSLPVTGPASPISCRSSQSLHSHNGY 55

RESULT 15

S40342

Ig kappa chain - human

C:Species: Homo sapiens (man)

C:Date: 06-Mar-1994 #sequence\_revision 26-May-1995 #text\_change 21-Jan-2000

C:Accession: S40342

R:Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A:Title: Expressed human immunoglobulin chi genes and their hypermutation.

A:Reference number: S40312; MUID:94080891

A:Accession: S40342

A:Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-135 <KLE>

A:Cross-references: EMBL:X72452; NID:g441372; PID:g441373

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:29-108/Domain: immunoglobulin homology <IMM>

Query Match

14.18; Score 31; DB 2; Length 135;

Best Local Similarity 100.0%; Pred. No. 3.6e-23;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TQSPSLPVTGPASPISCRSSQSLHSHNGY 35

|||||

Db 18 TQSPSLPVTGPASPISCRSSQSLHSHNGY 48

Search completed: October 9, 2002, 19:25:52  
Job time : 12.7857 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run On: October 9, 2002, 19:13:25 ; Search time 6.73469 Seconds  
(without alignments)  
1264.839 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 220

Sequence: 1 EIVLTQSLPLSVPTGEPAS.....EVTHQGLSSPVTKSENRGEC 220

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 106   | 48.2        | 106    | 1     | KAC_HUMAN   |
| 2          | 31    | 14.1        | 117    | 1     | KV2E_HUMAN  |
| 3          | 28    | 12.7        | 113    | 1     | KV2D_HUMAN  |
| 4          | 26    | 11.8        | 112    | 1     | KV2C_HUMAN  |
| 5          | 23    | 10.5        | 115    | 1     | KV2A_HUMAN  |
| 6          | 22    | 10.0        | 112    | 1     | KV2D_MOUSE  |
| 7          | 22    | 10.0        | 113    | 1     | KV2E_MOUSE  |
| 8          | 20    | 9.1         | 113    | 1     | KV2F_MOUSE  |
| 9          | 17    | 7.7         | 133    | 1     | KV2F_HUMAN  |
| 10         | 14    | 6.4         | 108    | 1     | KV1_CANFA   |
| 11         | 13    | 5.9         | 107    | 1     | KV1D_HUMAN  |
| 12         | 11    | 5.0         | 113    | 1     | KV2B_HUMAN  |
| 13         | 11    | 5.0         | 113    | 1     | KV2G_MOUSE  |
| 14         | 10    | 4.5         | 109    | 1     | KV1F_HUMAN  |
| 15         | 10    | 4.5         | 109    | 1     | KV2E_HUMAN  |
| 16         | 10    | 4.5         | 111    | 1     | KV1A_HUMAN  |
| 17         | 10    | 4.5         | 111    | 1     | KV2F_HUMAN  |
| 18         | 10    | 4.5         | 111    | 1     | KV2G_HUMAN  |
| 19         | 10    | 4.5         | 111    | 1     | KV2H_HUMAN  |
| 20         | 10    | 4.5         | 111    | 1     | KV6C_HUMAN  |
| 21         | 10    | 4.5         | 112    | 1     | KV1B_HUMAN  |
| 22         | 10    | 4.5         | 112    | 1     | KV6A_HUMAN  |
| 23         | 10    | 4.5         | 114    | 1     | KV4A_HUMAN  |
| 24         | 10    | 4.5         | 120    | 1     | KV2B_MOUSE  |
| 25         | 10    | 4.5         | 121    | 1     | KV4D_HUMAN  |
| 26         | 10    | 4.5         | 133    | 1     | KV4B_HUMAN  |
| 27         | 10    | 4.5         | 134    | 1     | KV4C_HUMAN  |
| 28         | 9     | 4.1         | 106    | 1     | KACA_RAT    |
| 29         | 9     | 4.1         | 106    | 1     | KACB_RAT    |
| 30         | 9     | 4.1         | 106    | 1     | KAC_MOUSE   |
| 31         | 9     | 4.1         | 108    | 1     | KV5P_MOUSE  |
| 32         | 9     | 4.1         | 112    | 1     | KV2A_MOUSE  |
| 33         | 9     | 4.1         | 113    | 1     | KV2C_MOUSE  |

|    |   |     |     |   |            |        |              |
|----|---|-----|-----|---|------------|--------|--------------|
| 34 | 9 | 4.1 | 131 | 1 | LV6E_HUMAN | P06319 | homo sapien  |
| 35 | 8 | 3.6 | 100 | 1 | KV3C_HUMAN | P01621 | homo sapien  |
| 36 | 8 | 3.6 | 106 | 1 | KACB_RABIT | P01839 | oryctolagus  |
| 37 | 8 | 3.6 | 107 | 1 | KV6A_MOUSE | P01675 | mus musculus |
| 38 | 8 | 3.6 | 107 | 1 | KV6B_MOUSE | P01676 | mus musculus |
| 39 | 8 | 3.6 | 107 | 1 | KV6C_MOUSE | P01677 | mus musculus |
| 40 | 8 | 3.6 | 107 | 1 | KV6D_MOUSE | P01678 | mus musculus |
| 41 | 8 | 3.6 | 107 | 1 | KV6E_MOUSE | P01679 | mus musculus |
| 42 | 8 | 3.6 | 108 | 1 | KV1E_HUMAN | P01597 | homo sapien  |
| 43 | 8 | 3.6 | 108 | 1 | KV1Y_HUMAN | P00362 | homo sapien  |
| 44 | 8 | 3.6 | 109 | 1 | KV3B_HUMAN | P01620 | homo sapien  |
| 45 | 8 | 3.6 | 109 | 1 | KV3D_HUMAN | P01622 | homo sapien  |

## ALIGNMENTS

RESULT 1

| ID | KAC_HUMAN                                                                                                                                                                                                                                           | STANDARD; | PRT; | 106 AA. |
|----|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------|------|---------|
| AC | P01834;                                                                                                                                                                                                                                             |           |      |         |
| DT | 21-JUL-1986 (Rel. 01, Created)                                                                                                                                                                                                                      |           |      |         |
| DT | 21-JUL-1986 (Rel. 01, Last sequence update)                                                                                                                                                                                                         |           |      |         |
| DT | 16-OCT-2001 (Rel. 40, Last annotation update)                                                                                                                                                                                                       |           |      |         |
| DE | Ig kappa chain C region.                                                                                                                                                                                                                            |           |      |         |
| GN | IGKC.                                                                                                                                                                                                                                               |           |      |         |
| OS | Homo sapiens (Human).                                                                                                                                                                                                                               |           |      |         |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                                                                                                                                                                                   |           |      |         |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                                                                                                                                                                                          |           |      |         |
| OX | NCBI_TaxID=9606;                                                                                                                                                                                                                                    |           |      |         |
| RN | [1]                                                                                                                                                                                                                                                 |           |      |         |
| RP | SEQUENCE (MYELOMA PROTEIN EU).                                                                                                                                                                                                                      |           |      |         |
| RX | MEDLINE=71064023; PubMed=5489770;                                                                                                                                                                                                                   |           |      |         |
| RA | Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;                                                                                                                                                                                       |           |      |         |
| RT | "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain.";                                                                                                                                            |           |      |         |
| RL | Biochemistry 9:3155-3161(1970).                                                                                                                                                                                                                     |           |      |         |
| RN | [2]                                                                                                                                                                                                                                                 |           |      |         |
| RP | DISULFIDE BONDS.                                                                                                                                                                                                                                    |           |      |         |
| RX | MEDLINE=71064027; PubMed=4923144;                                                                                                                                                                                                                   |           |      |         |
| RA | Gall W.E., Edelman G.M.;                                                                                                                                                                                                                            |           |      |         |
| RT | "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";                                                                                                                                                         |           |      |         |
| RL | Biochemistry 9:3188-3196(1970).                                                                                                                                                                                                                     |           |      |         |
| RN | [3]                                                                                                                                                                                                                                                 |           |      |         |
| RP | SEQUENCE (BENCE-JONES PROTEIN TI).                                                                                                                                                                                                                  |           |      |         |
| RX | MEDLINE=72188439; PubMed=5027703;                                                                                                                                                                                                                   |           |      |         |
| RA | Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;                                                                                                                                                                                                |           |      |         |
| RT | "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."; |           |      |         |
| RL | Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).                                                                                                                                                                                                 |           |      |         |
| RN | [4]                                                                                                                                                                                                                                                 |           |      |         |
| RP | SEQUENCE FROM N.A.                                                                                                                                                                                                                                  |           |      |         |
| RX | MEDLINE=81042304; PubMed=6775818;                                                                                                                                                                                                                   |           |      |         |
| RA | Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;                                                                                                                                                                                    |           |      |         |
| RT | "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments.";                                                                                                                                |           |      |         |
| RL | Cell 22:197-207(1980).                                                                                                                                                                                                                              |           |      |         |
| RN | [5]                                                                                                                                                                                                                                                 |           |      |         |
| RP | SEQUENCE (BENCE-JONES PROTEIN ROY).                                                                                                                                                                                                                 |           |      |         |
| RA | Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,                                                                                                                                                                                     |           |      |         |
| RA | Steinmetz-Kayne M., Suter L., Watanabe S.;                                                                                                                                                                                                          |           |      |         |
| RL | (In) Franek F., Shugar D. (eds.);                                                                                                                                                                                                                   |           |      |         |
| RL | Gamma globulins: structure and function, pp.57-74, Academic Press,                                                                                                                                                                                  |           |      |         |
| RL | New York (1969).                                                                                                                                                                                                                                    |           |      |         |
| RN | [6]                                                                                                                                                                                                                                                 |           |      |         |
| RP | SEQUENCE (BENCE-JONES PROTEIN CUM).                                                                                                                                                                                                                 |           |      |         |
| RX | MEDLINE=68242259; PubMed=5586923;                                                                                                                                                                                                                   |           |      |         |
| RA | Hilschmann N.;                                                                                                                                                                                                                                      |           |      |         |
| RT | "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";                                                                                                                                                                        |           |      |         |

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RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RA Titani K., Shinoda T., Putnam F.W.;
RT "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
chains.";
RL Science 169:56-59(1970).
CC -1- MISCELLANEOUS: THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
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CC -----
DR EMBL; J00241; AAA58989.1; -;
DR EMBL; V00557; CAA23823.1; -;
DR PIR; A02116; K3HU.
DR HSSP; P01842; 7FAB.
DR MIM; 147200; -.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003597; Ig_C1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00407; IGcl; 1.
DR PROSITE; PS00290; IG_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
FT VARIANT 83 83 * V-> L (IN INV(1,2) MARKER).
FT CONFLICT 14 14 D -> N (IN REF. 7 AND 8).
FT CONFLICT 57 57 E -> Q (IN REF. 5 AND 6).
SQ SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
Query Match 48.2%; Score 106; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 1.3e-103; Mismatches 0; Gaps 0;
Matches 106; Conservative 0; Indels 0;
QY 115 TVAAPSVFIFPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174
DB 1 TVAAPSVFIFPPSDQLKSGTASVVCCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
QY 175 KDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSNRGEK 220
DB 61 KDSYSLSTLTLSKADYKHKVYACEVTHOGLSSPVTKSNRGEK 106
RESULT 2
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RESULT 3
KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
Primary amyloidosis.";
RL Biochemistry 12:3763-3780(1973).
RN [2]
SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
patient with plasma cell dyscrasia and amyloidosis.";
RL J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
diversity.";
RL Nature 309:73-76(1984).
CC -----
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CC -----
DR EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IgV; 1.
DR Immunoglobulin V region; Signal.
FT NON_TER 1 1
FT SIGNAL <1 4
FT CHAIN 5 117 IG KAPPA CHAIN V-II REGION GM607.
FT DOMAIN 28 27 FRAMEWORK-1.
FT DOMAIN 44 58 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 59 65 FRAMEWORK-2.
FT DOMAIN 66 97 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 98 106 FRAMEWORK-3.
FT DOMAIN 107 116 COMPLEMENTARITY-DETERMINING-3.
FT DISULFID 27 97 FRAMEWORK-4.
FT NON_TER 117 117 BY SIMILARITY.
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
Query Match 14.1%; Score 31; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 4.8e-25;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 TQPSLSLPVTPGEPASISCRSSQSLHNSGY 35
DB 9 TQPSLSLPVTPGEPASISCRSSQSLHNSGY 39
RESULT 3
KV2D_HUMAN STANDARD; PRT; 113 AA.
ID KV2D_HUMAN
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
Primary amyloidosis.";
RL Biochemistry 12:3763-3780(1973).
RN [2]
SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;
RT "Structural identity of Bence Jones and amyloid fibril proteins in a
patient with plasma cell dyscrasia and amyloidosis.";
RL J. Clin. Invest. 52:1276-1281(1973).
CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL
```



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CC WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.
CC -I- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A
CC PATIENT WITH PLASMA CELL DYSCRASIA AND AMYLOIDOSIS.
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
DR PIR: A01888; K2HUTW.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein; Anyloid.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 39 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 40 54 FRAMEWORK-2.
FT DOMAIN 55 61 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 62 93 FRAMEWORK-3.
FT DOMAIN 94 102 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 103 112 FRAMEWORK-4.
FT DISULFID 23 93 BY SIMILARITY.
FT NON_TER 113
SQ SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 12.7%; Score 28; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 6.5e-22;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TQSPSLPVTGPEPASISCRSSQSLHS 32
DQ 5 TQSPSLPVTGPEPASISCRSSQSLHS 32
|||||
DQ 5 TQSPSLPVTGPEPASISCRSSQSLHS 32
|||||

RESULT 4
KV2C_HUMAN
ID KV2C_HUMAN STANDARD; PRT; 112 AA.
AC P01616;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region M1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA Dreyer W.J., Gray W.R., Hood L.E.;
RT "The genetic, molecular, and cellular basis of antibody formation:
RT some facts and a unifying hypothesis.";
RL Cold Spring Harb. Symp. Quant. Biol. 32:353-367(1967).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01887; K2HUTL.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 38 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 39 53 FRAMEWORK-2.
FT DOMAIN 54 60 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 61 92 FRAMEWORK-3.
FT DOMAIN 93 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 111 FRAMEWORK-4.
FT DISULFID 23 92 BY SIMILARITY.
FT NON_TER 112
SQ SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 11.8%; Score 26; DB 1; Length 112;
Best Local Similarity 100.0%; Pred. No. 8e-20;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IVLTQSPSLPVTGPEPASISCRSSQ 27

```

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DQ 2 IVLTQSPSLPVTGPEPASISCRSSQ 27
|||||
DQ 2 IVLTQSPSLPVTGPEPASISCRSSQ 27
|||||

RESULT 5
KV2A_HUMAN
ID KV2A_HUMAN STANDARD; PRT; 115 AA.
AC P01614;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region Cum.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=68242259; PubMed=5586923;
RA Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-
RT type).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [2]
RP REVISIONS TO 50; 52; 96 AND 97.
RX MEDLINE=70063440; PubMed=4188189;
RA Hilschmann N.;
RT "Molecular basis of antibody formation.";
RL Naturwissenschaften 56:195-205(1969).
CC -I- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -I- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR: A01885; K2HUCM.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig; 1.
DR SMART: SM00406; IGV; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DISULFID 24 95 BY SIMILARITY.
FT NON_TER 115
SQ SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 10.5%; Score 23; DB 1; Length 115;
Best Local Similarity 100.0%; Pred. No. 1.1e-16;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PLSLPVTGPEPASISCRSSQSL 30
DQ 9 PLSLPVTGPEPASISCRSSQSL 31
|||||
DQ 9 PLSLPVTGPEPASISCRSSQSL 31
|||||

RESULT 6
KV2D_MOUSE
ID KV2D_MOUSE STANDARD; PRT; 112 AA.
AC P01629;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 2S1.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RA MEDLINE=83055101; PubMed=7141411;
RA Herbst H., Chang J.Y., Abersold R., Braun D.G.;
RT "Murine VK25 isotype sequence: monoclonal antibody 2S1.3 specific for
RT the group A streptococcal polysaccharide.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).
CC -I- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL
CC ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.
DR PIR: A01911; KVMSS1.
DR InterPro: IPR003006; Ig_MHC.

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1

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 DR EMBL; Z00020; CAA77315.1; -.  
 DR PIR; A01890; K2HURP.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 KW Immunoglobulin V region; Signal.  
 FT SIGNAL 1 20  
 FT CHAIN 21 133 IG KAPPA CHAIN V-II REGION RPMI 6410.  
 FT DOMAIN 21 43 FRAMEWORK-1.  
 FT DOMAIN 44 59 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 60 74 FRAMEWORK-2.  
 FT DOMAIN 75 81 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 82 113 FRAMEWORK-3.  
 FT DOMAIN 114 122 COMPLEMENTARITY-DETERMINING-3.  
 FT DOMAIN 123 132 FRAMEWORK-4.  
 FT DISULFID 43 113 BY SIMILARITY.  
 FT NON\_TER 133 133  
 SQ SEQUENCE 133 AA; 14707 MW; 513CCAF3673009EE CRC64;

Query Match 7.7%; Score 17; DB 1; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-10;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 80 ISRVEADVGVYCMQG 96  
 DB 100 ISRVEADVGVYCMQG 116  
 |||||

RESULT 10  
 KVL\_CANFA STANDARD; PRT; 108 AA.  
 ID KVL\_CANFA  
 AC P01618;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V region GOM.  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=79026193; PubMed=100411;  
 RA Wasserman R.L., Capra J.D.;  
 RT "The amino acid sequence of the light chain variable region of a  
 RT canine myeloma immunoglobulin: evidence that the VK subgroups  
 RT predicated mammalian speciation."  
 RL Immunochimistry 15:303-305(1978).  
 CC -|- MISCELLANEOUS: PEPTIDES WERE ALIGNED BY HOMOLGY WITH HUMAN KAPPA  
 CC CHAINS.  
 CC -|- MISCELLANEOUS: THE SEQUENCE OF THE V REGION OF THE HEAVY CHAIN OF  
 CC THIS MYELOMA PROTEIN HAS ALSO BEEN DETERMINED.  
 CC PIR; A01907; K2DGGM.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 KW Immunoglobulin V region.  
 FT DOMAIN 1 23  
 FT DOMAIN 24 34 FRAMEWORK-1.  
 FT DOMAIN 35 49 COMPLEMENTARITY-DETERMINING-1.  
 FT DOMAIN 50 56 FRAMEWORK-2.  
 FT DOMAIN 57 88 COMPLEMENTARITY-DETERMINING-2.  
 FT DOMAIN 89 97 FRAMEWORK-3.  
 FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING-3.  
 FT DISULFID 23 88 BY SIMILARITY.  
 FT NON\_TER 108 108  
 SQ SEQUENCE 108 AA; 12005 MW; 02FBC498C47A3126 CRC64;

Query Match 6.4%; Score 14; DB 1; Length 108;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-07;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 PGEPASISCRSSQS 28  
 DB 15 PGEPASISCRSSQS 28  
 |||||

RESULT 11  
 KVID\_HUMAN STANDARD; PRT; 107 AA.  
 ID KVID\_HUMAN  
 AC P01596;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-I region CAR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=75075135; PubMed=4216454;  
 RA Milstein C.P., Deverson E.V.;  
 RT "Primary structure of kappa light chain from a human myeloma  
 RT protein."  
 RL Eur. J. Biochem. 49:377-391(1974).  
 CC -|- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)  
 CC MARKER.  
 CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.  
 DR PIR; A01864; KIHUAR.  
 DR HSSP; P80362; IWTL.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR InterPro; IPR003596; Ig\_V.  
 DR Pfam; PF00047; Ig; 1.  
 DR SMART; SM00406; IgV; 1.  
 KW Immunoglobulin V region; Glycoprotein.  
 FT CARBOHYD 28 N-LINKED (GLCNAC. . .).  
 FT NON\_TER 107 107  
 SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;

Query Match 5.9%; Score 13; DB 1; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-06;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 FTGPGTKVDIKR 113  
 DB 95 FTGPGTKVDIKR 107  
 |||||

RESULT 12  
 KV2B\_HUMAN STANDARD; PRT; 113 AA.  
 ID KV2B\_HUMAN  
 AC P01615;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Ig kappa chain V-II region FR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76253627; PubMed=821524;  
 RA Riesen W.F., Jaton J.-C.;  
 RT "Variable region sequence of the light chain from a Waldenstrom's IgM  
 RT with specificity for phosphorylcholine."  
 RL Biochemistry 15:3829-3833(1976).  
 CC -|- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S  
 CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.

```
DR PIR; A01886; K2HUPR.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 5.0%; Score 11; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 AEDGVVYCMQ 95
Db 85 AEDGVVYCMQ 95
|||||

RESULT 13
KV2G_MOUSE
ID KV2G_MOUSE STANDARD; PRT; 113 AA.
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 1
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies M.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
PROTEIN THAT BINDS DIGOXIN.
CC PIR; A01914; KWS26.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON_TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 5.0%; Score 11; DB 1; Length 113;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ASISCRSSQL 29
Db 19 ASISCRSSQL 29
|||||

RESULT 14
LV1F_HUMAN
ID LV1F_HUMAN STANDARD; PRT; 109 AA.
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
the lambda light chain.";
RL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
DR PIR; A01967; L1HUWA.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 97
FT DOMAIN 98 109
FT DISULFID 22 89
FT NON_TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match 4.5%; Score 10; DB 1; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVPDRFSGS 70
Db 57 SGVPDRFSGS 66
|||||

RESULT 15
LV2E_HUMAN
ID LV2E_HUMAN STANDARD; PRT; 109 AA.
AC P01708;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-II region BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN 1
RP SEQUENCE.
RX MEDLINE=80006606; PubMed=113407;
RA Infante A.J., Putnam F.W.;
RT "Primary structure of a human IgA1 immunoglobulin. V. Amino acid
sequence of a human IgA lambda light chain (Bur).";
RL J. Biol. Chem. 254:9006-9016(1979).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE KERN+ AND MCG+
MARKERS.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01974; L2HUBR.
DR HSSP; P01709; 2MCG.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
KW Immunoglobulin V region.
FT MOD_RES 1 90
FT DISULFID 22 90
BY SIMILARITY.
```

FT SITE 91 91 APPEARS TO BE A FREE BUT UNREACTIVE  
FT NON\_TER 109 109 SULFHYDRYL GROUP.  
SQ SEQUENCE 109 AA; 11506 MW; BFD8AE1C5D267FAB CRC64;  
Query Match 4.5%; Score 10; DB 1; Length 109;  
Best local similarity 100.0%; Pred. No. 0.0044;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 61 SGVPRFRSGS 70  
Db 58 SGVPRFRSGS 67

Search completed: October 9, 2002, 19:23:37  
Job time : 7.73469 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:14:10 ; Search time 18.801 Seconds  
(without alignments)  
2024.299 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 220

Sequence: 1 EIVLTQSLPLVTPGPAS.....EVTHOGLSPVTKSFNRGEC 220

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

SPTREMBL19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 17    | 7.7         | 114    | 4     | Q9UL80      |
| 2          | 14    | 6.4         | 108    | 4     | Q9UL83      |
| 3          | 13    | 5.9         | 109    | 4     | Q9UL86      |
| 4          | 11    | 5.0         | 104    | 11    | Q9UL82      |
| 5          | 11    | 5.0         | 116    | 4     | Q96PF6      |
| 6          | 10    | 4.5         | 107    | 4     | Q9UL81      |
| 7          | 10    | 4.5         | 108    | 4     | Q96SB0      |
| 8          | 10    | 4.5         | 112    | 4     | Q96JD2      |
| 9          | 10    | 4.5         | 112    | 4     | Q96JD1      |
| 10         | 10    | 4.5         | 116    | 4     | Q96JD0      |
| 11         | 10    | 4.5         | 235    | 11    | Q91WI2      |
| 12         | 10    | 4.5         | 236    | 4     | Q96E61      |
| 13         | 10    | 4.5         | 238    | 11    | Q99M37      |
| 14         | 9     | 4.1         | 211    | 11    | Q91XL0      |
| 15         | 9     | 4.1         | 214    | 11    | Q9RLA5      |
| 16         | 9     | 4.1         | 233    | 11    | Q91WS9      |

|    |   |     |     |    |        |
|----|---|-----|-----|----|--------|
| 17 | 9 | 4.1 | 234 | 11 | Q91WF8 |
| 18 | 8 | 3.6 | 97  | 11 | Q9JL76 |
| 19 | 8 | 3.6 | 109 | 4  | Q9UL78 |
| 20 | 8 | 3.6 | 258 | 16 | Q98DX9 |
| 21 | 8 | 3.6 | 278 | 11 | Q921K1 |
| 22 | 8 | 3.6 | 337 | 6  | Q95M34 |
| 23 | 8 | 3.6 | 468 | 11 | Q99L31 |
| 24 | 8 | 3.6 | 473 | 11 | Q9DL4  |
| 25 | 8 | 3.6 | 473 | 11 | Q99L25 |
| 26 | 8 | 3.6 | 473 | 11 | Q91Z05 |
| 27 | 8 | 3.6 | 480 | 4  | Q96JV4 |
| 28 | 8 | 3.6 | 490 | 16 | P74334 |
| 29 | 7 | 3.2 | 75  | 16 | O50840 |
| 30 | 7 | 3.2 | 77  | 12 | Q84508 |
| 31 | 7 | 3.2 | 95  | 16 | Q9RVD5 |
| 32 | 7 | 3.2 | 99  | 11 | Q9JL74 |
| 33 | 7 | 3.2 | 105 | 17 | Q96ZF1 |
| 34 | 7 | 3.2 | 106 | 5  | Q9U410 |
| 35 | 7 | 3.2 | 107 | 4  | Q9NSD6 |
| 36 | 7 | 3.2 | 107 | 4  | Q96SA9 |
| 37 | 7 | 3.2 | 107 | 11 | Q9ERZ9 |
| 38 | 7 | 3.2 | 108 | 4  | Q9UL79 |
| 39 | 7 | 3.2 | 108 | 4  | Q9UL77 |
| 40 | 7 | 3.2 | 108 | 4  | Q9UL70 |
| 41 | 7 | 3.2 | 111 | 11 | Q920S9 |
| 42 | 7 | 3.2 | 116 | 16 | Q92CR3 |
| 43 | 7 | 3.2 | 130 | 4  | Q9NP29 |
| 44 | 7 | 3.2 | 159 | 16 | Q9RXP4 |
| 45 | 7 | 3.2 | 164 | 5  | Q9GN43 |

#### ALIGNMENTS

RESULT 1

Q9UL80  
ID Q9UL80 PRELIMINARY; PRT; 114 AA.  
AC Q9UL80;  
DT 01-MAY-2000 (TRENBLrel. 13, Created)  
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
DE 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035034; AAD56270.1; -  
DR HSSP; P80362; 1WTL.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; Igv; 1.  
FT NON\_TER 1  
FT NON\_TER 114  
SQ SEQUENCE 114 AA; 12175 MW; 070E31E210D1CB01 CRC64;

Query Match 7.7%; Score 17; DB 4; Length 114;  
Best Local Similarity 100.0%; Pred. No. 1.1e-09;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 ISRVEADVGYYCMQG 96

|||||

Db 80 ISRVEADVGYYCMQG 96

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RESULT 2
Q9UL83 ID Q9UL83 PRELIMINARY; PRT; 108 AA.
AC Q9UL83;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.",
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035031; AAD56267.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 108
SQ SEQUENCE 108 AA; 11834 MW; 9F9C5A92EBA96EEA CRC64;

Query Match 6.4%; Score 14; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 100 PTFGPGTKVDIKR 113
Db 95 PTFGPGTKVDIKR 108
|||||

RESULT 3
Q9UL86 ID Q9UL86 PRELIMINARY; PRT; 109 AA.
AC Q9UL86;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE MYOSIN-REACTIVE IMMUNOGLOBULIN KAPPA CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.",
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035028; AAD56264.1; -.
DR HSSP; P80362; 1WTL.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 109
SQ SEQUENCE 109 AA; 11928 MW; 243325F72C7DAC83 CRC64;

Query Match 5.9%; Score 13; DB 4; Length 109;

Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 101 FTFGPGTKVDIKR 113
Db 97 FTFGPGTKVDIKR 109
|||||

RESULT 4
Q9JL82 ID Q9JL82 PRELIMINARY; PRT; 104 AA.
AC Q9JL82;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ANTI-MYOSIN IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION
DE (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALB/C;
RC MEDLINE=20448942; PubMed=10992488;
RA Malkiel S., Liao L., Cunningham M.W., Diamond B.;
RT "T-Cell-dependent antibody response to the dominant epitope of
RT streptococcal polysaccharide, N-acetyl-glucosamine, is cross-reactive
RT with cardiac myosin.",
RL Infect. Immun. 68:5803-5808(2000).
DR EMBL; AF206024; AAF69322.1; -.
DR HSSP; P01607; 1REI.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; Igv; 1.
FT NON_TER 1 104
SQ SEQUENCE 104 AA; 11360 MW; 5DA8BBFD5F0AALAE CRC64;

Query Match 5.0%; Score 11; DB 11; Length 104;
Best Local Similarity 100.0%; Pred. No. 0.002;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ASISCRSSQSL 29
Db 11 ASISCRSSQSL 21
|||||

RESULT 5
Q96PF6 ID Q96PF6 PRELIMINARY; PRT; 116 AA.
AC Q96PF6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE KAPPA 1 LIGHT CHAIN VARIABLE REGION (FRAGMENT).
GN SDNKL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21361171; PubMed=11468171;
RA Comenzo R.L., Zhang Y., Martinez C., Osman K., Herrera G.A.;
RT "The tropism of organ involvement in primary systemic amyloidosis:
RT contributions of Ig V(L) germ line gene use and clonal plasma cell
RT burden.",
RL Blood 98:714-720(2001).
DR EMBL; AF361758; AAK51465.1; -.
FT NON_TER 1 116
SQ SEQUENCE 116 AA; 1116 MW; 116
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SQ SEQUENCE 116 AA; 12735 MW; E796FC2217BFCF57 CRC64;  
Query Match 5.0%; Score 11; DB 4; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.0022;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 100 PFTFGPGTKVD 110  
Db 95 PFTFGPGTKVD 105  
RESULT 6  
Q9UL81  
ID Q9UL81 PRELIMINARY; PRT; 107 AA.  
AC Q9UL81  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE MYOSIN-REACTIVE IMMUNOGLOBULIN LIGHT CHAIN VARIABLE REGION  
DE (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98277139; PubMed=9614934;  
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,  
RA Young D.C.;  
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal  
RT fetus.";  
RL Clin. Immunol. Immunopathol. 87:184-192(1998).  
DR EMBL; AF035033; AAD56269.1; -;  
DR HSSP; P01607; IREI.  
DR InterPro; IPR003006; Iq\_MHC.  
DR InterPro; IPR003596; Iq\_V.  
DR Pfam; PF00047; Iq; 1.  
DR SMART; SM00406; IGV; 1.  
FT NON\_TER 1  
FT NON\_TER 107  
SQ SEQUENCE 107 AA; 11501 MW; 070549FDE0754748 CRC64;

Query Match 4.5%; Score 10; DB 4; Length 107;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 TFGPGTKVDI 111  
Db 96 TFGPGTKVDI 105

RESULT 7  
Q96SB0  
ID Q96SB0 PRELIMINARY; PRT; 108 AA.  
AC Q96SB0  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ANTI-STREPTOCOCCAL/ANTI-MYOSIN IMMUNOGLOBULIN LAMBDA LIGHT CHAIN  
DE VARIABLE REGION (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98375893; PubMed=9712075;  
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;  
RT "Molecular analysis of polyreactive monoclonal antibodies from  
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-myosin  
RT antibody V region genes.";  
RL J. Immunol. 161:2020-2031(1998).  
DR EMBL; U96394; AAB68783.1; -;

FT NON\_TER 1  
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;  
Query Match 4.5%; Score 10; DB 4; Length 108;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 61 SGVPDRFSGS 70  
Db 57 SGVPDRFSGS 66

RESULT 8  
Q96JD2  
ID Q96JD2 PRELIMINARY; PRT; 112 AA.  
AC Q96JD2  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION NEG (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE-BONE MARROW;  
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;  
RT "Amyloid lambda 6 light chain variable region NEG.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF267873; AAK58585.1; -;  
FT NON\_TER 1  
FT NON\_TER 112  
SQ SEQUENCE 112 AA; 11908 MW; 080B4B37E2360B06 CRC64;

Query Match 4.5%; Score 10; DB 4; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVPDRFSGS 70  
Db 57 SGVPDRFSGS 66

RESULT 9  
Q96JDI  
ID Q96JDI PRELIMINARY; PRT; 112 AA.  
AC Q96JDI  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE AMYLOID LAMBDA 6 LIGHT CHAIN VARIABLE REGION PIP (FRAGMENT).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE-BONE MARROW;  
RA Perfetti V., Casarini S., Colli Vignarelli M., Merlini G.;  
RT "Amyloid lambda 6 light chain variable region PIP.";  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF267874; AAK58586.1; -;  
FT NON\_TER 1  
FT NON\_TER 112  
SQ SEQUENCE 112 AA; 12047 MW; 0D3885AC23567B9F CRC64;

Query Match 4.5%; Score 10; DB 4; Length 112;  
Best Local Similarity 100.0%; Pred. No. 0.023;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 SGVPDRFSGS 70  
Db 57 SGVPDRFSGS 66

|                          |                                                                   |
|--------------------------|-------------------------------------------------------------------|
| OC                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC                       | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.        |
| OX                       | NCBI_TaxID=9606;                                                  |
| [1]                      |                                                                   |
| RN                       | SEQUENCE FROM N.A.                                                |
| RP                       | TISSUE=BRAIN, AND GLOBLASTOMA WITH EGFR AMPLIFICATION;            |
| RC                       | Strausberg R.;                                                    |
| RA                       | Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.           |
| RL                       | EMBL; BC012876; AAH12876.1; -. 7EC9FB3622FED957 CRC64;            |
| DQ                       | SEQUENCE 236 AA; 24712 MW; 24712 MW;                              |
| Query Match              | 4.5%; Score 10; DB 4; Length 236;                                 |
| Best Local Similarity    | 100.0%; Pred. No. 0.046;                                          |
| Matches 10; Conservative | 0; Mismatches 0; Indels 0; Gaps 0;                                |
| OY                       | 61 SGVPRDFSGS 70<br>                                              |
| Db                       | 77 SGVPRDFSGS 86<br>                                              |
| RESULT 13                |                                                                   |
| Q99M37                   | PRELIMINARY; PRT; 238 AA.                                         |
| ID                       | Q99M37                                                            |
| AC                       | Q99M37;                                                           |
| DT                       | 01-JUN-2001 (TREMBLrel. 17, Created)                              |
| DT                       | 01-JUN-2001 (TREMBLrel. 17, Last sequence update)                 |
| DE                       | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)               |
| DE                       | HYPOTHETICAL 26.3 KDA PROTEIN.                                    |
| OS                       | Mus musculus (Mouse).                                             |
| OC                       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; |
| OC                       | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.         |
| OX                       | NCBI_TaxID=10090;                                                 |
| [1]                      |                                                                   |
| RN                       | SEQUENCE FROM N.A.                                                |
| RP                       | TISSUE=MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS OLD, GROSS    |
| RC                       | TISSUE:                                                           |
| RA                       | Strausberg R.;                                                    |
| RL                       | Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.           |
| DR                       | EMBL; BC020335; AAH02035.1; -. HSP; P01679; 2FEJ.                 |
| DR                       | InterPro: IPR003599; Ig.                                          |
| DR                       | InterPro: IPR003597; Ig_c1.                                       |
| DR                       | InterPro: IPR003600; Ig_like.                                     |
| DR                       | InterPro: IPR003006; Ig_MHC.                                      |
| DR                       | InterPro: IPR003596; Ig_v.                                        |
| DR                       | Pfam; PF00047; Ig; 2.                                             |
| DR                       | SMART; SM00409; IG; 2.                                            |
| DR                       | SMART; SM00407; IGc1; 1.                                          |
| DR                       | SMART; SM00406; IGV; 1.                                           |
| DR                       | SMART; SM00410; IG_Like; 1.                                       |
| DR                       | PROSITE; PS00290; IG_MHC; UNKNOWN_1.                              |
| KW                       | Hypothetical protein.                                             |
| SQ                       | SEQUENCE 238 AA; 26344 MW; FB2B06A0B801330A CRC64;                |
| Query Match              | 4.5%; Score 10; DB 11; Length 238;                                |
| Best Local Similarity    | 100.0%; Pred. No. 0.046;                                          |
| Matches 10; Conservative | 0; Mismatches 0; Indels 0; Gaps 0;                                |
| Oy                       | 19 ASISCRSSQS 28<br>                                              |
| Db                       | 38 ASISCRSSQS 47<br>                                              |
| RESULT 14                |                                                                   |
| Q91XL0                   | PRELIMINARY; PRT; 211 AA.                                         |
| ID                       | Q91XL0                                                            |
| AC                       | Q91XL0;                                                           |
| DT                       | 01-DEC-2001 (TREMBLrel. 19, Created)                              |
| DT                       | 01-DEC-2001 (TREMBLrel. 19, Last sequence update)                 |
| DT                       | 01-DEC-2001 (TREMBLrel. 19, Last annotation update)               |
| DE                       | ADULT MALE KIDNEY CDNA, RIKEN FULL-LENGTH ENRICHED LIBRARY,       |
| DE                       | CLONE:O61001OP20, FULL INSERT SEQUENCE.                           |
| OS                       | Mus musculus (Mouse).                                             |

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RA Adachi J., Aizawa K., Akahira S., Akimura T., Aono H., Arai A.,
RA Arakawa T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Haraoka T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kato H., Kawai J., Kojima Y.,
RA Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Okazaki Y., Okido T.,
RA Owa C., Saito H., Saito R., Sakai C., Sakai K., Sano H., Sasaki D.,
RA Shibata K., Shibata Y., Shinagawa A., Shiraki T., Sogabe Y.,
RA Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., Tejima Y.,
RA Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA RIKEN FANTOM Consortium.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX MEDLINE=20499374; PubMed=11042159;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=KIDNEY;
RX STRAIN=20530913; PubMed=11076861;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
DR EMBL; AK002514; BAB22154.1; .
SQ SEQUENCE 211 AA; 23182 MW; 1A5FFA0F8A50163 CRC64;

Query Match 4.1%; Score 9; DB 11; Length 211;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 QDSKDSYSTS 180
DB 163 QDSKDSYSTS 171

RESULT 15
Q9RIA5 PRELIMINARY; PRT; 214 AA.
AC Q9RIA5;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
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DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE KAPPA LIGHT CHAIN OF MAB7 (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramoddoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; .
DR HSSP; P01679; 2FBJ.
DR InterPro; IPR003600; Ig_like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00410; IG_like; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 4.1%; Score 9; DB 11; Length 214;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 QDSKDSYSTS 180
DB 166 QDSKDSYSTS 174

Search completed: October 9, 2002, 19:24:57
Job time : 18.801 secs
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:04:24 ; Search time 23.5714 Seconds  
(without alignments)  
1036.689 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSPVSLPVTGPAS.....EVTHQGLSPVTKSFNRGEC 220

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

- 1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*
- 2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*
- 3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.\*
- 4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.\*
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- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.\*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.\*
- 22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query Match | Length | ID       | Description        |
|------------|--------|-------------|--------|----------|--------------------|
| 1          | 1146   | 100.0       | 220    | AAE12714 | Human recombinant  |
| 2          | 1073.5 | 93.7        | 239    | AAE12714 | Human PTHRP monocl |
| 3          | 1069.5 | 93.3        | 239    | AAE12714 | Human PTHRP monocl |
| 4          | 1065.5 | 93.0        | 239    | AAE12714 | Human PTHRP monocl |
| 5          | 1058.5 | 92.4        | 239    | AAE12714 | Human PTHRP monocl |
| 6          | 1053.5 | 91.9        | 239    | AAE12714 | Human PTHRP monocl |
| 7          | 1048.5 | 91.5        | 239    | AAE12714 | Human PTHRP monocl |
| 8          | 1034.5 | 90.3        | 239    | AAE12714 | Human PTHRP monocl |
| 9          | 1034.5 | 90.3        | 239    | AAE12714 | Human PTHRP monocl |
| 10         | 1031.5 | 90.0        | 239    | AAE12714 | Human PTHRP monocl |
| 11         | 1021.5 | 89.1        | 239    | AAE12714 | Human PTHRP monocl |

|    |        |      |     |          |                     |
|----|--------|------|-----|----------|---------------------|
| 12 | 1015.5 | 88.6 | 238 | AAE12714 | Humanised 323/A3 (  |
| 13 | 1015.5 | 88.6 | 238 | AAE12714 | Humanised 323/A3 (  |
| 14 | 1015.5 | 88.6 | 238 | AAE12714 | Humanised 323/A3 (  |
| 15 | 1015.5 | 88.6 | 238 | AAE12714 | Humanised 323/A3 (  |
| 16 | 992.5  | 86.6 | 239 | AAE12714 | Primate anti-hu     |
| 17 | 992.5  | 86.6 | 239 | AAE12714 | Anti-human Fas hum  |
| 18 | 992.5  | 86.6 | 239 | AAE12714 | Anti-human Fas hum  |
| 19 | 992.5  | 86.6 | 239 | AAE12714 | Macaque primatized  |
| 20 | 992.5  | 86.6 | 239 | AAE12714 | Anti-human Fas hum  |
| 21 | 992.5  | 86.6 | 239 | AAE12714 | Anti-human Fas hum  |
| 22 | 988.5  | 86.3 | 239 | AAE12714 | Anti-human Fas hum  |
| 23 | 988.5  | 86.3 | 239 | AAE12714 | Anti-human Fas hum  |
| 24 | 988.5  | 86.3 | 239 | AAE12714 | Anti-human Fas hum  |
| 25 | 988.5  | 86.3 | 239 | AAE12714 | Anti-human Fas hum  |
| 26 | 987.5  | 86.2 | 238 | AAE12714 | Humanised monoclon  |
| 27 | 987    | 86.1 | 238 | AAE12714 | Monoclonal antibod  |
| 28 | 986.5  | 86.1 | 238 | AAE12714 | 3F4 Human IgG4 exp  |
| 29 | 986.5  | 86.1 | 238 | AAE12714 | Murine anti-porcine |
| 30 | 978.5  | 85.4 | 238 | AAE12714 | Chimeric 2403 IgG   |
| 31 | 963.5  | 84.1 | 241 | AAE12714 | Human IGFAM-15 imm  |
| 32 | 952.5  | 83.1 | 242 | AAE12714 | Chimeric 6G4.2.5.1  |
| 33 | 952.5  | 83.1 | 242 | AAE12714 | Murine variable re  |
| 34 | 952.5  | 83.1 | 242 | AAE12714 | Chimeric anti IL-8  |
| 35 | 952.5  | 83.1 | 242 | AAE12714 | Chimeric monoclon   |
| 36 | 952.5  | 83.1 | 242 | AAE12714 | Anti-IL-8 mouse-hu  |
| 37 | 952.5  | 83.1 | 242 | AAE12714 | Chimeric Mab 6G4.2  |
| 38 | 952.5  | 83.1 | 242 | AAE12714 | Chimeric anti IL-8  |
| 39 | 952.5  | 83.1 | 242 | AAE12714 | Chimeric 6G4.2.5.1  |
| 40 | 952.5  | 83.1 | 242 | AAE12714 | Murine 6G4-2.5 ant  |
| 41 | 952.5  | 83.1 | 242 | AAE12714 | Chimeric 6G4.2.5 a  |
| 42 | 929    | 81.1 | 218 | AAE12714 | Chimeric antibody   |
| 43 | 917    | 80.0 | 226 | AAE12714 | Human interleukin   |
| 44 | 917    | 80.0 | 226 | AAE12714 | Anti-IL8 monoclon   |
| 45 | 914    | 79.8 | 234 | AAE12714 | The kappa chain of  |

#### ALIGNMENTS

RESULT 1  
AAE12714  
ID AAE12714 standard; Protein; 220 AA.  
XX AC AAE12714;  
XX AC AAE12714;  
DT 04-JAN-2002 (first entry)  
XX Human recombinant immunoglobulin (Ig) light chain region.  
DE Human; tumour-associated antigen mucin-1; MUC-1; adenocarcinoma;  
KW light chain region; cancer; breast; ovary; lung; bladder;  
KW cytotatic; therapy; immunoglobulin; Ig.  
XX Homo sapiens.  
XX WO200175110-A2.  
XX 11-OCT-2001.  
XX 30-MAR-2001; 2001WO-US10589.  
XX 30-MAR-2000; 2000US-0538913.  
XX (DYAX-) DYAX CORP.  
XX Hoogenboom HRJM, Henderikx MPG;  
DR WPI; 2001-626437/72.  
XX N-PSDB; RAD20744.  
PT Novel isolated tumor-associated antigen mucin-1-specific binding member  
PT for diagnosing and treating cancer, comprises mucin-1 binding domain or  
PT its portion for binding to an epitope of the protein core of mucin-1 -





Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

## RESULT 5

AA82611

ID AAY82611 standard; Protein; 239 AA.

XX AC AAY82611;

XX DT 02-AUG-2000 (first entry)

XX DE Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:5.

XX KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
KW sepsis; systemic inflammatory response syndrome; SIRS;  
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX OS Homo sapiens.

XX PN JP2000080100-A.

XX PD 21-MAR-2000.

XX PF 12-OCT-1998; 98JP-0304793.

XX PR 17-JUN-1998; 98JP-0188196.

XX PR 26-JUN-1998; 98JP-0196729.

XX PA (NISB ) JAPAN TOBACCO INC.

XX DR WPI; 2000-285723/25.

XX DR N-PSDB; AAA13921.

XX PT A human monoclonal antibody to parathyroid hormone related protein. -  
XX PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
XX PT including metastasis, and pain

XX PS Claim 31; Page 34-35; 88pp; Japanese.

XX CC The present invention describes a human monoclonal antibody to  
XX CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
XX CC its fragments, following the stimulation of PTHrP has the following  
XX CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
XX CC the release of calcium from bone; or (c) inhibits elevation of blood  
XX CC calcium content. The monoclonal antibody can be used in the treatment  
XX CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
XX CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
XX CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
XX CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
XX CC antiinflammatory activities. The present sequence represents a  
XX CC human PTHrP monoclonal antibody clone protein sequence from the  
XX CC present invention.

XX SQ Sequence 239 AA;

Query Match 92.4%; Score 1058.5; DB 21; Length 239;

Best Local Similarity 92.7%; Pred. No. 2.3e-64;

Matches 204; Conservative 8; Mismatches 7; Indels 1; Gaps 1;

Qy 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLISGSHRA 60

Db 21 DIVMTQSPSLPVTGPEPATISCRSSQSLHNSGNYLDWFLQKPGQSPOLLISGSHRA 80

Qy 61 SGVDPDRFSGSVGCTDFTLRISRVEAEDGVGYCYMQGLQSPFTFGPGTKVDIKRGTVAAPS 120

Db 81 SGVDPDRFSGSGGDFDTLKLRSRVEAEDGVGLYCMQALQIPFTFGPGTKVDIKR-TVAAPS 139

Qy 121 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSTS 180

Db 140 VFIFPPSDEQLKSGTASVCLNNFYPREAKVQWVDNALQSGNSQESVTEQDSKDSYSTS 199

Qy 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

## RESULT 6

AA82610

ID AAY82610 standard; Protein; 239 AA.

XX AC AAY82610;

XX DT 02-AUG-2000 (first entry)

XX DE Human PTHrP monoclonal antibody clone 15H7-8-3 protein SEQ ID NO:4.

XX KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
KW sepsis; systemic inflammatory response syndrome; SIRS;  
KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys

XX FT Misc-difference 156 /label= Phe, Ser, Tyr, Cys

XX FT Misc-difference 164 /label= Phe, Ser, Tyr, Cys

XX FT /label= Phe, Leu

XX PN JP2000080100-A.

XX PD 21-MAR-2000.

XX PF 12-OCT-1998; 98JP-0304793.

XX PR 17-JUN-1998; 98JP-0188196.

XX PR 26-JUN-1998; 98JP-0196729.

XX PA (NISB ) JAPAN TOBACCO INC.

XX DR WPI; 2000-286723/25.

XX DR N-PSDB; AAA13920.

XX PT A human monoclonal antibody to parathyroid hormone related protein. -  
XX PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
XX PT including metastasis, and pain

XX PS Claim 31; Page 33; 88pp; Japanese.

XX CC The present invention describes a human monoclonal antibody to  
XX CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
XX CC its fragments, following the stimulation of PTHrP has the following  
XX CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
XX CC the release of calcium from bone; or (c) inhibits elevation of blood  
XX CC calcium content. The monoclonal antibody can be used in the treatment  
XX CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
XX CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal  
XX CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
XX CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
XX CC antiinflammatory activities. The present sequence represents a  
XX CC human PTHrP monoclonal antibody clone protein sequence from the  
XX CC present invention.

XX SQ Sequence 239 AA;

Query Match 91.9%; Score 1053.5; DB 21; Length 239;

Best Local Similarity 92.7%; Pred. No. 5e-64;

Matches 204; Conservative 5; Mismatches 10; Indels 1; Gaps 1;

Qy 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLISGSHRA 60

Db 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPOLLISGSHRA 60



Db 21 DIVMTQXPLSLPVTGEPASISCRFSQSLLHSNGNYYLDWYLOKPGSQPQLIYLGSNRA 80  
 Qy 61 SGVPDRFSGSGVSGTDFTLIRSRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120  
 Db 81 SGVPDRFSGSGVSGTDFTLIRSRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR-TVAAPS 139  
 Qy 121 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
 Db 140 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 199  
 Qy 181 LSSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 220  
 Db 200 LSSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 7  
 AAY82614  
 ID AAY82614 standard; Protein; 239 AA.  
 XX  
 AC AAY82614;  
 XX  
 DT 02-AUG-2000 (first entry)  
 XX  
 DE Human PTHrP monoclonal antibody clone 2F8-10-3 protein SEQ ID NO:12.  
 XX  
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
 KW sepsis; systemic inflammatory response syndrome; SIRS;  
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 25 /label= Ile, Thr, Asn, Ser  
 FT Misc-difference 27  
 FT Misc-difference 117 /label= Phe, Ser, Tyr, Cys  
 FT Misc-difference 146 /label= Leu, Ile, Val  
 FT Misc-difference 146 /label= Phe, Ser, Tyr, Cys  
 FT Misc-difference 216 /note= "possible Val"  
 XX  
 PN JP2000080100-A.  
 XX  
 PD 21-MAR-2000.  
 XX  
 PF 12-OCT-1998; 98JP-0304793.  
 XX  
 PR 17-JUN-1998; 98JP-0188196.  
 PR 26-JUN-1998; 98JP-0196729.  
 XX  
 PA (NISB ) JAPAN TOBACCO INC.  
 XX  
 DR WPI; 2000-286723/25.  
 DR N-PSDB; AAA13924.  
 XX  
 PT A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain  
 XX  
 PS Claim 31; Page 43; 88pp; Japanese.  
 XX  
 CC The present invention describes a human monoclonal antibody to  
 CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or  
 CC its fragments, following the stimulation of PTHrP has the following  
 CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  
 CC the release of calcium from bone; or (c) inhibits elevation of blood  
 CC calcium content. The monoclonal antibody can be used in the treatment  
 CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including  
 CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal

CC diseases and gingiva, sepsis, systemic inflammatory response syndrome  
 CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and  
 CC antiinflammatory activities. The present sequence represents a  
 CC human PTHrP monoclonal antibody clone protein sequence from the  
 CC present invention.  
 XX  
 SQ Sequence 239 AA;  
 Query Match 91.5%; Score 1048.5; DB 21; Length 239;  
 Best Local Similarity 92.3%; Pred. No. 1.1e-63;  
 Matches 203; Conservative 4; Mismatches 12; Indels 1; Gaps 1;  
 Qy 1 EIVLTQSLPLSPLVTPGEPASISCRFSQSLLHSNGNYYLDWYLOKPGSQPQLIYLGSNRA 60  
 Db 21 DIVMTQXPLSLPVTGEPASISCRFSQSLLHSNGNYYLDWYLOKPGSQPQLIYLGSNRA 80  
 Qy 61 SGVPDRFSGSGVSGTDFTLIRSRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120  
 Db 81 SGVPDRFSGSGVSGTDFTLIRSRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKR-TVAAPS 139  
 Qy 121 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
 Db 140 VFIFPPSDEQLKSGTASVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 199  
 Qy 181 LSSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 220  
 Db 200 LSSLTLSKADYEHKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 8  
 AAY82612  
 ID AAY82612 standard; Protein; 239 AA.  
 XX  
 AC AAY82612;  
 XX  
 DT 02-AUG-2000 (first entry)  
 XX  
 DE Human PTHrP monoclonal antibody clone 1B3-9-16 protein SEQ ID NO:8.  
 XX  
 KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;  
 KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;  
 KW fracture; cachexia; tooth disease; periodontal disease; gingiva;  
 KW sepsis; systemic inflammatory response syndrome; SIRS;  
 KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 25 /label= Ile, Thr, Asn, Ser  
 FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys  
 FT Misc-difference 84 /note= "possibly Pro"  
 XX  
 PN JP2000080100-A.  
 XX  
 PD 21-MAR-2000.  
 XX  
 PF 12-OCT-1998; 98JP-0304793.  
 XX  
 PR 17-JUN-1998; 98JP-0188196.  
 PR 26-JUN-1998; 98JP-0196729.  
 XX  
 PA (NISB ) JAPAN TOBACCO INC.  
 XX  
 DR WPI; 2000-286723/25.  
 DR N-PSDB; AAA13922.  
 XX  
 PT A human monoclonal antibody to parathyroid hormone related protein. -  
 PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone  
 PT including metastasis, and pain  
 XX

|           |     |                                                                          |
|-----------|-----|--------------------------------------------------------------------------|
| XX        | PA  | (NISB ) JAPAN TOBACCO INC.                                               |
| XX        | WPI | 2000-286723/25.                                                          |
| XX        | DR  | N-PSDB; AAA13923.                                                        |
| XX        | PT  | A human monoclonal antibody to parathyroid hormone related protein. -    |
| XX        | PT  | useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone |
| XX        | PT  | including metastasis, and pain                                           |
| XX        | PS  | Claim 31; Page 40; 88pp; Japanese.                                       |
| XX        | CC  | The present invention describes a human monoclonal antibody to           |
| XX        | CC  | parathyroid hormone related protein (PTHrP). The monoclonal antibody or  |
| XX        | CC  | its fragments, following the stimulation of PTHrP has the following      |
| XX        | CC  | properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits   |
| XX        | CC  | the release of calcium from bone; or (c) inhibits elevation of blood     |
| XX        | CC  | calcium content. The monoclonal antibody can be used in the treatment    |
| XX        | CC  | of hypercalcaemia, rheumatoid arthritis, cancer of bone including        |
| XX        | CC  | metastasis, pain, fracture, cachexia, diseases of teeth, periodontal     |
| XX        | CC  | diseases and gingiva, sepsis, systemic inflammatory response syndrome    |
| XX        | CC  | (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and       |
| XX        | CC  | antiinflammatory activities. The present sequence represents a           |
| XX        | CC  | human PTHrP monoclonal antibody clone protein sequence from the          |
| XX        | CC  | present invention.                                                       |
| XX        | CC  |                                                                          |
| XX        | CC  | Sequence 239 AA;                                                         |
| XX        | CC  |                                                                          |
| XX        | CC  | Query Match 90.3%; Score 1034.5; DB 21; Length 239;                      |
| XX        | CC  | Best Local Similarity 91.8%; Pred. No. 9.6e-63;                          |
| XX        | CC  | Matches 202; Conservative 5; Mismatches 12; Indels 1; Gaps               |
| XX        | CC  |                                                                          |
| Qy        | 1   | EIVLTQSPISLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 50           |
| Db        | 21  | :  :    :    :    :    :    :    :    :    :    :    :    :    : 80      |
| Qy        | 61  | SGVDPDRFSGVSGTDTFLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120         |
| Db        | 81  | 139                                                                      |
| Qy        | 121 | VFIFPPSDEQLKSGTAVVYCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 180         |
| Db        | 140 | VFIFPPSDEQLKSGTAVVYCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS 199         |
| Qy        | 191 | LSSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 220                               |
| Db        | 200 | LSSTLTLSKADYKHKVYACEVTHOGLSPVTKSFNRGEC 239                               |
| RESULT 10 |     |                                                                          |
| AAy82619  | ID  | AAy82619 standard; Protein; 239 AA.                                      |
| XX        | AC  | AAy82619;                                                                |
| XX        | DT  | 02-AUG-2000 (first entry)                                                |
| XX        | XX  | Human PTHrP monoclonal antibody clone 5B12-16-12 protein SEQ ID NO:22.   |
| XX        | DE  |                                                                          |
| XX        | DE  | Human parathyroid hormone related protein; PTHrP; monoclonal antibody;   |
| KW        | KW  | hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;     |
| KW        | KW  | fracture; cachexia; tooth disease; periodontal disease; gingiva;         |
| KW        | KW  | sepsis; systemic inflammatory response syndrome; SIRS;                   |
| KW        | KW  | hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.          |
| XX        | OS  | Homo sapiens.                                                            |
| XX        | XX  |                                                                          |
| XX        | XX  | Key Location/Qualifiers                                                  |
| FT        | FT  | Misc-difference 1                                                        |
| FT        | FT  | Misc-difference 3 /note= "possibly Met"                                  |
| FT        | FT  | Misc-difference 3 /label= Phe, Leu, Ile, Val                             |
| FT        | FT  | Misc-difference 4                                                        |

PS Claim 31; Page 37-38; 88pp; Japanese.

XX The present invention describes a human monoclonal antibody to

CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or

CC its fragments, following the stimulation of PTHrP has the following

CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits

CC the release of calcium from bone; or (c) inhibits elevation of blood

CC calcium content. The monoclonal antibody can be used in the treatment

CC of hypercalcaemia, rheumatoid arthritis, cancer of bone including

CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal

CC diseases and gingiva, sepsis, systemic inflammatory response syndrome

CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and

CC antiinflammatory activities. The present sequence represents a

CC human PTHrP monoclonal antibody clone protein sequence from the

XX present invention.

XX

SQ Sequence 239 AA;

Query Match 90.3%; Score 1034.5; DB 21; Length 239;

Best Local Similarity 91.8%; Pred. No. 9.6e-63;

Matches 202; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPILSPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60

DB 21 DIVMXQPLSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGQSLLIYLGSNRA 80

QY 61 SGVYDFRFGSGVSGTQFTLIRISRAEDGVYCYMGQLQSPFTFGPTKVDIKRGTVAAAPS 120

DB 81 SGVYDFRFGSGSGTQFTLIRISRAVEDGVYCYMGQLQSPFTFGPTKVDIKRGTVAAAPS 139

QY 121 VFIFPSPDEQLKSGTASVVYCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSITYS 180

DB 140 VFIFPSPDEQLKSGTASVVYCLNNFYPREAKVQMKVDNALQSGNSQESVTEQDSKDSITYS 199

QY 181 LSSTLTLSKADYEKKHYKVAACEVTHOGLSPVTKSFNNGEC 220

DB 200 LSSTLTLSKADYEKKHYKVAACEVTHOGLSPVTKSFNNGEC 239

RESULT 9

AY82613

ID AY82613 standard; Protein; 239 AA.

XX

AC AY82613;

XX

DT 02-AUG-2000 (first entry)

XX

DE Human PTHrP monoclonal antibody clone 1B4-10-13 protein SEQ ID NO:10.

XX

KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;

XX hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;

KW fracture; cachexia; tooth disease; periodontal disease; gingiva;

KW sepsis; systemic inflammatory response syndrome; SIRS;

KW hypophosphataemia; antiarthritic; cytostatic; antiinflammatory.

XX

OS Homo sapiens.

XX

XX

FH Key Location/Qualifiers

FT Misc-difference 77

FT /label= Phe, Ser, Tyr, Cys

FT Misc-difference 84

FT /note= "possibly Pro"

FT Misc-difference 117

FT /label= Leu, Ile, Val

XX

PN JP2000080100-A.

XX

XX

PD 21-MAR-2000.

XX

PF 12-OCT-1998; 98JP-0304793.

XX

XX 17-JUN-1998; 98JP-0188196.

PR 26-JUN-1998; 98JP-0196729.

PR

|    |                                                                         |                                 |
|----|-------------------------------------------------------------------------|---------------------------------|
| FT | Misc-difference 5                                                       | /label= Leu, Pro, His, Gln, Arg |
| FT |                                                                         |                                 |
| FT | Misc-difference 11                                                      | /label= Val, Ala, Asp, Gly      |
| FT |                                                                         |                                 |
| FT | Misc-difference 16                                                      | /label= Leu, Ile, Val           |
| FT |                                                                         |                                 |
| FT | Misc-difference 25                                                      | /label= Phe, Ser, Tyr, Cys      |
| FT |                                                                         |                                 |
| FT | Misc-difference 27                                                      | /label= Ile, Thr, Asn, Ser      |
| FT |                                                                         |                                 |
| FT | Misc-difference 29                                                      | /label= Phe, Ser, Tyr, Cys      |
| FT |                                                                         |                                 |
| FT | Misc-difference 30                                                      | /note= "possibly Leu"           |
| FT |                                                                         |                                 |
| FT | Misc-difference 117                                                     | /label= Phe, Leu, Ile, Val      |
| FT |                                                                         |                                 |
| FT | Misc-difference 216                                                     | /label= Leu, Ile, Val           |
| FT |                                                                         |                                 |
| FT | Misc-difference 231                                                     | /note= "possibly Val"           |
| FT |                                                                         |                                 |
| FT |                                                                         | /note= "possibly Thr"           |
| XX |                                                                         |                                 |
| PN | JP2000080100-A.                                                         |                                 |
| XX |                                                                         |                                 |
| PD | 21-MAR-2000.                                                            |                                 |
| XX |                                                                         |                                 |
| PX | 12-OCT-1998;                                                            | 98JP-0304793.                   |
| PF |                                                                         |                                 |
| XX |                                                                         |                                 |
| PR | 17-JUN-1998;                                                            | 98JP-0188196.                   |
| PP | 26-JUN-1998;                                                            | 98JP-0196729.                   |
| XX |                                                                         |                                 |
| PA | (NISB ) JAPAN TOBACCO INC.                                              |                                 |
| XX |                                                                         |                                 |
| PA |                                                                         |                                 |
| DR | WPI: 2000-286723/25.                                                    |                                 |
| DR | N-PSDB; AAAL3929.                                                       |                                 |
| XX |                                                                         |                                 |
| PT | A human monoclonal antibody to parathyroid hormone related protein. -   |                                 |
| PT | useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone |                                 |
| PT | including metastasis, and pain                                          |                                 |
| XX |                                                                         |                                 |
| PS | Claim 31; Page 60; 88pp; Japanese.                                      |                                 |
| XX |                                                                         |                                 |
| CC | The present invention describes a human monoclonal antibody to          |                                 |
| CC | parathyroid hormone related protein (PTHrP). The monoclonal antibody or |                                 |
| CC | its fragments, following the stimulation of PTHrP has the following     |                                 |
| CC | properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits  |                                 |
| CC | the release of calcium from bone; or (c) inhibits elevation of blood    |                                 |
| CC | calcium content. The monoclonal antibody can be used in the treatment   |                                 |
| CC | of hypercalcaemia, rheumatoid arthritis, cancer of bone including       |                                 |
| CC | metastasis, pain, fracture, cachexia, diseases of teeth, periodontal    |                                 |
| CC | diseases and gingiva, sepsis, systemic inflammatory response syndrome   |                                 |
| CC | (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and      |                                 |
| CC | antiinflammatory activities. The present sequence represents a          |                                 |
| CC | human PTHrP monoclonal antibody clone protein sequence from the         |                                 |
| CC | present invention..                                                     |                                 |
| XX |                                                                         |                                 |
| SQ | Sequence 239 AA;                                                        |                                 |
|    | Query Match 90.0%; Score 1031.5; DB 21; Length 239;                     |                                 |
|    | Best Local Similarity 90.9%; Pred. No. 1.5e-62;                         |                                 |
|    | Matches 200; Conservative 3; Mismatches 16; Indels 1; Gaps              |                                 |
| QY | 1 EIVLTQSPILSLVPTGEGPASISCRSSQSLSHNGTYTLDWYLKPGQSPQLLIYGSHRA 60         |                                 |
| Db | :::                                                                     |                                 |
| Db | 21 DIVMXPXLLPVTPGEFASISCRSGORLHRNGNTYLDWYLKPGQSPQLIYLGSDRA 80           |                                 |
| QY | 61 SGVPDFRFGSGVGTDTFLIRISRAEDVGVIYCMQGLOSFFTGPGETKVDIKRGTVAAFS 120      |                                 |
| Db |                                                                         |                                 |
| Db | 81 SGVPDFRFGSGSGCTDFTLKISRVEADVGVYICMQAQIIFTFGPGTKVDIKR-TVAAFS 139      |                                 |
| QY | 121 VFIFPPSDEOLKSGTASVVCLLNNEYPREAKVQMKNALOGNSQEVSFTEDSKDSTYS 180       |                                 |
| Db |                                                                         |                                 |
| Db | 140 VFIFPPSDEOLKSGTASVVCLLNNEYPREAKVQMKNALOGNSQEVSFTEDSKDSTYS 199       |                                 |



CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is  
CC co-administered to a patient with an anti-Ep-CAM antibody. The  
CC combination is useful for treating cancer, particularly colorectal  
CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell  
CC lung cancer. The present sequence represents the kappa light chain of  
CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG1) which can be  
CC used in the combination of the invention.  
XX  
SQ Sequence 238 AA;  
  
Query Match 88.6%; Score 1015.5; DB 22; Length 238;  
Best Local Similarity 90.5%; Pred. No. 1.8e-61;  
Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;  
  
QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLVDWYLOKPGQSPQLLIYSGSHRA 60  
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
20 DIVMTQSPVLPVTPGEPASISCRSSKNLHNSGITLYLYWYLOKPGQSPQLLIYQMSNLA 79  
QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
80 SGVPDRFSSSGSGTDFTLKISRVEAEDGVYYCAQNLPIPTFGQGTKEIKR-TVAAPS 138  
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
139 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 198  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
199 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
  
RESULT 14  
AAB72233  
ID AAB72233 standard; Protein: 238 AA.  
XX  
AC AAB72233;  
XX  
DT 10-MAY-2001 (first entry)  
XX  
DE Humanised 323/A3 (IgG4cys) antibody kappa light chain amino acid.  
XX  
DE Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;  
KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;  
KW light chain.  
XX  
OS Mus sp.  
OS Homo sapiens.  
XX  
PN WO200107082-A1.  
XX  
PD 01-FEB-2001.  
XX  
PF 23-JUL-1999; 99WO-EP05271.  
XX  
PR 23-JUL-1999; 99WO-EP05271.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Knick VC, Stimmel JB, Thurmond LM;  
XX  
DR WPI; 2001-182729/18.  
XX  
XX Combination for treating cancer (e.g. breast, gastric or prostate  
PT cancers), or in the manufacture of a medicament for anti-cancer  
PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody  
PT with a chemotherapeutic agent -  
XX  
XX Example 7; Fig 11; 103pp; English.  
XX  
XX This invention relates to a combination of an anti-Ep-CAM (cyclic  
CC adenosine monophosphate) antibody with a chemotherapeutic agent, that is  
CC capable of arresting Ep-CAM antigen expressing cells in the synthesis (S)  
CC phase or the second growth phase (M) of cell enlargement (G2)/DNA

CC replication. The antibody exhibits cytostatic activity and is useful in  
CC the manufacture of a medicament for use in anti-cancer therapy,  
CC characterised in that a chemotherapeutic agent, which is capable of  
CC arresting Ep-CAM antigen expressing cells in S or in G2/M, is  
CC co-administered to a patient with an anti-Ep-CAM antibody. The  
CC combination is useful for treating cancer, particularly colorectal  
CC cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell  
CC lung cancer. The present sequence represents the kappa light chain of  
CC anti-Ep-CAM antibody known as humanised 323/A3 (IgG4cys) which can be  
CC used in the combination of the invention.  
XX  
SQ Sequence 238 AA;  
  
Query Match 88.6%; Score 1015.5; DB 22; Length 238;  
Best Local Similarity 90.5%; Pred. No. 1.8e-61;  
Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;  
  
QY 1 EIVLTQSPVLPVTPGEPASISCRSSQSLHNSGYTLVDWYLOKPGQSPQLLIYSGSHRA 60  
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
20 DIVMTQSPVLPVTPGEPASISCRSSKNLHNSGITLYLYWYLOKPGQSPQLLIYQMSNLA 79  
QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVYYCMQGLQSPFTFGPGTKVDIKRGTVAAAPS 120  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
80 SGVPDRFSSSGSGTDFTLKISRVEAEDGVYYCAQNLPIPTFGQGTKEIKR-TVAAPS 138  
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
139 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 198  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
199 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 238  
  
RESULT 15  
AAB72235  
ID AAB72235 standard; Protein: 238 AA.  
XX  
AC AAB72235;  
XX  
DT 10-MAY-2001 (first entry)  
XX  
DE Humanised 323/A3 (IgG2cys) antibody kappa light chain amino acid.  
XX  
DE Anti-Ep-CAM antibody; cyclic adenosine monophosphate; cell synthesis;  
KW chemotherapeutic agent; cytostatic; anti-cancer therapy; cancer;  
KW light chain.  
XX  
OS Mus sp.  
OS Homo sapiens.  
XX  
PN WO200107082-A1.  
XX  
PD 01-FEB-2001.  
XX  
PF 23-JUL-1999; 99WO-EP05271.  
XX  
PR 23-JUL-1999; 99WO-EP05271.  
XX  
PA (GLAX ) GLAXO GROUP LTD.  
XX  
PI Knick VC, Stimmel JB, Thurmond LM;  
XX  
DR WPI; 2001-182729/18.  
XX  
XX Combination for treating cancer (e.g. breast, gastric or prostate  
PT cancers), or in the manufacture of a medicament for anti-cancer  
PT therapy, comprises an anti-Ep-cyclic adenosine monophosphate antibody  
PT with a chemotherapeutic agent -  
XX  
XX Example 8; Fig 13; 103pp; English.  
XX  
XX This invention relates to a combination of an anti-Ep-CAM (cyclic

adenosine monophosphate) antibody with a chemotherapeutic agent, that is capable of arresting Ep-CAM antigen expressing cells in the synthesis (S) phase or the second growth phase (M) of cell enlargement (G2)/DNA replication. The antibody exhibits cytostatic activity and is useful in the manufacture of a medicament for use in anti-cancer therapy, characterized in that a chemotherapeutic agent, which is capable of arresting Ep-CAM antigen expressing cells in S or in G2/M, is co-administered to a patient with an anti-Ep-CAM antibody. The combination is useful for treating cancer, particularly colorectal cancer, breast cancer, gastric cancer, prostate cancer or non-small-cell lung cancer. The present sequence represents the kappa light chain of anti-Ep-CAM antibody known as humanised 323/A3 (IgG2cys) which can be used in the combination of the invention.

|    |     |                       |                 |                                  |
|----|-----|-----------------------|-----------------|----------------------------------|
| xx | SQ  | Sequence              | 238             | AA;                              |
|    |     | Query Match           | 88.6%           | Score 1015.5; DB 22; Length 238; |
|    |     | Best Local Similarity | 90.5%           | Pred. No. 1.8e-61;               |
|    |     | Matches 199;          | Conservative 8; | Mismatches 12; Indels 1; Gaps 1; |
| QY | 1   | EIVLTQSP              | 60              |                                  |
| DB | 20  | DIVMTQSP              | 79              |                                  |
| QY | 61  | SGVPRFSG              | 120             |                                  |
| DB | 80  | SGVPRFSS              | 138             |                                  |
| QY | 121 | VFIFPPDQ              | 180             |                                  |
| DB | 139 | VFIFPPDQ              | 198             |                                  |
| QY | 181 | LSSTLTLS              | 220             |                                  |
| DB | 199 | LSSTLTLS              | 238             |                                  |

Search completed: October 9, 2002, 19:10:28  
Job time : 24.5714 secs



Qy 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVYVCMQGLSPFTFGPTKVDIKRGTVAAAPS 120  
Db 81 SGVPDRFSGSGAGTDTLTKISAVEAEDGVYFCQGTRPTFTGGTKVKEIKR-TVAAPS 139  
Qy 121 VFIPPPDEQLKSGTASVVCLLNNEFPRKAVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 140 VFIPPPDEQLKSGTASVVCLLNNEFPRKAVQWKVDNALQSGNSQESVTEQDSKSDSTYS 199  
Qy 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
RESULT 2  
US-08-398-613A-56  
; Sequence 56, Application US/08398613A  
; Patent No. 5677426  
; GENERAL INFORMATION:  
; APPLICANT: Fong, Sherman  
; APPLICANT: Hebert, Caroline Alice  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Leong, Steven R.  
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398, 613A  
; FILING DATE: 01-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/205864  
; FILING DATE: 03-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fitts, Renee A.  
; REGISTRATION NUMBER: 35,136  
; REFERENCE/DOCKET NUMBER: 874P1-3  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1489  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
US-08-398-613A-56  
Query Match 83.1%; Score 952.5; DB 1; Length 242;  
Best Local Similarity 84.1%; Pred. No. 2.9e-77;  
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;  
Qy 1 EIVLTQSPLSPLVPTGEPASISCRSSQSLHNSGYTYLDWYLPKPGSPQLLIYSGSHRA 60  
Db 24 DIVMTQTPLSPLVSLGDQASISCRSSQSLVHGIGNTYLHWYLPKPGSPKLLIYKVSNR 83  
Qy 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVYVCMQGLSPFTFGPTKVDIKRGTVAAAPS 120  
Db 84 SGVPDRFSGSGTDFTLRISRVEAEDGLVFCQSOSTHVLPTFGAGTKLEKR-AVAAPT 142  
Qy 121 VFIPPPDEQLKSGTASVVCLLNNEFPRKAVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 143 VFIPPPDEQLKSGTASVVCLLNNEFPRKAVQWKVDNALQSGNSQESVTEQDSKSDSTYS 202

Qy 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 203 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 242  
RESULT 3  
US-08-398-612A-56  
; Sequence 56, Application US/08398612A  
; Patent No. 5686070  
; GENERAL INFORMATION:  
; APPLICANT: Doershuk, Claire M.  
; APPLICANT: Fong, Sherman  
; APPLICANT: Hebert, Caroline Alice  
; APPLICANT: Kim, Kyung Jin  
; APPLICANT: Leong, Steven R.  
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for  
; NUMBER OF SEQUENCES: 58  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Winpatin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/398, 612A  
; FILING DATE: 01-MAR-1995  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/398611  
; FILING DATE: 01-MAR-1995  
; APPLICATION NUMBER: 08/205864  
; FILING DATE: 03-MAR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Love, Richard B.  
; REGISTRATION NUMBER: 34,659  
; REFERENCE/DOCKET NUMBER: P0874P1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-5530  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 56:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 242 amino acids  
; TYPE: Amino Acid  
; TOPOLOGY: Linear  
US-08-398-612A-56  
Query Match 83.1%; Score 952.5; DB 1; Length 242;  
Best Local Similarity 84.1%; Pred. No. 2.9e-77;  
Matches 185; Conservative 15; Mismatches 19; Indels 1; Gaps 1;  
Qy 1 EIVLTQSPLSPLVPTGEPASISCRSSQSLHNSGYTYLDWYLPKPGSPQLLIYSGSHRA 60  
Db 24 DIVMTQTPLSPLVSLGDQASISCRSSQSLVHGIGNTYLHWYLPKPGSPKLLIYKVSNR 83  
Qy 61 SGVPDRFSGSVGTDFTLRISRVEAEDGVYVCMQGLSPFTFGPTKVDIKRGTVAAAPS 120  
Db 84 SGVPDRFSGSGTDFTLRISRVEAEDGLVFCQSOSTHVLPTFGAGTKLEKR-AVAAPT 142  
Qy 121 VFIPPPDEQLKSGTASVVCLLNNEFPRKAVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
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Qy 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220











|    |     |                                 |                                |      |
|----|-----|---------------------------------|--------------------------------|------|
| Db | 143 | VFIFPPSEQLKSGTASVCLLNPNFY       | PREAKVQWKYDNLQSGNSQSEVTEQDSKDS | TSYS |
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| Db | 203 | LSSTLTLSKADYKPKHYACEVTHQGLSSPVT | KSFNRGEC                       | 242  |

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RESULT 14
US-08-804-444A-51
; Sequence 51, Application US/08804444A
; Patent No. 6117980
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania N
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,444A
; FILING DATE: 21-Feb-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-804-444A-51

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|-----------------------|--------|-------------------|--------------|-------------|--------------|------------|--------------------------|
| Query Match           | 78.0%; | Score             | 893.5;       | DB          | 3;           | Length     | 242;                     |
| Best local similarity | 79.5%; | Pred.             | No. 4.9e-72; |             |              |            |                          |
| Matches               | 175;   | Conservative      | 14;          | Mismatches  | 30;          | Indels     | 1;                       |
| Gaps                  |        |                   |              |             |              |            |                          |
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| Db                    | 24     | DIQMTQSP          | SSLASVGD     | RVTITCR     | SSQLVHG      | IGNITLHWY  | QOKPGKAPKLLIYKVSNNR      |
| QY                    | 61     | SGVPDR            | FSSVSGT      | DTLLIRIS    | VEADVGV      | YICMQGLQ   | SQPFTFGPGTKVDIKRGTVAAAPS |
| Db                    | 84     | SGVPDR            | FSSVSGT      | DTLLIRIS    | VEADVGV      | YICMQGLQ   | SQPFTFGPGTKVDIKRGTVAAAPS |
| QY                    | 121    | VFIFPSP           | DEQLKSGT     | ASVVCLLN    | NFYPREAK     | VQWKVDNALQ | SGNSQESVTEQDSKSDSYS      |
| Db                    | 143    | VFIFPSP           | DEQLKSGT     | ASVVCLLN    | NFYPREAK     | VQWKVDNALQ | SGNSQESVTEQDSKSDSYS      |
| QY                    | 181    | LSSTLT            | LSKADYEK     | HKVYACEV    | THQGLSP      | VTKSFNRGEC | 240                      |
| Db                    | 203    | LSSTLT            | LSKADYEK     | HKVYACEV    | THQGLSP      | VTKSFNRGEC | 242                      |
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|                       |        | ; Sequence        | 56,          | Application | US/08804444A |            |                          |
|                       |        | Patent            | No.          | 6117980     |              |            |                          |

GENERAL INFORMATION:  
APPLICANT: Gonzalez, Tania N  
APPLICANT: Leong, Steven R.  
APPLICANT: Presta, Leonard G.  
TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 1 DNA Way  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: WinPatIn (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/804,444A  
FILING DATE: 21-Feb-1997  
CLASSIFICATION: 530  
ATTORNEY/AGENT INFORMATION:  
NAME: Love, Richard B.  
REGISTRATION NUMBER: 34,659  
REFERENCE/DOCKET NUMBER: P1085  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650/225-5530  
TELEFAX: 650/952-9881  
INFORMATION FOR SEQ ID NO: 56:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 242 amino acids  
TYPE: Amino Acid  
TOPOLOGY: Linear  
US-08-804-444A-56

Query Match 78.0%; Score 893.5; DB 3; Length 242;  
Best Local Similarity 79.5%; Pred. No. 4.9e-72;  
Matches 175; Conservative 14; Mismatches 30; Indels 1; Gaps 1;  
Qy 1 EIVLTQSPSLPVTPGEPASISCRSSQSLLSNGYTYLDWYLOKPGQSPOLLIYSGSHRA 60  
Db 24 DIQMTQSPSSLSASVGDRVTITCRSSQSLVHGIGATYLVHWYQQKPKAPKLLIYKVSNR 83  
Qy 61 SGVPDRFSGSVSGTDFTLIRISRVEAEVGVVYCMQGLQSPFTFGPTKVDIKRGTVAA 120  
Db 84 SGVPSRFSGSGSGTDFLTISLQPEDFATYVCQSQSTHVLPTFGQGTKVEIKR-TVA 142  
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Search completed: October 9, 2002, 19:14:04  
Job time : 8.97959 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:10:35 ; Search time 86.7092 Seconds  
(without alignments)  
893.051 Million cell updates/sec

Title: US-09-822-698A-24  
Perfect score: 1146  
Sequence: 1 EIVLTQSLPLVPTGEPAS.....EVTHQGLSPVTKSFNRGSC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pep.\*
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- 25: /cgn2\_6/ptodata/2/paa/US101\_COMB.pep.\*
- 26: /cgn2\_6/ptodata/2/paa/US102\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | ID  | Description                         |
|------------|--------|-------------|-----|-------------------------------------|
| 1          | 1146   | 100.0       | 220 | US-09-822-698A-24                   |
| 2          | 1052.5 | 91.8        | 219 | Sequence 24, Appl Sequence 104, App |
| 3          | 1050.5 | 91.7        | 239 | Sequence 8, Appli                   |
| 4          | 1050.5 | 91.7        | 239 | Sequence 8, Appli                   |
| 5          | 1050.5 | 91.7        | 239 | Sequence 8, Appli                   |
| 6          | 1050.5 | 91.7        | 239 | Sequence 8, Appli                   |
| 7          | 1050.5 | 91.7        | 239 | Sequence 8, Appli                   |

|    |        |      |     |    |                   |                   |
|----|--------|------|-----|----|-------------------|-------------------|
| 8  | 1023.5 | 89.3 | 219 | 23 | US-09-972-656-94  | Sequence 94, Appl |
| 9  | 1016.5 | 88.7 | 219 | 23 | US-09-972-656-106 | Sequence 106, App |
| 10 | 992.5  | 86.6 | 239 | 14 | US-09-046-351-78  | Sequence 78, Appl |
| 11 | 992.5  | 86.6 | 239 | 14 | US-09-046-351-82  | Sequence 82, Appl |
| 12 | 992.5  | 86.6 | 239 | 17 | US-09-383-916-6   | Sequence 6, Appli |
| 13 | 992.5  | 86.6 | 239 | 19 | US-09-576-424-6   | Sequence 6, Appli |
| 14 | 988.5  | 86.3 | 239 | 14 | US-09-046-351-80  | Sequence 80, Appl |
| 15 | 988.5  | 86.3 | 239 | 14 | US-09-046-351-84  | Sequence 84, Appl |
| 16 | 986.5  | 86.1 | 238 | 11 | US-08-721-612B-19 | Sequence 19, Appl |
| 17 | 986.5  | 86.1 | 238 | 11 | US-08-721-612C-19 | Sequence 19, Appl |
| 18 | 978.5  | 85.4 | 238 | 20 | US-09-698-705-10  | Sequence 10, Appl |
| 19 | 976.5  | 85.2 | 262 | 21 | US-09-760-479-658 | Sequence 658, App |
| 20 | 971    | 84.7 | 228 | 23 | US-09-909-567-50  | Sequence 50, Appl |
| 21 | 969.5  | 84.6 | 219 | 23 | US-09-972-656-92  | Sequence 92, Appl |
| 22 | 966.5  | 84.3 | 244 | 21 | US-09-760-479-641 | Sequence 641, App |
| 23 | 963.5  | 84.1 | 241 | 26 | US-60-128-194-1   | Sequence 1, Appli |
| 24 | 952.5  | 83.1 | 242 | 7  | US-08-398-614A-56 | Sequence 56, Appl |
| 25 | 952.5  | 83.1 | 242 | 7  | US-08-398-616A-56 | Sequence 56, Appl |
| 26 | 952.5  | 83.1 | 242 | 12 | US-08-804-444-56  | Sequence 56, Appl |
| 27 | 952.5  | 83.1 | 242 | 14 | US-09-012-116-42  | Sequence 42, Appl |
| 28 | 952.5  | 83.1 | 242 | 15 | US-09-121-952A-42 | Sequence 42, Appl |
| 29 | 952.5  | 83.1 | 242 | 15 | US-09-122-513A-42 | Sequence 42, Appl |
| 30 | 952.5  | 83.1 | 242 | 16 | US-09-234-182A-42 | Sequence 42, Appl |
| 31 | 952.5  | 83.1 | 242 | 16 | US-09-234-340A-42 | Sequence 42, Appl |
| 32 | 952.5  | 83.1 | 242 | 18 | US-09-489-394-42  | Sequence 42, Appl |
| 33 | 952.5  | 83.1 | 242 | 21 | US-09-726-258-42  | Sequence 42, Appl |
| 34 | 929    | 81.1 | 218 | 20 | US-09-698-705-12  | Sequence 12, Appl |
| 35 | 917    | 80.0 | 226 | 1  | PCT-US00-27237-38 | Sequence 38, Appl |
| 36 | 917    | 80.0 | 226 | 1  | PCT-US00-33042-38 | Sequence 38, Appl |
| 37 | 917    | 80.0 | 226 | 18 | US-09-453-234-38  | Sequence 38, Appl |
| 38 | 917    | 80.0 | 226 | 18 | US-09-456-090-38  | Sequence 38, Appl |
| 39 | 917    | 80.0 | 226 | 18 | US-09-456-090A-38 | Sequence 38, Appl |
| 40 | 914    | 79.8 | 234 | 18 | US-09-472-087-17  | Sequence 17, Appl |
| 41 | 914    | 79.8 | 234 | 18 | US-09-472-087-69  | Sequence 69, Appl |
| 42 | 908    | 79.2 | 224 | 1  | PCT-US00-27237-44 | Sequence 44, Appl |
| 43 | 908    | 79.2 | 224 | 1  | PCT-US00-27237-78 | Sequence 78, Appl |
| 44 | 908    | 79.2 | 224 | 1  | PCT-US00-33042-44 | Sequence 44, Appl |
| 45 | 908    | 79.2 | 224 | 1  | PCT-US00-33042-78 | Sequence 78, Appl |

ALIGNMENTS

RESULT 1  
US-09-822-698A-24  
; Sequence 24, Application US/09822698A  
; GENERAL INFORMATION:  
; APPLICANT: Hooqenboom, Hendricus R.J.M.  
; APPLICANT: Henderikx, Maria P.G.  
; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof  
; FILE REFERENCE: DYX-015.1 US  
; CURRENT APPLICATION NUMBER: US/09/822,698A  
; CURRENT FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: US 09/538,913  
; PRIOR FILING DATE: 2000-03-30  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: Microsoft Word  
; SEQ ID NO 24  
; LENGTH: 220  
; TYPE: PRT  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Immunoglobulin kappa light chain of MUC1-specific PH1-IgG1  
US-09-822-698A-24

|                       |         |                    |                    |                                 |
|-----------------------|---------|--------------------|--------------------|---------------------------------|
| Query Match           | 100.0%; | Score 1146;        | DB 22;             | Length 220;                     |
| Best Local Similarity | 100.0%; | Pred. No. 4.1e-94; |                    |                                 |
| Matches               | 220;    | Conservative       | 0;                 | Mismatches 0; Indels 0; Gaps 0; |
| Qy                    | 1       | EIVLTQSLPLVPTGEPAS | TCRSSQSLHNSGYTLDWY | LQKPGSQPLLIIYSGSHRA 60          |
| Db                    | 1       | EIVLTQSLPLVPTGEPAS | TCRSSQSLHNSGYTLDWY | LQKPGSQPLLIIYSGSHRA 60          |

QY 61 SGVDPFRSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120  
Db 61 SGVDPFRSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120  
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180  
Db 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

RESULT 2  
US-09-972-656-104  
; Sequence 104, Application US/09972656  
; GENERAL INFORMATION:  
; APPLICANT: Deshpande, Rajendra  
; APPLICANT: Tsai, Mei-Mei  
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma  
; FILE REFERENCE: A-799  
; CURRENT APPLICATION NUMBER: US/09/972,656  
; CURRENT FILING DATE: 2001-10-05  
; NUMBER OF SEQ ID NOS: 135  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 104  
; LENGTH: 219  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-656-104

Query Match 91.8%; Score 1052.5; DB 23; Length 219;  
Best Local Similarity 93.2%; Pred. No. 9.7e-86;  
Matches 205; Conservative 6; Mismatches 8; Indels 1; Gaps 1;  
QY 1 EIVLTQSPSLPLPVTGPGSPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 60  
Db 1 EIVLTQSPSLPLPVTGPGSPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 60  
QY 61 SGVDPFRSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120  
Db 61 SGVDPFRSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 119  
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180  
Db 120 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 179  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 180 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 219

RESULT 3  
US-09-924-340-8  
; Sequence 8, Application US/09924340  
; GENERAL INFORMATION:  
; APPLICANT: Bejanin, Stephanie  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/924,340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: JPatent

; SEQ ID NO 8  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..20  
US-09-924-340-8  
Query Match 91.7%; Score 1050.5; DB 23; Length 239;  
Best Local Similarity 92.7%; Pred. No. 1.6e-85;  
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPLPVTGPGSPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 60  
Db 21 DIVMTQSPFLPVTGPGSPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 80  
QY 61 SGVDPFRSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120  
Db 81 SGVDPFRSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 139  
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 180  
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDYTS 199  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 4  
US-09-994-590-8  
; Sequence 8, Application US/09994590  
; GENERAL INFORMATION:  
; APPLICANT: Benjanin, Stephanie  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91.US3.DIV  
; CURRENT APPLICATION NUMBER: US/09/994,590  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR FILING DATE: US 09/924,340  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: JPatent  
; SEQ ID NO 8  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..20  
US-09-994-590-8

Query Match 91.7%; Score 1050.5; DB 23; Length 239;  
Best Local Similarity 92.7%; Pred. No. 1.6e-85;  
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;  
QY 1 EIVLTQSPSLPLPVTGPGSPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 60  
Db 21 DIVMTQSPFLPVTGPGSPASISCRSSQSLHNSGYTYLDWYLOKPGQSPOLLIYSGSHRA 80  
QY 61 SGVDPFRSGSVSGTDFTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120



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Db 81 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 139
Qy 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 180
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 199
Qy 181 LSSTLTLSKADYKHKHYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYKHKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 5
US-10-000-489-8
; Sequence 8, Application US/10000489
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-10-000-489-8

Query Match 91.7%; Score 1050.5; DB 24; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.6e-85;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSPFLSPVTPGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYSGSHRA 60
Db 21 DIVMTQSPFLPVPTEGEPASISCRSSQSLHNSGYTLDWYHQKPGQSPQLLIYLSNRA 80
Qy 61 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 120
Db 81 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 139
Qy 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 180
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 199
Qy 181 LSSTLTLSKADYKHKHYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYKHKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 6
US-10-000-986-8
; Sequence 8, Application US/10000986
; GENERAL INFORMATION:
; APPLICANT: Benjamin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US9.DIV
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; CURRENT APPLICATION NUMBER: US/10/000,986
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-10-000-986-8

Query Match 91.7%; Score 1050.5; DB 24; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.6e-85;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSPFLSPVTPGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYSGSHRA 60
Db 21 DIVMTQSPFLPVPTEGEPASISCRSSQSLHNSGYTLDWYHQKPGQSPQLLIYLSNRA 80
Qy 61 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 120
Db 81 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 139
Qy 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 180
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSYTS 199
Qy 181 LSSTLTLSKADYKHKHYACEVTHQGLSSPVTKSFNRGEC 220
Db 200 LSSTLTLSKADYKHKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 7
US-60-305-456-8
; Sequence 8, Application US/60305456
; GENERAL INFORMATION:
; APPLICANT: BEJANIN, Stephane
; APPLICANT: TANAKA, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS
; FILE REFERENCE: 97.US5.PRO
; CURRENT APPLICATION NUMBER: US/60/305,456
; CURRENT FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-305-456-8

Query Match 91.7%; Score 1050.5; DB 26; Length 239;
Best Local Similarity 92.7%; Pred. No. 1.6e-85;
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

Qy 1 EIVLTQSPFLSPVTPGEPASISCRSSQSLHNSGYTLDWYLQKPGQSPQLLIYSGSHRA 60
Db 21 DIVMTQSPFLPVPTEGEPASISCRSSQSLHNSGYTLDWYHQKPGQSPQLLIYLSNRA 80
Qy 61 SGVPDRFSGSGGDTFTLKISRVEAEDVGVYCMQALQTFTEGPTGTRVDIKR-TVAAPS 120
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; APPLICANT: Nakahara, Kaori
; APPLICANT: Yonehara, Shin
; TITLE OF INVENTION: HUMANIZED ANTI-HUMAN Fas ANTIBODY
; FILE REFERENCE: 980125/HG
; CURRENT APPLICATION NUMBER: US/09/046,351A
; CURRENT FILING DATE: 1998-03-23
; EARLIER APPLICATION NUMBER: JP HEI 9-67938
; EARLIER FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 189
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: L chain of a
; OTHER INFORMATION: humanized anti-Fas antibody
US-09-046-351-82

Query Match 86.6%; Score 992.5; DB 14; Length 239;
Best Local Similarity 88.2%; Pred. No. 2.6e-80;
Matches 194; Conservative 10; Mismatches 15; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPGEPAISCRSSQSLHNSGYTLDMYLRKPGQSPQLLIYSGSHRA 60
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Db 21 DVVMTQSPSLPVTLGOPASISCRSSKSLVHSGNTYLVHWYLRKPGQSPRLLIYKVSNR 80

QY 61 SGVPRDFSGSVSGTDFTLIRSRVEADGVYYCMQGLQSPFTFGPGTKVDIKRGTVAA 120
 ::::||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 SGVPRDFSGSGGDTFTLKISRVEADGVYYCQSTHVPPAFQGGTKVEIKR-TVAAPS 139

QY 121 VFIFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS 180
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Db 140 VFIFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS 199

QY 181 LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 220
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Db 200 LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 12
US-09-383-916-6
; Sequence 6, Application US/09383916
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-383-916-6

Query Match 86.6%; Score 992.5; DB 17; Length 239;
Best Local Similarity 87.7%; Pred. No. 2.6e-80;
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60
 ::::||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNR 80

QY 61 SGVPRDFSGSVSGTDFTLIRSRVEADGVYYCMQGLQSPFTFGPGTKVDIKRGTVAA 120
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 SGVPRDFSGSGAGDTFTLKISAVEADGVYFCGQGTPTPTFGGKVEIKR-TVAAPS 139

QY 121 VFIFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS 180
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 140 VFIFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS 199

QY 181 LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 220
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 200 LSSTLTLSKADYEKKHYACEVTHQGLSSPVTKSFNRGEC 239

RESULT 13
US-09-576-424-6
; Sequence 6, Application US/09576424
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, DARRELL R.
; APPLICANT: HANNA, NABIL
; APPLICANT: BRAMS, PETER
; APPLICANT: HEARD, CHERYL
; TITLE OF INVENTION: IDENTIFICATION OF UNIQUE BINDING INTERACTIONS BETWEEN
; TITLE OF INVENTION: CERTAIN ANTIBODIES AND THE HUMAN B7.1 AND B7.2
; TITLE OF INVENTION: CO-STIMULATORY ANTIGENS
; FILE REFERENCE: 37003-275681
; CURRENT APPLICATION NUMBER: US/09/576,424
; CURRENT FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: PCT/US97/19906
; PRIOR FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: 08/746,361
; PRIOR FILING DATE: 1996-11-08
; PRIOR APPLICATION NUMBER: 08/487,550
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-576-424-6

Query Match 86.6%; Score 992.5; DB 19; Length 239;
Best Local Similarity 87.7%; Pred. No. 2.6e-80;
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGPGEPAISCRSSQSLHNSGYTYLDWYLRKPGQSPQLLIYSGSHRA 60
 ::::||||| :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 21 EVVMTQSPSLPITPGEPASISCRSSQSLKHSNGDTFLSWYQQKPGQPPRLLIYKVSNR 80

QY 61 SGVPRDFSGSVSGTDFTLIRSRVEADGVYYCMQGLQSPFTFGPGTKVDIKRGTVAA 120
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 81 SGVPRDFSGSGAGDTFTLKISAVEADGVYFCGQGTPTPTFGGKVEIKR-TVAAPS 139

QY 121 VFIFPPSDQLKSGTASVVCLLNFFYPREAKVQWKVDNALQSGNSQESVTEQDSKDS 180
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:11:10 ; Search time 29,1837 seconds  
(without alignments)  
2085.589 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSPFLPVTGEPAS.....EVTHQGLSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1006125 seqs, 276659714 residues

Total number of hits satisfying chosen parameters: 1006125

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents\_AA\_New\*

- 1: /cgn2\_6/ptodata/1/paa/PCT\_NEW\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/1/paa/US05\_NEW\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*
- 7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score  | Query % | Length | ID | Description          |
|------------|--------|---------|--------|----|----------------------|
| 1          | 1050.5 | 91.7    | 239    | 5  | US-09-992-600A-8     |
| 2          | 1015.5 | 88.6    | 238    | 6  | US-10-031-355-2      |
| 3          | 1015.5 | 88.6    | 238    | 6  | US-10-031-355-11     |
| 4          | 1015.5 | 88.6    | 238    | 6  | US-10-031-355-13     |
| 5          | 1015.5 | 88.6    | 238    | 6  | US-10-031-355-15     |
| 6          | 1009.5 | 88.1    | 219    | 1  | PCT-US02-11854A-11   |
| 7          | 1009.5 | 88.1    | 238    | 1  | PCT-US02-11854A-19   |
| 8          | 992.5  | 86.6    | 239    | 5  | US-09-758-173-6      |
| 9          | 992.5  | 86.6    | 239    | 5  | US-09-326-098-6      |
| 10         | 992.5  | 86.6    | 239    | 5  | US-09-948-429B-6     |
| 11         | 992.5  | 86.6    | 239    | 5  | US-09-971-631-6      |
| 12         | 992.5  | 86.6    | 239    | 6  | US-10-124-807-6      |
| 13         | 992.5  | 86.6    | 239    | 6  | US-10-124-905-6      |
| 14         | 992.5  | 86.6    | 239    | 6  | US-10-030-390-6      |
| 15         | 987.5  | 86.2    | 219    | 1  | PCT-US02-21323-11    |
| 16         | 987.5  | 86.2    | 219    | 1  | PCT-US02-21324-11    |
| 17         | 987.5  | 86.2    | 219    | 1  | PCT-US02-26321-11    |
| 18         | 986.5  | 86.1    | 238    | 4  | US-08-721-612D-19    |
| 19         | 986.5  | 86.1    | 238    | 4  | US-08-721-612E-19    |
| 20         | 983.5  | 85.8    | 219    | 5  | US-09-791-537-129754 |
| 21         | 976.5  | 85.2    | 262    | 6  | US-10-206-008-658    |
| 22         | 971    | 84.7    | 228    | 5  | US-09-909-567B-50    |
| 23         | 966.5  | 84.3    | 244    | 6  | US-10-206-008-641    |
| 24         | 963.5  | 84.1    | 217    | 5  | US-09-791-537-116780 |
| 25         | 963.5  | 84.1    | 217    | 5  | US-09-791-537-116791 |
| 26         | 963.5  | 84.1    | 241    | 5  | US-09-831-805A-15    |

|    |       |      |     |   |                      |                    |
|----|-------|------|-----|---|----------------------|--------------------|
| 27 | 961.5 | 83.9 | 219 | 1 | PCT-US02-11853-11    | Sequence 11, Appl  |
| 28 | 961.5 | 83.9 | 239 | 1 | PCT-US02-11853-19    | Sequence 19, Appl  |
| 29 | 914   | 79.8 | 234 | 6 | US-10-153-382-15     | Sequence 15, Appl  |
| 30 | 905.5 | 79.0 | 235 | 6 | US-10-153-382-7      | Sequence 7, Appl   |
| 31 | 903   | 78.8 | 238 | 6 | US-10-153-382-107    | Sequence 107, Appl |
| 32 | 902.5 | 78.8 | 233 | 6 | US-10-153-382-11     | Sequence 11, Appl  |
| 33 | 901   | 78.6 | 240 | 6 | US-10-058-120-10     | Sequence 10, Appl  |
| 34 | 899   | 78.4 | 240 | 6 | US-10-159-006-36     | Sequence 36, Appl  |
| 35 | 898.5 | 78.4 | 235 | 1 | PCT-US02-20181-4     | Sequence 4, Appl   |
| 36 | 898   | 78.4 | 220 | 5 | US-09-791-537-122090 | Sequence 122090,   |
| 37 | 898   | 78.4 | 240 | 6 | US-10-216-310-8      | Sequence 8, Appl   |
| 38 | 895.5 | 78.1 | 219 | 5 | US-09-791-537-93645  | Sequence 93645, A  |
| 39 | 894   | 78.0 | 244 | 5 | US-09-831-805A-17    | Sequence 17, Appl  |
| 40 | 893.5 | 78.0 | 215 | 1 | PCT-US02-12801-129   | Sequence 129, Appl |
| 41 | 893.5 | 78.0 | 215 | 5 | US-09-791-537-5099   | Sequence 5099, Ap  |
| 42 | 891   | 77.7 | 238 | 6 | US-10-216-484-50     | Sequence 50, Appl  |
| 43 | 891   | 77.7 | 238 | 6 | US-10-216-484-109    | Sequence 109, App  |
| 44 | 889   | 77.6 | 220 | 5 | US-09-669-971-1      | Sequence 1, Appl   |
| 45 | 887.5 | 77.4 | 215 | 1 | PCT-US02-12801-118   | Sequence 118, App  |

#### ALIGNMENTS

##### RESULT 1

US-09-992-600A-8  
; Sequence 8, Application US/09992600A  
; GENERAL INFORMATION:  
; APPLICANT: Benjanin, Stephane  
; APPLICANT: Tanaka, Hiroaki  
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF  
; FILE REFERENCE: 91 US4.DIV  
; CURRENT APPLICATION NUMBER: US/09/992,600A  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 09/924,340  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: PCT/IB01/01715  
; PRIOR FILING DATE: 2001-08-06  
; PRIOR APPLICATION NUMBER: US 60/305,456  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/302,277  
; PRIOR FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: US 60/298,698  
; PRIOR FILING DATE: 2001-06-15  
; PRIOR APPLICATION NUMBER: US 60/293,574  
; PRIOR FILING DATE: 2001-05-25  
; NUMBER OF SEQ ID NOS: 114  
; SOFTWARE: JPatent  
; SEQ ID NO 8  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIGNAL  
; LOCATION: 1..20  
US-09-992-600A-8

Query Match 91.7%; Score 1050.5; DB 5; Length 239;  
Best Local Similarity 92.7%; Pred. No. 2.7e-54;  
Matches 204; Conservative 6; Mismatches 9; Indels 1; Gaps 1;

|    |     |                                                                |     |
|----|-----|----------------------------------------------------------------|-----|
| Qy | 1   | EIVLTQSPFLPVTGEPASISCRSSQSLHNSGTYTLDNYLQKPGSPOLLVYSGSHRA       | 60  |
| Db | 21  | DIVMTQSPFLPVTGEPASISCRSSQSLHNSGTYTLDNYLQKPGSPOLLVYSGSHRA       | 80  |
| Qy | 61  | SGVPRDRFSGSVSGTDFTLIRISRVEAEADVGVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS | 120 |
| Db | 81  | SGVPRDRFSGSVSGTDFTLIRISRVEAEADVGVYCMQGLQSPFTFGPGTKVDIKR-TVAAPS | 139 |
| Qy | 121 | VFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS  | 180 |
| Db | 140 | VFIFPPSDEQLKSGTASVVCVLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYS  | 199 |

QY 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 239

## RESULT 2

US-10-031-355-2

; Sequence 2, Application US/10031355  
; GENERAL INFORMATION:  
; APPLICANT: Glaxo Group Limited  
; APPLICANT: Knick, Vincent C  
; APPLICANT: Stimmel, Julie B  
; APPLICANT: Thurmond, Linda M  
; TITLE OF INVENTION: Antibody combination  
; FILE REFERENCE: PU3513  
; CURRENT APPLICATION NUMBER: US/10/031,355  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: sequence  
US-10-031-355-2

Query Match 88.6%; Score 1015.5; DB 6; Length 238;  
Best Local Similarity 90.5%; Pred. No. 3e-52;  
Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60  
Db 20 DIVMTQSPSLPVTGEPASISCRSSKNLLHNSGITLYLYWYLRKPGQSPQLLIYQMSNLA 79  
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMOGLOSPTFGPTGKTVDIKRGTVAAPS 120  
Db 80 SGVPDRFSSGSGTDFTLRISRVEAEDGVVYCAQNLEIPRTFGQGTKEIKR-TVAAPS 138  
QY 121 VFIFFPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 139 VFIFFPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 198  
QY 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
Db 199 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238

## RESULT 3

US-10-031-355-11

; Sequence 11, Application US/10031355  
; GENERAL INFORMATION:  
; APPLICANT: Glaxo Group Limited  
; APPLICANT: Knick, Vincent C  
; APPLICANT: Stimmel, Julie B  
; APPLICANT: Thurmond, Linda M  
; TITLE OF INVENTION: Antibody combination  
; FILE REFERENCE: PU3513  
; CURRENT APPLICATION NUMBER: US/10/031,355  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 11  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: sequence  
US-10-031-355-11

Query Match 88.6%; Score 1015.5; DB 6; Length 238;

Best Local Similarity 90.5%; Pred. No. 3e-52;  
Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;  
QY 1 EIVLTQSPSLPVTGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60  
Db 20 DIVMTQSPSLPVTGEPASISCRSSKNLLHNSGITLYLYWYLRKPGQSPQLLIYQMSNLA 79  
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMOGLOSPTFGPTGKTVDIKRGTVAAPS 120  
Db 80 SGVPDRFSSGSGTDFTLRISRVEAEDGVVYCAQNLEIPRTFGQGTKEIKR-TVAAPS 138  
QY 121 VFIFFPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 139 VFIFFPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 198  
QY 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
Db 199 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238

## RESULT 4

US-10-031-355-13

; Sequence 13, Application US/10031355  
; GENERAL INFORMATION:  
; APPLICANT: Glaxo Group Limited  
; APPLICANT: Knick, Vincent C  
; APPLICANT: Stimmel, Julie B  
; APPLICANT: Thurmond, Linda M  
; TITLE OF INVENTION: Antibody combination  
; FILE REFERENCE: PU3513  
; CURRENT APPLICATION NUMBER: US/10/031,355  
; CURRENT FILING DATE: 2002-05-15  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 238  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: sequence  
US-10-031-355-13

Query Match 88.6%; Score 1015.5; DB 6; Length 238;  
Best Local Similarity 90.5%; Pred. No. 3e-52;  
Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTGEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60  
Db 20 DIVMTQSPSLPVTGEPASISCRSSKNLLHNSGITLYLYWYLRKPGQSPQLLIYQMSNLA 79  
QY 61 SGVPDRFSGSVSGTDFTLRISRVEAEDGVVYCMOGLOSPTFGPTGKTVDIKRGTVAAPS 120  
Db 80 SGVPDRFSSGSGTDFTLRISRVEAEDGVVYCAQNLEIPRTFGQGTKEIKR-TVAAPS 138  
QY 121 VFIFFPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 139 VFIFFPSDEQLKSGTASVYVCLLNPFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 198  
QY 181 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 220  
Db 199 LSSTLTLSKADYKHKVYACEVTHOGLSSPVTKSFNRGEC 238

## RESULT 5

US-10-031-355-15

; Sequence 15, Application US/10031355  
; GENERAL INFORMATION:  
; APPLICANT: Glaxo Group Limited  
; APPLICANT: Knick, Vincent C  
; APPLICANT: Stimmel, Julie B  
; APPLICANT: Thurmond, Linda M  
; TITLE OF INVENTION: Antibody combination

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; FILE REFERENCE: PU3513
; CURRENT APPLICATION NUMBER: US/10/031,355
; CURRENT FILING DATE: 2002-03-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: sequence
US-10-031-355-15

Query Match 88.1%; Score 1015.5; DB 6; Length 238;
Best Local Similarity 90.5%; Pred. No. 3e-52;
Matches 199; Conservative 8; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 20 DIVMTQSPSLPVTPGEPASISCRSKNLLHNSGITYLYWYLOKPGQSPQLLIYQMSNLA 79
QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPTKVDIKRGTVAAPS 120
Db 80 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCAQNLEIPRTFGGQTKVEIKR-TVAAPS 138
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 180
Db 139 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 198
QY 181 LSSTLTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEC 220
Db 199 LSSTLTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEC 238

RESULT 6
PCT-US02-11854A-11
; Sequence 11, Application PC/TUS0211854A
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Humanized Antibodies
; FILE REFERENCE: X-14819
; CURRENT APPLICATION NUMBER: PCT/US02/11854A
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/287,653
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; LENGTH: 219
; TYPE: PRT
; ORGANISM: humanized antibody
PCT-US02-11854A-11

Query Match 88.1%; Score 1009.5; DB 1; Length 219;
Best Local Similarity 88.6%; Pred. No. 6.2e-52;
Matches 195; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DIVMTQSPSLPVTLGQPASISCRSQNIHNSGNTYLEWYLOKPGQSPRLLIYKVSNR 60
QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPTKVDIKRGTVAAPS 120
Db 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCFQGSHPVLTFTGGGKVEIKR-TVAAPS 119
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 180
Db 120 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 179
QY 181 LSSTLTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEC 220
Db 180 LSSTLTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEC 219
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RESULT 7
PCT-US02-11854A-19
; Sequence 19, Application PC/TUS0211854A
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Humanized Antibodies
; FILE REFERENCE: X-14819
; CURRENT APPLICATION NUMBER: PCT/US02/11854A
; CURRENT FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/287,653
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 238
; TYPE: PRT
; ORGANISM: humanized antibody
PCT-US02-11854A-19

Query Match 88.1%; Score 1009.5; DB 1; Length 238;
Best Local Similarity 88.6%; Pred. No. 6.7e-52;
Matches 195; Conservative 12; Mismatches 12; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 20 DIVMTQSPSLPVTLGQPASISCRSQNIHNSGNTYLEWYLOKPGQSPRLLIYKVSNR 79
QY 61 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCMQGLQSPFTFGPTKVDIKRGTVAAPS 120
Db 80 SGVPDRFSGSVSGTDFTLIRISRVEAEDGVVYCFQGSHPVLTFTGGGKVEIKR-TVAAPS 138
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 180
Db 139 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 198
QY 181 LSSTLTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEC 220
Db 199 LSSTLTLSKADYKHKYVACEVTHQGLSPVTKSFNRGEC 238

RESULT 8
US-09-758-173-6
; Sequence 6, Application US/09758173
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,173
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
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QY 61 SGVDRFSGSVSGTDTFLIRSRVEADVGYYCMQGLQSPFTFGGTVKVDIKRGTVAAAPS 120  
Db 81 SGVDRFSGSGAGDTFLKISAVEADVGYYFCGGGTRTPPTFGGTVKVEIKR-TVAAPS 139  
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 199  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
RESULT 13  
US-10-124-905-6  
; Sequence 6, Application US/10124905  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/124,905  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/383,916  
; FILING DATE:  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-10-124-905-6  
Query Match 86.6%; Score 992.5; DB 6; Length 239;  
Best Local Similarity 87.7%; Pred. No. 6.6e-51;  
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60  
Db 21 EVVMTQSPSLPITGPEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80  
QY 61 SGVDRFSGSVSGTDTFLIRSRVEADVGYYCMQGLQSPFTFGGTVKVDIKRGTVAAAPS 120  
Db 81 SGVDRFSGSGAGDTFLKISAVEADVGYYFCGGGTRTPPTFGGTVKVEIKR-TVAAPS 139  
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 180

Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 199  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239  
RESULT 14  
US-10-030-390-6  
; Sequence 6, Application US/10030390  
; GENERAL INFORMATION:  
; APPLICANT: Anderson, Darrell R.  
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince Street  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22314  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/030,390  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/383,916  
; FILING DATE:  
; FILING DATE: 07-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin, Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-131  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 239 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-10-030-390-6  
Query Match 86.6%; Score 992.5; DB 6; Length 239;  
Best Local Similarity 87.7%; Pred. No. 6.6e-51;  
Matches 193; Conservative 12; Mismatches 14; Indels 1; Gaps 1;  
QY 1 EIVLTQSPSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLQKPGQSPQLLIYSGSHRA 60  
Db 21 EVVMTQSPSLPITGPEPASISCRSSQSLKHSNGDTFLSWYQKPGQPPRLIIYKVSNRD 80  
QY 61 SGVDRFSGSVSGTDTFLIRSRVEADVGYYCMQGLQSPFTFGGTVKVDIKRGTVAAAPS 120  
Db 81 SGVDRFSGSGAGDTFLKISAVEADVGYYFCGGGTRTPPTFGGTVKVEIKR-TVAAPS 139  
QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 180  
Db 140 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKSDSTYS 199  
QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220  
Db 200 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 239

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RESULT 15
PCT-US02-21323-11
; Sequence 11, Application PC/TUS0221323
; GENERAL INFORMATION:
; APPLICANT: Eli Lilly and Company
; TITLE OF INVENTION: Rapid Improvement of Cognition in Conditions Related to A-beta
; FILE REFERENCE: X-15240
; CURRENT APPLICATION NUMBER: PCT/US02/21323
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 60/313,222
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 60/383,846
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 219
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized antibody
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(219)
; OTHER INFORMATION: humanized 266 antibody preferred light chain
PCT-US02-21323-11

Query Match 86.2%; Score 987.5; DB 1; Length 219;
Best Local Similarity 87.3%; Pred. No. 1.2e-50;
Matches 192; Conservative 13; Mismatches 14; Indels 1; Gaps 1;

QY 1 EIVLTQSPFLSPVTPGEPASISCRSSQSLHSGCYLYLDWYLOKPGQSPQLLIYSGSHRA 60
Db 1 DVVMTQSPFLSPVTLGQSPASISCRSSQSLIYSDGNAYLHWFLQKPGOSPRLLIYKVSNRF 60

QY 61 SGVPRFSGSVSGTDFTLRISRVEAEDVGYYCMQGLQSPFTFGPTKVDIKRGTVAAPS 120
Db 61 SGVPRFSGSGGTDFTLRISRVEAEDVGYYCSQSTHVPWTFGGTKVEIKR-TVAAPS 119

QY 121 VFIFPPSDEQLKSGTASVVCVLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYS 180
Db 120 VFIFPPSDEQLKSGTASVVCVLLNFPYPREAKVQKVDNALQSGNSQESVTEQDSKDSSTYS 179

QY 181 LSSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 220
Db 180 LSSTLTLSKADYKHKYKACEVTHQGLSSPVTKSFNRGEC 219

```

Search completed: October 9, 2002, 19:21:23  
Job time : 30.1837 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 9, 2002, 19:07:45 ; Search time 11.7857 Seconds  
(without alignments)  
1793.668 Million cell updates/sec

Title: US-09-822-698A-24

Perfect score: 1146

Sequence: 1 EIVLTQSLPLPVTGPGEAS.....EVTHQGLSPVTKSFNRGEC 220

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_71.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description        |
|------------|-------|-------------|--------|----------|--------------------|
| 1          | 893.5 | 78.0        | 215    | 2 JE0242 | Ig kappa chain NIG |
| 2          | 877.5 | 76.6        | 215    | 2 JE0244 | Ig kappa chain NIG |
| 3          | 869.5 | 75.9        | 215    | 2 JE0243 | Ig kappa chain NIG |
| 4          | 847.5 | 74.0        | 215    | 2 A23746 | Ig kappa chain V-I |
| 5          | 823   | 71.8        | 216    | 2 JE0241 | Ig kappa chain Am3 |
| 6          | 785.5 | 68.5        | 219    | 2 S52028 | Ig kappa chain - m |
| 7          | 782.5 | 68.3        | 219    | 2 PC4203 | Ig kappa chain (mo |
| 8          | 777.5 | 67.8        | 217    | 2 S42772 | Ig kappa chain - m |
| 9          | 777.5 | 67.8        | 219    | 2 S16112 | Ig kappa chain V r |
| 10         | 769.5 | 67.1        | 219    | 2 S38865 | Ig kappa chain - m |
| 11         | 750.5 | 65.5        | 225    | 2 JL0029 | Ig kappa chain pre |
| 12         | 725   | 63.3        | 240    | 2 S06084 | Ig kappa chain pre |
| 13         | 690   | 60.2        | 220    | 2 A31790 | Ig kappa chain V r |
| 14         | 677   | 59.1        | 218    | 2 S68241 | Ig kappa chain V r |
| 15         | 671   | 58.6        | 218    | 2 JC5810 | monoclonal antibod |
| 16         | 662   | 57.8        | 214    | 2 S68212 | Ig kappa chain (Ma |
| 17         | 651.5 | 56.8        | 197    | 2 S29593 | Ig kappa chain (WM |
| 18         | 640   | 55.8        | 210    | 2 A56169 | Ig kappa chain V r |
| 19         | 640   | 55.8        | 234    | 2 S14237 | Ig kappa chain pre |
| 20         | 636   | 55.5        | 234    | 2 S01320 | Ig kappa chain pre |
| 21         | 634.5 | 55.4        | 225    | 2 S37484 | Ig kappa chain - m |
| 22         | 627   | 54.7        | 230    | 2 S33161 | Ig kappa chain - s |
| 23         | 621.5 | 54.2        | 235    | 2 S25058 | Ig kappa chain - m |
| 24         | 611.5 | 53.4        | 178    | 2 PT0219 | Ig kappa chain V-C |
| 25         | 587.5 | 51.3        | 135    | 2 S52059 | JC-kappa protein - |
| 26         | 549.5 | 47.9        | 121    | 2 S40371 | Ig kappa chain - h |
| 27         | 548   | 47.8        | 106    | 1 K3HU   | Ig kappa chain C r |
| 28         | 546.5 | 47.7        | 135    | 2 S40342 | Ig kappa chain - h |
| 29         | 535.5 | 46.7        | 136    | 2 S40357 | Ig kappa chain V-J |

#### ALIGNMENTS

##### RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda

A:Submitted to JIPID, November 1998

A:Description: Structure relationship of kappatype light chains with AL amyloidosis:

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 78.0%; Score 893.5; DB 2; Length 215;

Best Local Similarity 81.4%; Pred. No. 2.4e-56;

Matches 179; Conservative 14; Mismatches 22; Indels 5; Gaps 3;

Qy 1 EIVLTQSLPLPVTGPGEASISCRSSQLHNSNGYTVLDWYLKQPGSPOLLIYSSSHRA 60

Db 1 EIVLTQSGPTLSLSPGERATLSRASOSV--SN--NYLAWYQQKPGQAPSLIYDASSRA 56

Qy 61 SGVPDRFSGSVSGTDTLRISRVEAEDGVVYCMQGLQSPFTFGPGTKVDIKRGTVAAPS 120

Db 57 TGIPDRFSGSGTDTLTISGLEPDEFVYVYCOQYDRPPTFGQGTVEIKR-TVAAPS 115

Qy 121 VFIFPPDEQLKSGTASVVLNNFYPREAKVQWKNALQSGNSQESVTEQDSKDYTS 180

Db 116 VFIFPPDEQLKSGTASVVLNNFYPREAKVQWKNALQSGNSQESVTEQDSKDYTS 175

Qy 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

Db 176 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 215

##### RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence\_revision 05-Dec-1998 #text\_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.

A:Submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:16-90/Domain: immunoglobulin homology <IMM>

|                                                                                       |                                                                      |
|---------------------------------------------------------------------------------------|----------------------------------------------------------------------|
| C:Superfamily: immunoglobulin V region; immunoglobulin homology                       |                                                                      |
| C:Keywords: heterotetramer; immunoglobulin                                            |                                                                      |
| F:16-91/Domain: immunoglobulin homology <IMM>                                         |                                                                      |
| Query Match                                                                           | 74.0%; Score 847.5; DB 2; Length 215;                                |
| Best Local Similarity                                                                 | 80.4%; Pred. No. 4.3e-53;                                            |
| Matches                                                                               | 176; Conservative 13; Mismatches 25; Indels 5; Gaps 3;               |
| QY                                                                                    | 1 EIVLTQSPPLSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60    |
| DB                                                                                    | 1 EIVLTQSPATLSLSPGERATLISGGASQS-VSN---YLAWYQKPGQAPRLLIYDASSRA 56     |
| QY                                                                                    | 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYVYCMQGLQSPFFGPGTKVDIKRGTVAAAPS 120  |
| DB                                                                                    | 57 TGIPDRFSGSGSTDFTLTISRLEPEDFAVYGYQYGSPLTFGGGTGKVEIKR-TVAAPS 115    |
| QY                                                                                    | 121 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180 |
| DB                                                                                    | 116 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 175 |
| QY                                                                                    | 181 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 219                    |
| DB                                                                                    | 176 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 214                    |
| RESULT 5                                                                              |                                                                      |
| JE0241                                                                                |                                                                      |
| Ig kappa chain Am37 precursor - human                                                 |                                                                      |
| C:Species: Homo sapiens (man)                                                         |                                                                      |
| C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000           |                                                                      |
| C:Accession: JE0241                                                                   |                                                                      |
| R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda |                                                                      |
| submitted to JIPID, November 1998                                                     |                                                                      |
| A:Description: Structure relationship of kappa type light chains with AL amyloidosis: |                                                                      |
| A:Reference number: JE0241                                                            |                                                                      |
| A:Accession: JE0241                                                                   |                                                                      |
| A:Molecule type: protein                                                              |                                                                      |
| A:Residues: 1-216 <ALI>                                                               |                                                                      |
| C:Superfamily: immunoglobulin V region; immunoglobulin homology                       |                                                                      |
| F:16-92/Domain: immunoglobulin homology <IMM>                                         |                                                                      |
| Query Match                                                                           | 71.8%; Score 823; DB 2; Length 216;                                  |
| Best Local Similarity                                                                 | 76.4%; Pred. No. 2.3e-51;                                            |
| Matches                                                                               | 168; Conservative 20; Mismatches 28; Indels 4; Gaps 4;               |
| QY                                                                                    | 1 EIVLTQSPPLSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60    |
| DB                                                                                    | 1 DIVLTQSPDFLAVSLGERATINCKSQSVLY-NSKNFLAWYQKPGQ-PKLLIWA-NVRE 57      |
| QY                                                                                    | 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYVYCMQGLQSPFFGPGTKVDIKRGTVAAAPS 120  |
| DB                                                                                    | 58 SGVPDRFSGSVSGTDFTLTISNLAELVAVYCYQYVSTPTPSFGQGRLEIKR-TVAAPS 116    |
| QY                                                                                    | 121 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180 |
| DB                                                                                    | 117 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 176 |
| QY                                                                                    | 181 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 220                    |
| DB                                                                                    | 177 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 216                    |
| RESULT 6                                                                              |                                                                      |
| S52028                                                                                |                                                                      |
| Ig kappa chain - mouse                                                                |                                                                      |
| C:Species: Mus musculus (house mouse)                                                 |                                                                      |
| C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000           |                                                                      |
| C:Accession: S52028                                                                   |                                                                      |
| R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A |                                                                      |
| submitted to the EMBL Data Library, August 1994                                       |                                                                      |
| A:Description: Coordinate expression of antibody subunit genes yields high levels of  |                                                                      |
| A:Reference number: S52028                                                            |                                                                      |
| A:Accession: S52028                                                                   |                                                                      |

|                                                                                          |                                                                      |
|------------------------------------------------------------------------------------------|----------------------------------------------------------------------|
| Query Match                                                                              | 76.6%; Score 877.5; DB 2; Length 215;                                |
| Best Local Similarity                                                                    | 79.6%; Pred. No. 3.2e-55;                                            |
| Matches                                                                                  | 176; Conservative 16; Mismatches 22; Indels 7; Gaps 4;               |
| QY                                                                                       | 1 EIVLTQSPPLSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60    |
| DB                                                                                       | 1 EIVLTQSPATLSVSPGERATLISCRASQS-VHSN---LAWYQKPGQAPRLLIYRASTRA 55     |
| QY                                                                                       | 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYVYCMQ-GLQSPFFGPGTKVDIKRGTVAAAP 119  |
| DB                                                                                       | 56 TGIPARFSGSGSTDFTLTISLQSEDFALYCYQYNTWPLTFGGGTGKVEIKR-TVAAP 114     |
| QY                                                                                       | 120 SVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTY 179 |
| DB                                                                                       | 115 SVFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTY 174 |
| QY                                                                                       | 180 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 220                    |
| DB                                                                                       | 175 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 215                    |
| RESULT 3                                                                                 |                                                                      |
| JE0243                                                                                   |                                                                      |
| Ig kappa chain NIC93 precursor - human                                                   |                                                                      |
| C:Species: Homo sapiens (man)                                                            |                                                                      |
| C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000              |                                                                      |
| C:Accession: JE0243                                                                      |                                                                      |
| R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T |                                                                      |
| submitted to JIPID, November 1998                                                        |                                                                      |
| A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy |                                                                      |
| A:Reference number: JE0243                                                               |                                                                      |
| A:Accession: JE0243                                                                      |                                                                      |
| A:Molecule type: protein                                                                 |                                                                      |
| A:Residues: 1-215 <ALI>                                                                  |                                                                      |
| C:Superfamily: immunoglobulin V region; immunoglobulin homology                          |                                                                      |
| F:16-90/Domain: immunoglobulin homology <IMM>                                            |                                                                      |
| Query Match                                                                              | 75.9%; Score 869.5; DB 2; Length 215;                                |
| Best Local Similarity                                                                    | 77.7%; Pred. No. 1.2e-54;                                            |
| Matches                                                                                  | 171; Conservative 18; Mismatches 26; Indels 5; Gaps 1;               |
| QY                                                                                       | 1 EIVLTQSPPLSLPVTGPEPASISCRSSQSLHNSGYTYLDWYLOKPGQSPQLLIYSGSHRA 60    |
| DB                                                                                       | 1 EIVLTQSPATLSVSPGERATLISCRASQSA-----TNVVTWQKLGQAPRLLIYDASTRA 55     |
| QY                                                                                       | 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGYVYCMQGLQSPFFGPGTKVDIKRGTVAAAPS 120  |
| DB                                                                                       | 56 TGVPARFSGSGSTDFTLTISLQSEDFAIYCYQHNNAWPPTFGQGTGKVKTRRTVAAPS 115    |
| QY                                                                                       | 121 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 180 |
| DB                                                                                       | 116 VFIFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSDSTYS 175 |
| QY                                                                                       | 181 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 220                    |
| DB                                                                                       | 176 LSSTLTLSKADYEKKHKVYACEVTHQGLSSPVTKSFNRGEC 215                    |
| RESULT 4                                                                                 |                                                                      |
| A23746                                                                                   |                                                                      |
| Ig kappa chain V-III (KAU cold agglutinin) - human                                       |                                                                      |
| C:Species: Homo sapiens (man)                                                            |                                                                      |
| C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000              |                                                                      |
| C:Accession: A23746                                                                      |                                                                      |
| R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.                                           |                                                                      |
| J. Biol. Chem. 266, 2836-2842, 1991                                                      |                                                                      |
| A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl |                                                                      |
| A:Reference number: A23746; MUID:91131575                                                |                                                                      |
| A:Accession: A23746                                                                      |                                                                      |
| A>Status: preliminary                                                                    |                                                                      |
| A:Molecule type: protein                                                                 |                                                                      |
| A:Residues: 1-215 <LEO>                                                                  |                                                                      |

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(continued from page 1)

01234567891011121314151617181920212223242526272829303132333435363738394041424344454647484950515253545556575859606162636465666768697071727374757677787980818283848586878889909192939495969798991001011021031041051061071081091101111121131141151161171181191201211221231241251261271281291301311321331341351361371381391401411421431441451461471481491501511521531541551561571581591601611621631641651661671681691701711721731741751761771781791801811821831841851861871881891901911921931941951961971981992002012022032042052062072082092102112122132142152162172182192202212222232242252262272282292302312322332342352362372382392402412422432442452462472482492502512522532542552562572582592602612622632642652662672682692702712722732742752762772782792802812822832842852862872882892902912922932942952962972982993003013023033043053063073083093103113123133143153163173183193203213223233243253263273283293303313323333343353363373383393403413423433443453463473483493503513523533543553563573583593603613623633643653663673683693703713723733743753763773783793803813823833843853863873883893903913923933943953963973983994004014024034044054064074084094104114124134144154164174184194204214224234244254264274284294304314324334344354364374384394404414424434444454464474484494504514524534544554564574584594604614624634644654664674684694704714724734744754764774784794804814824834844854864874884894904914924934944954964974984995005015025035045055065075085095105115125135145155165175185195205215225235245255265275285295305315325335345355365375385395405415425435445455465475485495505515525535545555565575585595605615625635645655665675685695705715725735745755765775785795805815825835845855865875885895905915925935945955965975985996006016026036046056066076086096106116126136146156166176186196206216226236246256266276286296306316326336346356366376386396406416426436446456466476486496506516526536546556566576586596606616626636646656666676686696706716726736746756766776786796806816826836846856866876886896906916926936946956966976986997007017027037047057067077087097107117127137147157167177187197207217227237247257267277287297307317327337347357367377387397407417427437447457467477487497507517527537547557567577587597607617627637647657667677687697707717727737747757767777787797807817827837847857867877887897907917927937947957967977987998008018028038048058068078088098108118128138148158168178188198208218228238248258268278288298308318328338348358368378388398408418428438448458468478488498508518528538548558568578588598608618628638648658668678688698708718728738748758768778788798808818828838848858868878888898908918928938948958968978988999009019029039049059069079089099109119129139149159169179189199209219229239249259269279289299309319329339349359369379389399409419429439449459469479489499509519529539549559569579589599609619629639649659669679689699709719729739749759769779789799809819829839849859869879889899909919929939949959969979989991000100110021003100410051006100710081009101010111012101310141015101610171018101910201021102210231024102510261027102810291030103110321033103410351036103710381039104010411042104310441045104610471048104910501051105210531054105510561057105810591060106110621063106410651066106710681069107010711072107310741075107610771078107910801081108210831084108510861087108810891090109110921093109410951096109710981099110011011102110311041105110611071108110911101111111211131114111511161117111811191120112111221123112411251126112711281129113011311132113311341135113611371138113911401141114211431144114511461147114811491150115111521153115411551156115711581159116011611162116311641165116611671168116911701171117211731174117511761177117811791180118111821183118411851186118711881189119011911192119311941195119611971198119912001201120212031204120512061207120812091210121112121213121412151216121712181219122012211222122312241225122612271228122912301231123212331234123512361237123812391240124112421243124412451246124712481249125012511252125312541255125612571258125912601261126212631264126512661267126812691270127112721273127412751276127712781279128012811282128312841285128612871288128912901291129212931294129512961297129812991300

```
RESULT 10
S38865
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S38865
R:Klipp, B.; Becker, W.; Schlaak, M.
A:Description: Combination of a defined specificity and desired isotype by cloning of an
A:Reference number: S38864
A:Accession: S38865
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <KIP>
A:Cross-references: EMBL:Z27396; NID:g416538; PIDN:CAA81787.1; PID:g416539
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 67.1%; Score 769.5; DB 2; Length 219;
Best Local Similarity 67.3%; Pred. No. 1.4e-47;
Matches 148; Conservative 29; Mismatches 42; Indels 1; Gaps 1;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHSGNYVLDWYLOKPGSPOLLIIYSGSHRA 60
DB 1 ELVNTQSPLESLVSLGDSQASISCRSSQSLVHTNGNTYLVHWYLOKPGSLPKLLIYVSNRF 60

QY 61 SGVPDRFSGVSGTDFTLIRISRVEAEDGVGYCMOGLQSPFTFGPGTKVDIKRGTVAAAPS 120
DB 61 ELVNTQSPLESLVSLGDSQASISCRSSQSLVHTNGNTYLVHWYLOKPGSLPKLLIYVSNRF 60

QY 61 SGVPDRFSGVSGTDFTLIRISRVEAEDGVGYCMOGLQSPFTFGPGTKVDIKRGTVAAAPS 120
DB 61 SGVPDRFSGVSGTDFTLIRISRVEAEDGVGYCMOGLQSPFTFGPGTKVDIKRGTVAAAPS 120

QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSY 180
DB 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSY 180

QY 120 VSIFFPPTSEQLTSGGASVVCFLNNFYPKDINVKWIDGSEKQNGVLSWTDQDSKDSY 195
DB 120 VSIFFPPTSEQLTSGGASVVCFLNNFYPKDINVKWIDGSEKQNGVLSWTDQDSKDSY 195

QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
DB 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220

QY 180 MSSTLTLTCKDEYERHNSYTCETHTKTSTPIVKSFNREK 240
DB 180 MSSTLTLTCKDEYERHNSYTCETHTKTSTPIVKSFNREK 240

RESULT 11
JL0029
Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desaynard, C.; Scharff, M.D.
J. Exp. Med. 167, 934-973, 1988
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphospho
A:Reference number: JL0029; MUID:88171315
A:Accession: JL0029
A:Molecule type: mRNA
A:Residues: 1-225 <CHI>
A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A:Note: the authors translated the codon CCG for residue 106 as Pro, ACC for residue 132
A:Note: the nucleotide sequence shown is inconsistent with authors' translation because
A:Note: except for four positions shown above
C:Comment: The protein is an anti-phosphorylcholine antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

F:7-225/Product: Ig kappa chain #status predicted <IIC>
F:7-106/Domain: V region #status predicted <VAR>
F:107-119/Domain: J region #status predicted <J1R>
F:120-225/Domain: C region #status predicted <COR>

Query Match 65.5%; Score 750.5; DB 2; Length 225;
Best Local Similarity 64.5%; Pred. No. 3.2e-46;
Matches 142; Conservative 31; Mismatches 46; Indels 1; Gaps 1;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHSGNYVLDWYLOKPGSPOLLIIYSGSHRA 60
DB 7 DVLMTQIPLESLVSLGDSQASISCRSSQSLVHTNGNTYLVHWYLOKPGSPNLLIYKISNRF 66

Query Match 60.2%; Score 690; DB 2; Length 220;
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```
QY 61 SGVPDRFSGVSGTDFTLIRISRVEAEDGVGYCMOGLQSPFTFGPGTKVDIKRGTVAAAPS 120
DB 67 SGVPDRFSGVSGTDFTLIRISRVEAEDGVGYCMOGLQSPFTFGPGTKVDIKRGTVAAAPS 125

QY 121 VFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSY 180
DB 126 VSIFFPPTSEQLTSGGASVVCFLNNFYPKDINVKWIDGSEKQNGVLSWTDQDSKDSY 185

QY 181 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
DB 186 MSSTLTLTCKDEYERHNSYTCETHTKTSTPIVKSFNREK 225

RESULT 12
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain c
A:Reference number: S06084; MUID:90016888
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-240/Product: Ig kappa chain #status predicted <SIG>
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 63.3%; Score 725; DB 2; Length 240;
Best Local Similarity 63.3%; Pred. No. 2.2e-44;
Matches 140; Conservative 31; Mismatches 48; Indels 2; Gaps 2;

QY 1 EIVLTQSPLESLPVTPGEPASISCRSSQSLHSGNYVLDWYLOKPGSPOLLIIYSGSHR 59
DB 21 DFVMTQSPSSLAIVAGEIVTINCKSSQSLFYSGNKNYLAHWYQKPGSPKLLIYWASTR 80

QY 60 ASGVDRFSGVSGTDFTLIRISRVEAEDGVGYCMOGLQSPFTFGPGTKVDIKRGTVAAAP 119
DB 81 QSGVDRFSGVSGTDFTLIRISRVEAEDGVGYCMOGLQSPFTFGPGTKVDIKRGTVAAAP 139

QY 120 VSIFFPPTSEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSGNSQESVTEQDSKDSY 179
DB 140 TVSIFFPPTSEQLKSGTASVVCCLNNFYPRDISVKWKIDGTERRDGVLSVTDQDSKDSY 199

QY 180 LSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 220
DB 200 SMSSTLTLSKADYKHKVYACEVTHQGLSSPVTKSFNRGEC 240

RESULT 13
A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an
A:Reference number: A92686; MUID:89034213
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:M23626; GB:J04061; NID:g533234; PIDN:AAA39162.1; PID:g533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 60.2%; Score 690; DB 2; Length 220;
```



C:Accession: JC5810  
R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, Biochem. Biophys. Res. Commun. 240, 566-572, 1997  
A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porph  
A:Reference number: JC5810; MUID:98063277  
A:Accession: JC5810  
A:Molecule type: protein  
A:Residues: 1-218 <AKA>  
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a p  
C:Superfamily: immunoglobulin v region; immunoglobulin homology  
E:16-94/Domain: immunoglobulin homology <IMM>

Search completed: October 9, 2002, 19:13:19  
Job time : 11.7857 secs

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Best Local Similarity 60.6%; Pred. No. 6e-42;
Matches 134; Conservative 29; Mismatches 56; Indels 2; Gaps 2;

QY 1 EIVLTQSPLSLPVTPGEPASISCRSSQSLIHSNGY-TYLDWYLQKPGQSPQLLIYSGSHR 59
Db 1 DIWVTQSPSLTVAGEKVTMCTSSQSLFNSGKQKNYLTWYQKPGQPKVLIYWASTR 60

QY 60 ASGVPDRFGSGVSGTDFTLIRSRVEADGVGYVCMOGLQSPPTFGPGTKVDIKRGTVAAP 119
Db 61 ESGVPDRFTGSGSGTDFTLTISSQAEADLAIVYQNDYSNPLTFGGGTKLELRAD-AAP 119

QY 120 SVFIPPSDEOLKSGTASVYVCLLNPFYPREAKYQWKNALQSGNSQESVTEQDSKDY 179
Db 120 TVSIFPPSDEQLTSGGASVYVCFLNPFYPKDINVKWIDGERQNGVLNSWTQDQSKDY 179

QY 180 LSSLTLSKADYEKKHYACEVTHQGLSGSPVTKSNRNEC 220
Db 180 SMSSTLTATKDEYRHNSYTCETATHTKSTSPIVKSFNRNEC 220

RESULT 14
S68241
Ig kappa chain V region (Mab13-1) - mouse (fragment)
N:Alternate names: immunoglobulin light chain
C:Species: Mus musculus (house mouse)
C:Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68241; S68214
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.;
submitted to the EMBL Data Library, March 1994
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin
A:Reference number: S68241
A:Accession: S68241
A:Molecule type: mRNA
A:Residues: 1-218 <TAK>
A:Cross-references: EMBL:D29670; NID:g473962; PID:BAA06141.1; PID:g473963
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.;
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223
A:Accession: S68214
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'NI', 3-212 <TAK>
A:Cross-references: EMBL:D29670
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 59.1%; Score 677; DB 2; Length 218;
Best Local Similarity 59.5%; Pred. No. 4.9e-41;
Matches 131; Conservative 33; Mismatches 55; Indels 2; Gaps 2;

QY 1 EIVLTQSPLSLPVTPGEPASISCRSSQSLIHSNGYTYLDWYLQKPGQSPQLLIYSGSHRA 60
Db 1 ELVLTQSPASLAVSLGQRATISCRASKS-VSASGVYIMHWYQKPGQPKLLISLATNLE 59

QY 61 SGVPDRFGSGVSGTDFTLIRSRVEADGVGYVCMOGLQSPPTFGPGTKVDIKRGTVAPAS 120
Db 60 SGVPARFSGSGSGTDFTLINHPVEEDVATYVQHSRELPLTFGAGTKLELRAD-AAPT 118

QY 121 VFIFPPSDEOLKSGTASVYVCLLNPFYPREAKYQWKNALQSGNSQESVTEQDSKDY 180
Db 119 VSIFFPPSDEQLTSGGASVYVCFLNPFYPKDINVKWIDGERQNGVLNSWTQDQSKDY 178

QY 181 LSSLTLSKADYEKKHYACEVTHQGLSGSPVTKSNRNEC 220
Db 179 MSSLTATKDEYRHNSYTCETATHTKSTSPIVKSFNRNEC 218

```

RESULT 15  
JC5810  
monoclonal antibody 13-1 light chain - mouse  
C:Species: Mus musculus (house mouse)  
~:Date: 04-Feb-1998 #sequence revision 13-Mar-1998 #text\_change 21-Jan-2000



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 9, 2002, 19:04:54 ; Search time 6.73469 Seconds  
(without alignments)  
1264.839 Million cell updates/sec

Title: US-09-822-698A-24  
Perfect score: 1146  
Sequence: 1 EIVLTQSLPLSPVTPGEPAS.....EYTHQGLSSPVTKSFNRGEC 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query | Score | Match | Length | ID         | Description        |
|------------|-------|-------|-------|--------|------------|--------------------|
| 1          | 548   | 47.8  | 106   | 1      | KAC_HUMAN  | P01834 homo sapien |
| 2          | 527   | 46.0  | 117   | 1      | KV2E_HUMAN | P06309 homo sapien |
| 3          | 500   | 43.6  | 113   | 1      | KV2D_HUMAN | P01617 homo sapien |
| 4          | 478.5 | 41.8  | 112   | 1      | KV2C_HUMAN | P01616 homo sapien |
| 5          | 467.5 | 40.8  | 115   | 1      | KV2A_HUMAN | P01614 homo sapien |
| 6          | 455   | 39.7  | 113   | 1      | KV2B_HUMAN | P01615 homo sapien |
| 7          | 444   | 38.7  | 133   | 1      | KV2F_HUMAN | P06310 homo sapien |
| 8          | 432   | 37.7  | 113   | 1      | KV2E_MOUSE | P03976 mus musculu |
| 9          | 429   | 37.4  | 113   | 1      | KV2G_MOUSE | P01631 mus musculu |
| 10         | 423   | 36.9  | 113   | 1      | KV2F_MOUSE | P01630 mus musculu |
| 11         | 402   | 35.1  | 112   | 1      | KV2D_MOUSE | P01629 mus musculu |
| 12         | 394.5 | 34.4  | 108   | 1      | KV1_CANFA  | P01618 canis famil |
| 13         | 394   | 34.4  | 113   | 1      | KV2C_MOUSE | P01628 mus musculu |
| 14         | 387   | 33.8  | 112   | 1      | KV2A_MOUSE | P01626 mus musculu |
| 15         | 370   | 32.3  | 129   | 1      | KV3L_HUMAN | P18135 homo sapien |
| 16         | 369   | 32.2  | 129   | 1      | KV3M_HUMAN | P18136 homo sapien |
| 17         | 368.5 | 32.2  | 114   | 1      | KV4A_HUMAN | P01623 homo sapien |
| 18         | 367   | 32.0  | 106   | 1      | KACB_RAT   | P01835 rattus norv |
| 19         | 366.5 | 32.0  | 134   | 1      | KV4C_HUMAN | P06314 homo sapien |
| 20         | 366   | 31.9  | 109   | 1      | KV3B_HUMAN | P01620 homo sapien |
| 21         | 366   | 31.9  | 109   | 1      | KV3D_HUMAN | P01622 homo sapien |
| 22         | 362   | 31.6  | 120   | 1      | KV2B_MOUSE | P01627 mus musculu |
| 23         | 359   | 31.3  | 106   | 1      | KACA_RAT   | P01836 rattus norv |
| 24         | 357   | 31.2  | 109   | 1      | KV3E_HUMAN | P01623 homo sapien |
| 25         | 357   | 31.2  | 109   | 1      | KV3G_HUMAN | P04206 homo sapien |
| 26         | 354   | 30.9  | 133   | 1      | KV4B_HUMAN | P06313 homo sapien |
| 27         | 351   | 30.6  | 108   | 1      | KV3A_HUMAN | P01619 homo sapien |
| 28         | 350   | 30.5  | 106   | 1      | KAC_MOUSE  | P01837 mus musculu |
| 29         | 349.5 | 30.5  | 128   | 1      | KV3K_HUMAN | P06311 homo sapien |
| 30         | 343.5 | 30.0  | 111   | 1      | KV3M_MOUSE | P01665 mus musculu |
| 31         | 340.5 | 29.7  | 111   | 1      | KV3L_MOUSE | P01664 mus musculu |
| 32         | 340   | 29.7  | 109   | 1      | KV3F_HUMAN | P01624 homo sapien |
| 33         | 338.5 | 29.5  | 111   | 1      | KV3O_MOUSE | P01667 mus musculu |

|    |       |      |     |   |            |                    |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 338.5 | 29.5 | 111 | 1 | KV3U_MOUSE | P01673 mus musculu |
| 35 | 338   | 29.5 | 129 | 1 | KV3H_HUMAN | P04207 homo sapien |
| 36 | 336.5 | 29.4 | 111 | 1 | KV3S_MOUSE | P01671 mus musculu |
| 37 | 335.5 | 29.3 | 111 | 1 | KV3N_MOUSE | P01666 mus musculu |
| 38 | 334.5 | 29.2 | 111 | 1 | KV3R_MOUSE | P01670 mus musculu |
| 39 | 333.5 | 29.1 | 111 | 1 | KV3H_MOUSE | P01660 mus musculu |
| 40 | 332   | 29.0 | 110 | 1 | KV3P_MOUSE | P01668 mus musculu |
| 41 | 331.5 | 28.9 | 111 | 1 | KV3O_MOUSE | P01669 mus musculu |
| 42 | 326.5 | 28.5 | 111 | 1 | KV3J_MOUSE | P01662 mus musculu |
| 43 | 326.5 | 28.5 | 111 | 1 | KV3T_MOUSE | P01672 mus musculu |
| 44 | 324.5 | 28.3 | 111 | 1 | KV3C_MOUSE | P01656 mus musculu |
| 45 | 324.5 | 28.3 | 131 | 1 | KV3I_MOUSE | P01661 mus musculu |

ALIGNMENTS

| RESULT 1 |                                                                                                                                                                                                                                                    |           |      |         |  |
|----------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------|------|---------|--|
| ID       | KAC_HUMAN                                                                                                                                                                                                                                          | STANDARD; | PRT; | 106 AA. |  |
| AC       | P01834;                                                                                                                                                                                                                                            |           |      |         |  |
| DT       | 21-JUL-1986 (Rel. 01, Created)                                                                                                                                                                                                                     |           |      |         |  |
| DT       | 21-JUL-1986 (Rel. 01, Last sequence update)                                                                                                                                                                                                        |           |      |         |  |
| DT       | 16-OCT-2001 (Rel. 40, Last annotation update)                                                                                                                                                                                                      |           |      |         |  |
| DE       | Ig kappa chain C region.                                                                                                                                                                                                                           |           |      |         |  |
| GN       | IGKC.                                                                                                                                                                                                                                              |           |      |         |  |
| OS       | Homo sapiens (Human).                                                                                                                                                                                                                              |           |      |         |  |
| OC       | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;                                                                                                                                                                                  |           |      |         |  |
| OC       | Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.                                                                                                                                                                                         |           |      |         |  |
| OX       | NCBI_TaxID=9606;                                                                                                                                                                                                                                   |           |      |         |  |
| RN       | [1]                                                                                                                                                                                                                                                |           |      |         |  |
| RP       | SEQUENCE (MYELOMA PROTEIN EU).                                                                                                                                                                                                                     |           |      |         |  |
| RX       | MEDLINE=71064023; PubMed=5489770;                                                                                                                                                                                                                  |           |      |         |  |
| RA       | Gottlieb P.D., Cunningham B.A., Rutishauser U., Edelman G.M.;                                                                                                                                                                                      |           |      |         |  |
| RT       | "The covalent structure of a human gamma G-immunoglobulin. VI. Amino acid sequence of the light chain."                                                                                                                                            |           |      |         |  |
| RL       | Biochemistry 9:3155-3161(1970).                                                                                                                                                                                                                    |           |      |         |  |
| RN       | [2]                                                                                                                                                                                                                                                |           |      |         |  |
| RP       | DISULFIDE BONDS.                                                                                                                                                                                                                                   |           |      |         |  |
| RX       | MEDLINE=71064027; PubMed=4923144;                                                                                                                                                                                                                  |           |      |         |  |
| RA       | Gall W.E., Edelman G.M.;                                                                                                                                                                                                                           |           |      |         |  |
| RT       | "The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds."                                                                                                                                                         |           |      |         |  |
| RL       | Biochemistry 9:3188-3196(1970).                                                                                                                                                                                                                    |           |      |         |  |
| RN       | [3]                                                                                                                                                                                                                                                |           |      |         |  |
| RP       | SEQUENCE (BENCE-JONES PROTEIN TI).                                                                                                                                                                                                                 |           |      |         |  |
| RX       | MEDLINE=72188439; PubMed=5027703;                                                                                                                                                                                                                  |           |      |         |  |
| RA       | Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;                                                                                                                                                                                               |           |      |         |  |
| RT       | "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein TI). IV. The complete amino acid sequence and its significance for the mechanism of antibody production." |           |      |         |  |
| RL       | Hoppe-Seyler's Z. Physiol. Chem. 353:189-208(1972).                                                                                                                                                                                                |           |      |         |  |
| RN       | [4]                                                                                                                                                                                                                                                |           |      |         |  |
| RP       | SEQUENCE FROM N.A.                                                                                                                                                                                                                                 |           |      |         |  |
| RX       | MEDLINE=81042304; PubMed=6775818;                                                                                                                                                                                                                  |           |      |         |  |
| RA       | Hietter P.A., Max E.E., Seidman J.G., Maizel J.V. Jr., Leder P.;                                                                                                                                                                                   |           |      |         |  |
| RT       | "Cloned human and mouse kappa immunoglobulin constant and J region genes conserve homology in functional segments."                                                                                                                                |           |      |         |  |
| RL       | Cell 22:197-207(1980).                                                                                                                                                                                                                             |           |      |         |  |
| RN       | [5]                                                                                                                                                                                                                                                |           |      |         |  |
| RP       | SEQUENCE (BENCE-JONES PROTEIN ROY).                                                                                                                                                                                                                |           |      |         |  |
| RA       | Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,                                                                                                                                                                                    |           |      |         |  |
| RA       | Steinmetz-Kayne M., Suter L., Watanabe S.;                                                                                                                                                                                                         |           |      |         |  |
| RL       | (in) Franek F., Shugar D. (eds.);                                                                                                                                                                                                                  |           |      |         |  |
| RL       | Gamma globulins: structure and function, pp.57-74, Academic Press, New York (1969).                                                                                                                                                                |           |      |         |  |
| RN       | [6]                                                                                                                                                                                                                                                |           |      |         |  |
| RP       | SEQUENCE (BENCE-JONES PROTEIN CUM).                                                                                                                                                                                                                |           |      |         |  |
| RX       | MEDLINE=68242259; PubMed=5586923;                                                                                                                                                                                                                  |           |      |         |  |
| RA       | Hilschmann N.;                                                                                                                                                                                                                                     |           |      |         |  |
| RT       | "The complete amino acid sequence of Bence Jones protein Cum (kappa-type)."                                                                                                                                                                        |           |      |         |  |

```

RL Hoppe-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).
RN [7]
RP SEQUENCE (BENCE-JONES PROTEIN AG).
RX MEDLINE=69234734; PubMed=4893682;
RT Titani K., Shinoda T., Putnam F.W.;
RA "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges."
RL J. Biol. Chem. 244:3550-3560(1969).
RN [8]
RP SEQUENCE (WALDENSTROM'S MACROGLOBULIN OU).
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
RT chains."
RL Science 169:56-59(1970).
RN [9]
RP SEQUENCE (THE EU SEQUENCE HAS THE INV (3) ALLOTYPIC MARKER,
CC 45-ALA & 83-VAL. THE ROY SEQUENCE HAS THE INV (1,2) ALLOTYPIC
CC MARKER, 45-ALA AND 83-LEU.
CC -----
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CC -----
CC EMBL; J00241; AAA58989.1; -
CC EMBL; V00557; CAA23823.1; -
CC PIR; A02116; K3HU.
CC HSSP; P01842; 7FAB.
CC MIN; 147200; -
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003597; Ig_C1.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00407; IGCL; 1.
CC PROSITE; PS00290; IG_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region.
CC NON_TER 1 1
CC DISULFID 26 86
CC VARIANT 106 106
CC INTERCHAIN (WITH A HEAVY CHAIN).
CC V -> L (IN INV(1,2) MARKER).
CC /FTID=VAR_003897.
CC D -> N (IN REF. 7 AND 8).
CC E -> Q (IN REF. 5 AND 6).
CC CONFLICT 14 14
CC CONFLICT 57 57
CC SEQUENCE 106 AA; 11609 MW; 51984D1FDD372CE8 CRC64;
SQ
Query Match 47.8%; Score 548; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 4.2e-40; Mismatches 0; Indels 0; Gaps 0;
Matches 106; Conservative 0;
QY 115 TVAAPSVFFPPSDQLSGTASVYCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 174
Db 1 TVAAPSVFFPPSDQLSGTASVYCLNNFYPREAKVQWKVDNALQSGNSQESVTEQDS 60
QY 175 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGEK 220
Db 61 KDSYSLSTLTLSKADYKHKVYACEVTHQGLSSPVTKSNRGEK 106
RESULT 2
KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

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RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity."
RL Nature 309:73-76(1984).
CC -----
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CC -----
CC EMBL; Z00009; -; NOT_ANNOTATED_CDS.
CC PIR; A01889; K2HUGM.
CC InterPro; IPR003006; Ig_MHC.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC Immunoglobulin V region; Signal.
CC NON_TER 1 1
CC SIGNAL <1 4
CC CHAIN 5 117
CC DOMAIN 28 43
CC COMPLEMENTARITY-DETERMINING-1.
CC DOMAIN 44 58
CC COMPLEMENTARITY-DETERMINING-2.
CC DOMAIN 66 97
CC COMPLEMENTARITY-DETERMINING-3.
CC DOMAIN 98 106
CC COMPLEMENTARITY-DETERMINING-4.
CC DOMAIN 107 116
CC DISULFID 27 97
CC NON_TER 117 117
CC SEQUENCE 117 AA; 12664 MW; 92C57DC719E558B1 CRC64;
SQ
Query Match 46.0%; Score 527; DB 1; Length 117;
Best Local Similarity 89.4%; Pred. No. 2.9e-38; Mismatches 6; Indels 0; Gaps 0;
Matches 101; Conservative 6;
QY 1 EIVLTQSPISLPTVTPGEPASISCRSSQSLHNSGYIYLDWYLQKQPSQPLLIIYSGSHRA 60
Db 5 DIVTQSPISLPTVTPGEPASISCRSSQSLHNSGYIYLDWYLQKQPSQPLLIIYSGNRA 64
QY 61 SGVPDRFSGSVSGTDTLRLISRVEAEADVGYICMQLQSPFTFGPGTKVDIAR 113
Db 65 SGVPDRFSGSVSGTDTLRLISRVEAEADVGYICMQLQSPFTFGPGTKVDIAR 117
RESULT 3
KV2D_HUMAN STANDARD; PRT; 113 AA.
AC P01617;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region TEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (BENCE-JONES PROTEIN TEW).
RX MEDLINE=74148480; PubMed=4596149;
RA Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT "Amino acid sequence of a kappa Bence Jones protein from a case of
RT primary amyloidosis."
RL Biochemistry 12:3763-3780(1973).
RN [2]
RP SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RX MEDLINE=73166638; PubMed=4700495;
RA Terry W.D., Page D.L., Kimura S., Isobe T., Osserman E.F.,
RA Glenner G.G.;

```

RT Structural identity of Bence Jones and amyloid fibril proteins in a patient with plasma cell dyscrasia and amyloidosis.";

RL J. Clin. Invest. 52:1276-1281(1973).

CC -1- MISCELLANEOUS: THE MAJOR AMYLOID PROTEIN APPEARS TO BE IDENTICAL WITH THE BENCE JONES PROTEIN ISOLATED FROM THE SAME PATIENT.

CC -1- MISCELLANEOUS: THIS PROTEIN WAS ISOLATED FROM THE URINE OF A PATIENT WITH PLASMA CELL DYSKRASIA AND AMYLOIDOSIS.

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2) MARKER.

CC PIR: A01888; K2HUTW.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam: PF00047; Ig; 1.

DR SMART: SM00406; IGV; 1.

KW Immunoglobulin V region; Bence-Jones protein; Amyloid.

FT DOMAIN 1 23

FT DOMAIN 24 39

FT DOMAIN 40 54

FT DOMAIN 55 61

FT DOMAIN 62 93

FT DOMAIN 94 102

FT DOMAIN 103 112

FT DISULFID 23 93

FT NON\_TER 113 113

FT SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query Match 43.6%; Score 500; DB 1; Length 113;

Best Local Similarity 82.3%; Pred. No. 5.5e-36;

Matches 93; Conservative 14; Mismatches 6; Indels 0; Gaps 0;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLOKPGSQPOLLIYSGSRA 60

Db 1 DIVMTQSPSLPVTPGEPASISCRSSQSLHSGDFYLNWYLOKPGSQPOLLIYLSNRA 60

QY 61 SGVPRFSGSGVSGDTFLIRSRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113

Db 61 SGVPRFSGSGSGDTFLTKISRVQAEADVGVYCMQALQAPITFGQGRLEIKR 113

RESULT 4

ID KV2C\_HUMAN STANDARD; PRT; 112 AA.

AC P01616;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE Ig kappa chain V-II region MIL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

FT NON\_TER 112 112

FT SEQUENCE 112 AA; 12055 MW; E5B22E2FA7ABE481 CRC64;

Query Match 41.8%; Score 478.5; DB 1; Length 112;

Best Local Similarity 78.8%; Pred. No. 3.6e-34;

Matches 89; Conservative 15; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLOKPGSQPOLLIYSGSRA 60

Db 1 DIVLTQSPSLPVTPGEPASISCRSSQSLHSG-BYLDWYLOKPGSZPLLIIYLSNRA 59

QY 61 SGVPRFSGSGVSGDTFLIRSRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113

Db 60 SGVPRFSGSGSGDTFLTKISRVQAEADVGVYCMQALQAPITFGGQGVNVEIKR 112

RESULT 5

ID KV2A\_HUMAN STANDARD; PRT; 115 AA.

AC P01614;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region Cum.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=68242259; PubMed=5586923;

RA Hilschmann N.;

RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";

RL Hope-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).

RN [2]

RP REVISIONS TO 50; 52; 96 AND 97.

RX MEDLINE=70063440; PubMed=4188189;

RA Hilschmann N.;

RT "Molecular basis of antibody formation.";

RL Naturwissenschaften 56:195-205(1969).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01885; K2HUCM.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DISULFID 24 95

FT NON\_TER 115 115

FT SEQUENCE 115 AA; 12676 MW; 59E9F90A379569EC CRC64;

Query Match 40.8%; Score 467.5; DB 1; Length 115;

Best Local Similarity 79.8%; Pred. No. 3.2e-33;

Matches 91; Conservative 14; Mismatches 8; Indels 1; Gaps 1;

QY 1 EIVLTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLOKPGSQPOLLIYSGSRA 59

Db 2 DIVMTQSPSLPVTPGEPASISCRSSQSLHSGNYTLDWYLOKPGSQPOLLIYLSYR 61

QY 60 ASGVPRFSGSGVSGDTFLIRSRVEADVGVYCMQGLQSPFTFGPGTKVDIKR 113

Db 62 ASGVPRFSGSGSGDTFLTKISRVQAEADVGVYCMQALQAPITFGQGRLEIKR 115

RESULT 6

ID KV2B\_HUMAN STANDARD; PRT; 113 AA.

AC P01615;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-II region Cum.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE.

RX MEDLINE=68242259; PubMed=5586923;

RA Hilschmann N.;

RT "The complete amino acid sequence of Bence Jones protein Cum (kappa-type).";

RL Hope-Seyler's Z. Physiol. Chem. 348:1718-1722(1967).

RN [2]

RP REVISIONS TO 50; 52; 96 AND 97.

RX MEDLINE=70063440; PubMed=4188189;

RA Hilschmann N.;

RT "Molecular basis of antibody formation.";

RL Naturwissenschaften 56:195-205(1969).

CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.

CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.

DR PIR; A01885; K2HUCM.

DR InterPro; IPR003006; Ig\_MHC.

DR InterPro; IPR003596; Ig\_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

KW Immunoglobulin V region; Bence-Jones protein.

FT DISULFID 23 92

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DE DE Ig kappa chain V-II region FR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76253627; PubMed=821524;
RZ Riesen W.F., Jaton J.-C.;
RA "Variable region sequence of the light chain from a Waldenstroms IgM
RT with specificity for phosphorylcholine.";
RL Biochemistry 15:3829-3833(1976).
CC CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
CC CC MACROGLOBULIN THAT BINDS PHOSPHORYLCHOLINE.
CC CC PIR; A01886; K2HUFR.
DR DR InterPro; IPR003006; Ig_MHC.
DR DR InterPro; IPR003596; Ig_V.
DR DR Pfam; PF00047; Ig; 1.
DR DR SMART; SM00406; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 123 93
FT NON_TER 113
FT SEQUENCE 113 AA; 12660 MW; 0C0DA39E46DB96BE CRC64;

Query Match 39.7%; Score 455; DB 1; Length 113;
Best Local Similarity 74.3%; Pred. No. 3.7e-32;
Matches 84; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EIVVTQSLPLSVTPGEPASISCRSSOLSHSGNYIYLDWYLOKPGSQPOLLIYSGSHRA 60
Db 1 DVMVTQSLPLSVTPGEPASISCRSSQSLVRYLWYLOKPGSQPELLIYLSYRD 60
Qy 61 SGVPDRSGSGVGTDFLTRISRVAEADGVYVCMQGLQSPFTFGPTKVDIKR 113
Db 61 SGVPDRSGSGVGTDFLTRIRVQAEADGVYVCMQATZSPYTFGQGTKLZIKR 113

RESULT 7
KV2F_HUMAN STANDARD; PRT; 133 AA.
AC P06310;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE DE Ig kappa chain V-II region RPMI 6410 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Weindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and
RT III.";
RL Nucleic Acids Res. 13:6499-6513(1985).
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CC CC EMBL; 20020; CAA77315.1; -.

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|                                                               |                                                                       |
|---------------------------------------------------------------|-----------------------------------------------------------------------|
| CC                                                            | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.    |
| OX                                                            | NCBI_TaxID=10090;                                                     |
| RN                                                            | [1]                                                                   |
| RP                                                            | SEQUENCE                                                              |
| RX                                                            | MEDLINE=83256427; PubMed=6409088;                                     |
| RA                                                            | Chang J.-Y., Herbst H., Abersold R., Braun D.G.;                      |
| RT                                                            | "A new isotype sequence (V kappa 27) of the variable region of kappa- |
| RT                                                            | light chains from a mouse hybridoma-derived anti-(streptococcal group |
| RT                                                            | A polysaccharide) antibody containing an additional cysteine residue. |
| RT                                                            | Application of the dimethylaminoazobenzene isothiocyanate technique   |
| RT                                                            | for the isolation of peptides.";                                      |
| RL                                                            | Biochem. J. 211:173-180(1983).                                        |
| CC                                                            | -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL  |
| CC                                                            | ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.            |
| CC                                                            | PIR: A01913; KVM57S.                                                  |
| DR                                                            | InterPro: IPR003006; Ig_MHC.                                          |
| DR                                                            | InterPro: IPR003596; Ig_v.                                            |
| DR                                                            | Pfam: PF00047; Ig; 1.                                                 |
| DR                                                            | SMART: SM00406; IGV; 1.                                               |
| KW                                                            | Immunoglobulin V region; Monoclonal antibody; Hybridoma.              |
| FT                                                            | DOMAIN 1 23                                                           |
| FT                                                            | DOMAIN 24 39                                                          |
| FT                                                            | DOMAIN 40 54                                                          |
| FT                                                            | DOMAIN 55 61                                                          |
| FT                                                            | DOMAIN 62 93                                                          |
| FT                                                            | DOMAIN 94 102                                                         |
| FT                                                            | DOMAIN 103 112                                                        |
| FT                                                            | DISULFID 23 93                                                        |
| FT                                                            | NON_TER 113 113                                                       |
| SEQ                                                           | SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;                    |
| Query Match 36.9%; Score 423; DB 1; Length 113;               |                                                                       |
| Best Local Similarity 74.3%; Pred. No. 1.9e-29;               |                                                                       |
| Matches 84; Conservative 11; Mismatches 18; Indels 0; Gaps 0; |                                                                       |
| Qy                                                            | 1 EIVLTQSPLSLPVTGPEPASISCRSSQSLHNSGYTYLDWTYLPQPGSPOLLTYSGSHRA 60      |
| Db                                                            | 1 DIVMTQTAPSAVLTVPGESVTSICRSKSLHNSGNTLYWFLQRPQGPOLLTYRMSNLA 60        |
| Qy                                                            | 61 SGVPRFRFSVSGTDFTLIRISKVAEDGVVYCMQGLSQSPETFGTGTVDIKR 113            |
| Db                                                            | 61 SGVPRFRFSGSGSGTAFTLIRISKVAEDGVVYCMQQRPEYTFGGGTKLEIKR 113           |
| RESULT 11                                                     |                                                                       |
| KV2D_MOUSE                                                    |                                                                       |
| ID                                                            | KV2D_MOUSE STANDARD; PRT; 112 AA.                                     |
| AC                                                            | P01629;                                                               |
| DC                                                            | 21-JUL-1986 (Rel. 01, Created)                                        |
| DT                                                            | 21-JUL-1986 (Rel. 01, Last sequence update)                           |
| DT                                                            | 15-JUL-1999 (Rel. 38, Last annotation update)                         |
| DE                                                            | Ig kappa chain V-II region 251.3.                                     |
| OS                                                            | Mus musculus (Mouse).                                                 |
| OC                                                            | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |
| OC                                                            | Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.    |
| NCBI_TaxID=10090;                                             |                                                                       |
| RN                                                            | [1]                                                                   |
| RP                                                            | SEQUENCE                                                              |
| RX                                                            | MEDLINE=83055101; PubMed=7141411;                                     |
| RA                                                            | Herbst H., Chang J.Y., Abersold R., Braun D.G.;                       |
| RT                                                            | "Murine VK25 isotype sequence: monoclonal antibody 2s1.3 specific for |
| RT                                                            | the group A streptococcal polysaccharide.";                           |
| RT                                                            | Hoppe-Seyler's Z. Physiol. Chem. 363:1069-1076(1982).                 |
| CC                                                            | -!- MISCELLANEOUS: THIS CHAIN IS FROM A HYBRIDOMA-DERIVED MONOCLONAL  |
| CC                                                            | ANTIBODY AGAINST THE STREPTOCOCCAL GROUP A POLYSACCHARIDE.            |
| CC                                                            | PIR: A01911; KVM51.                                                   |
| DR                                                            | InterPro: IPR003006; Ig_MHC.                                          |
| DR                                                            | InterPro: IPR003596; Ig_v.                                            |
| DR                                                            | Pfam: PF00047; Ig; 1.                                                 |
| DR                                                            | SMART: SM00406; IGV; 1.                                               |
| KW                                                            | Immunoglobulin V region; Monoclonal antibody.                         |
| FT                                                            | DOMAIN 1 23                                                           |
| FT                                                            | DOMAIN 24 39                                                          |
| FT                                                            | DOMAIN 40 54                                                          |
| FT                                                            | DOMAIN 55 61                                                          |
| FT                                                            | DOMAIN 62 93                                                          |
| FT                                                            | DOMAIN 94 102                                                         |
| FT                                                            | DOMAIN 103 112                                                        |
| FT                                                            | DISULFID 23 93                                                        |
| FT                                                            | NON_TER 113 113                                                       |
| SEQ                                                           | SEQUENCE 113 AA; 12496 MW; 42C019D10ADA3C91 CRC64;                    |





CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT  
CC BINDS PHOSPHORYLCHOLINE. THE SEQUENCE OF THE V REGION OF THE HEAVY  
CC CHAIN HAS ALSO BEEN DETERMINED.

DR PIR; A01908; KVM516.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region.  
FT DOMAIN 1 23  
FT DOMAIN 24 39  
FT DOMAIN 40 54  
FT DOMAIN 55 61  
FT DOMAIN 62 93  
FT DOMAIN 94 102  
FT DOMAIN 103 112  
FT DISULFID 23 93  
FT NON\_TER 112 112  
SQ SEQUENCE 112 AA; 12349 MW; A58EDFD6404B9726 CRC64;

Query Match 33.8%; Score 387; DB 1; Length 112;  
Best Local Similarity 68.8%; Pred. No. 2.2e-26;  
Matches 77; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

Qy 1 EIVLTQSPPLSLPVTGPEPASISCRSSQSLHNSGYTYLDWYKQPGSPQLLIYSGSHRA 60  
Db 1 DIVITQDELSNPVTSGESVSISCRSSKSLLYKDGKTYLNNFLQRPQSGPQLLIYSLMSTRA 60  
Qy 61 SGVPDRFSGSGSGTDFTLTISRVEAEDVGVYVCMQGLQSPFTFGPGTKVDIKR 112  
Db 61 SGVSDRFSGSGSGRTDFTLTISRVAEDVGVYVCOQLVEYPLTFGAGTKLEIKR 112

RESULT 15  
KV3L\_HUMAN  
ID KV3L\_HUMAN STANDARD; PRT; 129 AA.  
AC P18135;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Ig kappa chain V-III region HAH precursor.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=88171307; PubMed=3127527;  
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;  
RT "Autoantibody-associated kappa light chain variable region gene  
RT expressed in chronic lymphocytic leukemia with little or no somatic  
RT mutation. Implications for etiology and immunotherapy.";  
RL J. Exp. Med. 167:840-852(1988).  
CC -!- DISEASE: THE PROTEIN IS ONE OF THE SURFACE IMMUNOGLOBULIN M  
CC AUTOANTIBODIES EXPRESSED IN PATIENTS WITH CHRONIC LYMPHOCYTIC  
CC LEUKEMIA.  
DR PIR; PL0022; K3HUHA.  
DR HSSP; P01789; IMCP.  
DR InterPro; IPR003006; Ig\_MHC.  
DR InterPro; IPR003596; Ig\_v.  
DR Pfam; PF00047; Ig; 1.  
DR SMART; SM00406; IGV; 1.  
KW Immunoglobulin V region; Signal.  
FT SIGNAL 1 20  
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.  
FT DOMAIN 21 43  
FT DOMAIN 44 55  
FT DOMAIN 56 70  
FT DOMAIN 71 77  
FT DOMAIN 78 109  
FT DOMAIN 110 118  
FT DOMAIN 119 129  
FT DISULFID 43 109

FT NON\_TER 129 129  
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 32.3%; Score 370; DB 1; Length 129;  
Best Local Similarity 66.4%; Pred. No. 7.3e-25;  
Matches 75; Conservative 13; Mismatches 21; Indels 4; Gaps 1;

Qy 1 EIVLTQSPPLSLPVTGPEPASISCRSSQSLHNSGYTYLDWYKQPGSPQLLIYSGSHRA 60  
Db 21 EIVLTQSPGTLSLSPGERATLSCRASQSVSSS-----YLAWYQQKPGQAPRLIIYGASSRA 76  
Qy 61 SGVPDRFSGSVSGTDFTLRISRVEAEDVGVYVCMQGLQSPFTFGPGTKVDIKR 113  
Db 77 TGIPDRFSGSGSGTDFTLTISRLEPEDFAVYVCCQYGTSPRTFGQGTKEIKR 129

Search completed: October 9, 2002, 19:11:04  
Job time : 6.73469 secs

